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OM nucleic - nucleic search, using sw model

Run on: December 14, 2005, 02:17:22 ; Search time 934 Seconds
(without alignments)

1440.553 Million cell updates/sec

Title: US-10-647-956A-5

Perfect score: 2745

Sequence: 1 atgagcagttacaattctgc.....taggaatcgaggaaacttca 2745

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4161359 seqs, 245077644 residues

Total number of hits satisfying chosen parameters: 8322718

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA_New.*

1: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
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6: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2.*
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3.*
10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2745	100.0	2745	6	US-10-647-956A-5
C 2	44.6	1.6	3352	6	US-10-750-185-46142
3	42.4	1.5	2025	6	US-10-750-185-36257
4	41	1.5	152335	7	US-11-121-086-73
C 5	40	1.5	199321	7	US-11-121-086-10
6	39.8	1.4	40000	6	US-10-995-561-13509
7	39.4	1.4	1423	6	US-10-750-185-59139
C 8	39	1.4	151828	7	US-11-117-187-197
9	38.2	1.4	1306	6	US-10-750-185-25909
C 10	38	1.4	82596	7	US-11-117-187-207
11	38	1.4	1082144	7	US-11-117-187-211
C 12	37.8	1.4	1624	6	US-10-750-185-29572
13	37.6	1.4	1908	6	US-10-750-185-59139
C 14	37.6	1.4	50959	7	US-11-117-187-210
15	37.6	1.4	72600	7	US-11-117-187-206
C 16	37.4	1.4	4417	6	US-10-821-234-350
17	37.2	1.4	53323	6	US-10-995-561-13345
C 18	37.2	1.4	398287	6	US-10-995-561-13396
19	36.6	1.3	1513	6	US-10-750-185-26295
C 20	36.4	1.3	1720	6	US-10-750-185-25513
21	36.4	1.3	193084	7	US-11-121-086-82
C 22	36.4	1.3	207908	7	US-11-112-908-21
23	36.2	1.3	146656	7	US-11-121-086-68

24	36.2	1.3	150437	7	US-11-112-908-44	Sequence 44, Appl
25	36.2	1.3	150491	7	US-11-112-908-46	Sequence 46, Appl
C 26	36	1.3	600	6	US-10-750-185-363	Sequence 363, App
27	35.8	1.3	633	6	US-10-793-626-2863	Sequence 2863, App
28	35.8	1.3	633	6	US-10-793-626-3319	Sequence 3319, App
29	35.8	1.3	3030	6	US-10-793-626-4246	Sequence 4246, App
30	35.8	1.3	3734	6	US-10-793-626-4103	Sequence 4103, App
C 31	35.6	1.3	3032	7	US-11-000-463-659	Sequence 659, App
C 32	35.6	1.3	3405	7	US-11-000-463-187	Sequence 187, App
33	35.6	1.3	3535	6	US-10-750-185-48788	Sequence 48788, A
34	35.4	1.3	600	6	US-10-750-185-368	Sequence 368, App
C 35	35.4	1.3	600	6	US-10-750-185-3634	Sequence 3634, App
C 36	35.2	1.3	482	7	US-11-123-896-301	Sequence 301, App
37	35.2	1.3	1523	6	US-10-750-185-36494	Sequence 36494, A
C 38	35.2	1.3	1540	6	US-10-485-517-39	Sequence 39, Appl
C 39	35.2	1.3	1565	6	US-10-750-185-46922	Sequence 46922, A
40	35	1.3	399	6	US-10-467-657-8213	Sequence 8213, App
41	35	1.3	1659	6	US-10-750-185-53431	Sequence 53431, A
C 42	35	1.3	4399	6	US-10-750-185-44371	Sequence 44371, A
C 43	35	1.3	170837	7	US-11-121-086-97	Sequence 97, Appl
C 44	35	1.3	199130	6	US-10-995-561-13233	Sequence 13233, A
C 45	35	1.3	241805	6	US-10-995-561-13215	Sequence 13215, A

ALIGNMENTS

RESULT 1

US-10-647-956A-5

; Sequence 5, Application US/10647956A

; Publication No. US20050251878A1

; GENERAL INFORMATION:

; APPLICANT: firench-Constant, Richard

; APPLICANT: Bowen, David

; APPLICANT: Rocheleau, Thomas

; APPLICANT: Waterfield, Nicholas

; TITLE OF INVENTION: DNA SEQUENCES FROM PHOTORHABDUS LUMINESCENS

; FILE REFERENCE: 61645

; CURRENT APPLICATION NUMBER: US/10/647,956A

; CURRENT FILING DATE: 2003-08-26

; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/817,514

; PRIOR FILING DATE: CURRENT FILING DATE: 2000-03-26

; PRIOR APPLICATION NUMBER: US 60/191806

; PRIOR FILING DATE: 2000-03-24

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 5

; LENGTH: 2745

; TYPE: DNA

; ORGANISM: Photorhabdus luminescens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(2745)

US-10-647-956A-5

Query Match 100.0%; Score 2745; DB 6; Length 2745;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2745; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGAGCAGTTACAAATTCGCAATTTGACCAAAAGACCCCTCGATTAAAGTTAGATTAAC	60
Db	1	ATGAGCAGTTACAAATTCGCAATTTGACCAAAAGACCCCTCGATTAAAGTTAGATTAAC	60
Qy	61	AGGAATTAATTAATCTAGCTACTTTAGAAATATCTACGCACTCAAGCTGACGAAACAGTGAT	120
Db	61	AGGAATTAATTAATCTAGCTACTTTAGAAATATCTACGCACTCAAGCTGACGAAACAGTGAT	120
Qy	121	GAATTAATTAATCTAGCTACTTTAGAAATATCTACGCACTCAAGCTGACGAAACAGTGAT	180
Db	121	GAATTAATTAATCTAGCTACTTTAGAAATATCTACGCACTCAAGCTGACGAAACAGTGAT	180
Qy	181	CGTAAATTAATTAATCTAGCTACTTTAGAAATATCTACGCACTCAAGCTGACGAAACAGTGAT	240

Db 181 CGTAAAAATAAAACCAGAGCGGCCCAAATTTTCATTCGTGCTTTTAATCTTGC CGGTCAA 240
Qy 241 GTTTTACGTGAGAAAGTGTGATGCGCGTCGGACTATTACCCCTCAATGATATTGAAGT 300
Db 241 GTTTTACGTGAGAAAGTGTGATGCGCGTCGGACTATTACCCCTCAATGATATTGAAGT 300
Qy 301 CGCCCGGTGTGTGATCATCAATGCAACCGGTGTCCGCCAAAACCACTCGTTATGAAGATAAC 360
Db 301 CGCCCGGTGTGTGATCATCAATGCAACCGGTGTCCGCCAAAACCACTCGTTATGAAGATAAC 360
Qy 361 ACCCTTCCCGTCTGCTGCTGCTATCACCGAAACAAGTACAGGAGAGAGAAACGACC 420
Db 361 ACCCTTCCCGTCTGCTGCTGCTATCACCGAAACAAGTACAGGAGAGAGAAACGACC 420
Qy 421 GAACGTCTTATCTGGGCGGCAATACGCGCGCAAGAAAAGATTACAACCTCGCCGCTCAG 480
Db 421 GAACGTCTTATCTGGGCGGCAATACGCGCGCAAGAAAAGATTACAACCTCGCCGCTCAG 480
Qy 481 TGTGTCCGCCATTACGATACCGCGGACTTACTCAACTCAATAGCCTTTCTCTGGCTGGC 540
Db 481 TGTGTCCGCCATTACGATACCGCGGACTTACTCAACTCAATAGCCTTTCTCTGGCTGGC 540
Qy 541 GTGTGTCTATCACAACTCTCAAACTGCTTACCGATAACCAAGGATGCCGACTGGACAGGT 600
Db 541 GTGTGTCTATCACAACTCTCAAACTGCTTACCGATAACCAAGGATGCCGACTGGACAGGT 600
Qy 601 GAAGACCAGAGCCTCTGGCAACAAAACCTGAGTAGTAGTCTATATACCCAAAGTAAC 660
Db 601 GAAGACCAGAGCCTCTGGCAACAAAACCTGAGTAGTAGTCTATATACCCAAAGTAAC 660
Qy 661 ACTGATGCCACCGGGCTTTACTGACCCAGACCGATGCAAGGCAACATTCAGCGGCTG 720
Db 661 ACTGATGCCACCGGGCTTTACTGACCCAGACCGATGCAAGGCAACATTCAGCGGCTG 720
Qy 721 GCCTATGATGTGGCGGCGAGCTAAAAGGGAGTTGGTTAAACACTCAAAGGTTCAGCGGAA 780
Db 721 GCCTATGATGTGGCGGCGAGCTAAAAGGGAGTTGGTTAAACACTCAAAGGTTCAGCGGAA 780
Qy 781 CAGGTGATTATCAAACTCGCTAACCTACTCCGCGCGCGGGGCAAAAATTCGTGAAGAGCAC 840
Db 781 CAGGTGATTATCAAACTCGCTAACCTACTCCGCGCGCGGGGCAAAAATTCGTGAAGAGCAC 840
Qy 841 GGTAAACGGGATTGTCACTGAATACAGCTACGAAACCGGAAACCCAAACCGCTTATCGGCATT 900
Db 841 GGTAAACGGGATTGTCACTGAATACAGCTACGAAACCGGAAACCCAAACCGCTTATCGGCATT 900
Qy 901 ACCACTCGCGTCCATCAGACGCGCAAGGTGTGCAAGACCTACGCTATCAATATGACCCA 960
Db 901 ACCACTCGCGTCCATCAGACGCGCAAGGTGTGCAAGACCTACGCTATCAATATGACCCA 960
Qy 961 GTAGGCAATGTCAATTAATCCGTAATGATGCGGAAGCCACTCGCTTTTGGCGCAATCAG 1020
Db 961 GTAGGCAATGTCAATTAATCCGTAATGATGCGGAAGCCACTCGCTTTTGGCGCAATCAG 1020
Qy 1021 AAAGTAGCCCGGAGAAATAGCTATACCTACGATTCCTGTATCAGCTTATCAGCGCCACC 1080
Db 1021 AAAGTAGCCCGGAGAAATAGCTATACCTACGATTCCTGTATCAGCTTATCAGCGCCACC 1080
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Db 1081 GGGCGGAAATGGGCAATATCGGTGAGCAAAACCAACCTTCCTCCCTGCGCTACCT 1140
Qy 1141 TCTGACAAACAATACCTACACTAATCTACTCGAGCTTACAGCTATGATCAAGTGGTAAT 1200
Db 1141 TCTGACAAACAATACCTACACTAATCTACTCGAGCTTACAGCTATGATCAAGTGGTAAT 1200
Qy 1201 CTGACGAAATTCGSCACAGCTCGCAGTACCAGAACCACTACCGTGGCTATCAC 1260
Db 1201 CTGACGAAATTCGSCACAGCTCGCAGTACCAGAACCACTACCGTGGCTATCAC 1260
Qy 1261 CTCTCAAAACCGCAGCAATTCGGGGTGTCTCAGTAGCTTAACCCGATCCAAATCAAGTG 1320
Db 1261 CTCTCAAAACCGCAGCAATTCGGGGTGTCTCAGTAGCTTAACCCGATCCAAATCAAGTG 1320

Qy 1321 GATACGTTGTTTCATGTCGCGTGTACCAAAACCAAGTTTATTATCCCGGACAGACTTATC 1380
Db 1321 GATACGTTGTTTCATGTCGCGTGTACCAAAACCAAGTTTATTATCCCGGACAGACTTATC 1380
Qy 1381 TGGACACCAAGAGAGTAAAGCAGGTAAATAATGGCCCGGAAATAGTGGTACCGC 1440
Db 1381 TGGACACCAAGAGAGTAAAGCAGGTAAATAATGGCCCGGAAATAGTGGTACCGC 1440
Qy 1441 TAGCAGACCAACCGCATGAGACAACTGAAAAGTGAAGTGAACAGCAACCCAGAAATACACG 1500
Db 1441 TAGCAGACCAACCGCATGAGACAACTGAAAAGTGAAGTGAACAGCAACCCAGAAATACACG 1500
Qy 1501 CAGCAACACCGGTAAATCTATTTGCGGACTCGAGCTACGCAACCCAGAGCAACGCC 1560
Db 1501 CAGCAACACCGGTAAATCTATTTGCGGACTCGAGCTACGCAACCCAGAGCAACGCC 1560
Qy 1561 ACAACACGGAAGATTACACGTTATCACCTCGGTGAAGCCGCTCGCGCACAGGTACGG 1620
Db 1561 ACAACACGGAAGATTACACGTTATCACCTCGGTGAAGCCGCTCGCGCACAGGTACGG 1620
Qy 1621 GTGTTGCACTGGAGAGCGGTAAAGCCAGAAAGATGTCAAATAATCAACTACGTACAGC 1680
Db 1621 GTGTTGCACTGGAGAGCGGTAAAGCCAGAAAGATGTCAAATAATCAACTACGTACAGC 1680
Qy 1681 TAGCATTAATCTGATCGGCTCCAGCCAGCTTGAACCTGACAAACCAAGGACAAATATCAGC 1740
Db 1681 TAGCATTAATCTGATCGGCTCCAGCCAGCTTGAACCTGACAAACCAAGGACAAATATCAGC 1740
Qy 1741 GAGGAGAGATTATTCATTTGCGGGGACAGCGCTGTGGGCGAGCAACACAGCCAAACAGAA 1800
Db 1741 GAGGAGAGATTATTCATTTGCGGGGACAGCGCTGTGGGCGAGCAACACAGCCAAACAGAA 1800
Qy 1801 GCCAGCTATAAAACGATTCGCTATTCCGCAAAAGACAGAGATGCCACCGGCTGTATTAT 1860
Db 1801 GCCAGCTATAAAACGATTCGCTATTCCGCAAAAGACAGAGATGCCACCGGCTGTATTAT 1860
Qy 1861 TAGGTTATCGTTATTACCAACCGTGGCGGCGAGATGGTTAAGCGGAGCCCGGCGAGGA 1920
Db 1861 TAGGTTATCGTTATTACCAACCGTGGCGGCGAGATGGTTAAGCGGAGCCCGGCGAGGA 1920
Qy 1921 ACCATTGATGGGTGAATCTATACCGAAATGGTAAGAAATAATCTCTGTAGTTTACAAGAT 1980
Db 1921 ACCATTGATGGGTGAATCTATACCGAAATGGTAAGAAATAATCTCTGTAGTTTACAAGAT 1980
Qy 1981 GAAAAATGGATTAGCGCCAGAAAAAGGAAATATACCAAGAGGTAAATTTCTTTGATGAA 2040
Db 1981 GAAAAATGGATTAGCGCCAGAAAAAGGAAATATACCAAGAGGTAAATTTCTTTGATGAA 2040
Qy 2041 TTAATAATTCAAATTTGGCAGCCAAAGTTTCAATGTTGTCAATGGAACAGAAAGAGAGC 2100
Db 2041 TTAATAATTCAAATTTGGCAGCCAAAGTTTCAATGTTGTCAATGGAACAGAAAGAGAGC 2100
Qy 2101 AGTTATACAAAAATAATCAATTTGAAAGTGGTTCGTCGCTGATTCGGATCCGTCGGGT 2160
Db 2101 AGTTATACAAAAATAATCAATTTGAAAGTGGTTCGTCGCTGATTCGGATCCGTCGGGT 2160
Qy 2161 TATTTGCTAAGCCAGAGAGTTACTAAAGAGGTATAGAAAAAGTCAAATCATATATAGC 2220
Db 2161 TATTTGCTAAGCCAGAGAGTTACTAAAGAGGTATAGAAAAAGTCAAATCATATATAGC 2220
Qy 2221 CGACTTGAAGAAACAGCTCCCTTTTCAGAAAAATCAAAAACGAATCTTTCTTTAGGATCT 2280
Db 2221 CGACTTGAAGAAACAGCTCCCTTTTCAGAAAAATCAAAAACGAATCTTTCTTTAGGATCT 2280
Qy 2281 GAAATATCCGGTTATATGGCAAGAACCATACAGATACGATATCAGAAATATGCCGAAGAG 2340
Db 2281 GAAATATCCGGTTATATGGCAAGAACCATACAGATACGATATCAGAAATATGCCGAAGAG 2340
Qy 2341 CATAAATATAGAGTAATCACCTGATTTTTTATTCAGAAACCGATTTCTTTGGGTTAATG 2400
Db 2341 CATAAATATAGAGTAATCACCTGATTTTTTATTCAGAAACCGATTTCTTTGGGTTAATG 2400

QY 2401 GATAAAGTGAAAAAATGATTATCCGGTGAAGAAAAATTTATCGCGCAATGGAGTT 2460
Db 2401 GATAAAGTGAAAAAATGATTATCCGGTGAAGAAAAATTTATCGCGCAATGGAGTT 2460
QY 2461 AAGGTTTATCATGATTAAATAAATAAACAATCAGATTACATGTCACATTCATTCGCGC 2520
Db 2461 AAGGTTTATCATGATTAAATAAATAAACAATCAGATTACATGTCACATTCATTCGCGC 2520
QY 2521 CATCCCTATACGCAATTTAGTAATGAAGAAAGAGCGCTGTTCAGAAAAACAGAACCCGCT 2580
Db 2521 CATCCCTATACGCAATTTAGTAATGAAGAAAGAGCGCTGTTCAGAAAAACAGAACCCGCT 2580
QY 2581 ATTGCAATAGATAGAAATATAATTTCAAAAGGTTGGCAAAATTCCTGCAATGAAGA 2640
Db 2581 ATTGCAATAGATAGAAATATAATTTCAAAAGGTTGGCAAAATTCCTGCAATGAAGA 2640
QY 2641 ATTAAAAATCATTTGAAGGACATAAATTTATAGGATATCAACAGAGCTATTATATT 2700
Db 2641 ATTAAAAATCATTTGAAGGACATAAATTTATAGGATATCAACAGAGCTATTATATT 2700
QY 2701 CGCTCTCGCGCTATCGCTGAGAAATTTAGGAATCGGAGAACTTCA 2745
Db 2701 CGCTCTCGCGCTATCGCTGAGAAATTTAGGAATCGGAGAACTTCA 2745

RESULT 2
US-10-750-185-46142/c
; Sequence 46142, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46142
; LENGTH: 3352
; TYPE: DNA
; ORGANISM: Bovine 19866881360268
US-10-750-185-46142

Query Match 1.6%; Score 44.6; DB 6; Length 3352;
Best Local Similarity 49.2%; Pred. No. 0.12;
Matches 146; Conservative 0; Mismatches 149; Indels 2; Gaps 1;
QY 2201 AAAGTCAATCATATATAGCCGACTTGAAGAAAAACAGCTCCCTTTTCAGAAAAATCAAAA 2260
Db 3323 AATGTCATATATACAAATAAACTGGAGGAAAAACGTCATAAATAAATTTCTAAAA 3264
QY 2261 CGAATCTTTTATGATCTGAATATCCGGTTTATATGGCAAGAACCATCAAGATACGA 2320
Db 3263 TAAATCCAAAGAACGACATGATGAACCAACAAAGCAAGAAATTCATAATATGAAAA 3204
QY 2321 TATCAGATATGCGAAGACATAAATATAGATGATACCCCTGATTTTATTCAGAA 2380
Db 3203 AAAAATCTATAAAGATAAGTAAAAAATCATTTTATTTAAAGACTTATATTTGCAAA 3144
QY 2381 CCATTTCTTTGCTTAATGATAAAGTCAAAAAATGATTATTCGGTGAAGAAAAA 2440
Db 3143 CCCTCACA--GGATTATTAAGACAAAGAGACATGAATAAAGAGATGTTATCATTA 3086
QY 2441 TTTATCGCGCAATGGAGTTTAAAGTTTATCATGATTTTAAAAATAAACAATCAGAA 2497

Db 3085 CAGATGAGGTATAGTATATTAAAGATACTTCATGTTAATAATAGAGAAAAACCAGAT 3029
RESULT 3
US-10-750-185-36257
; Sequence 36257, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36257
; LENGTH: 2025
; TYPE: DNA
; ORGANISM: Bovine 19866881087862
US-10-750-185-36257

Query Match 1.5%; Score 42.4; DB 6; Length 2025;
Best Local Similarity 57.6%; Pred. No. 0.34;
Matches 76; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
QY 2506 AACTATGCAATGGCCCATCCCTATACGCAATTTGAGTAATGAAGAAAAAGAGCGCTTTGCAA 2565
Db 45 AATAATCCATTTGTCAAAACCTTTGTACACACCCCAATGAAGAAAAAGAACTATTTAAGA 104
QY 2566 GAAACAGAACCGCTATTGCAATAGATAGAGAAATATAATTTCAAAGTGTGGCAAATTC 2625
Db 105 GCAACTGNAATCAAAATTTACAAATTAAGAGAGATCACAATTTCAAGGCTTTATACAGATTA 164
QY 2626 CTGACAAATGAAA 2637
Db 165 ATAAAAAACTAAA 176

RESULT 4
US-11-121-086-73
; Sequence 73, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR FILING DATE: 2005-05-04
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 73
; LENGTH: 152335
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-73

Query Match 1.5%; Score 41; DB 7; Length 152335;
Best Local Similarity 46.4%; Pred. No. 7.7;
Matches 134; Conservative 0; Mismatches 155; Indels 0; Gaps 0;
QY 2194 ATAGAAAAAAGTCAATCATATATATATACCGCACTTGAAGAAAAACAGTCCCTTTTCAGAAAAA 2253

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Db 58783 ATACATATACATCTATATGTATATAGATATATAGATATATAGATATATAGATATATAGAT 58842
Qy 2254 TCAAAAACGAATCTTTCTTTAGGATCTGAATATATCCGGTTATATGCGCAACATACAA 2313
Db 58843 ATATATCCATATATTTATATAGATATATACATATGTATATAGATATATTTATATATGTAT 58902
Qy 2314 GATACGATATCAGAAATATCGGAAGACATATAATATAGAAAGTATACCCCTGATTTTAT 2373
Db 58903 ATACCTATATACGTATATAGATATATACATATATACATATATGTATATATAGATATATAT 58962
Qy 2374 TCAGAAACCGATTTCTTTTGGTTTAATGATATAAAGTGAAAAAATGATTATTCGGTGAA 2433
Db 58963 ACATATATACATATGTATACATAGATGTATACATATGTATATATGTATATATCTATGTAT 59022
Qy 2434 AGAAAAATTTATGCGGCAATGGAGTTAAGGTTTATCATGATTTAAAAA 2482
Db 59023 ACATAGATGTATACATCTATGTATACATAGATGTATACATAGATATATA 59071

RESULT 5
US-11-121-086-10/c
; Sequence 10, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121.086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 10
; LENGTH: 199321
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-10

Query Match 1.5%; Score 40; DB 7; Length 199321;
Best Local Similarity 50.5%; Pred. No. 16;
Matches 97; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

Qy 2481 AAATAACAATCAGAAATACATGTCACTATGTCAATGGCCCATCCCTATACGCAATTTGAG 2540
Db 51397 AAAAAAACCTGGAGATATAGGTTTCTGTCTGCTTTGCCACTAATTTATGTGACCTTGA 51338
Qy 2541 TAATGAAGAAGAGCGCTTTGCAAGAAACAGAACCCGCTATTGCAATAGATAGAGAATA 2600
Db 51337 TAAGTCACTTAATGATTATTAAGTATCCCTAACATAGAGGTTAGTTTACATGAATC 51278
Qy 2601 TAATTTCAAAGGTTTGGCAAAATTCCTGACAAATGAAAGCAATTAATAAATCATTTGAAAGG 2660
Db 51277 CAAGTGTCTGTGCTTTAAAGTCTGTAAGTCTAGCACTTGAAGCACTTGAAGCACTACAG 51218
Qy 2661 ACATAAAATTA 2672
Db 51217 AAAAAAAAAAAAA 51206

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RESULT 6
US-10-995-561-13509
; Sequence 13509, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24

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; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13509
; LENGTH: 40000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(40000)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-);
US-10-995-561-13509

Query Match 1.4%; Score 39.8; DB 6; Length 40000;
Best Local Similarity 48.2%; Pred. No. 7.9;
Matches 144; Conservative 0; Mismatches 152; Indels 3; Gaps 1;

Qy 2144 ATTCCGATCCGTCGGGTTATTTGCTTAAGCCACGAGGTTACTAAAGGTTATGAAAAA 2203
Db 14127 ATTTAAATACTTCTGTCNAATTAGGACAGTTTGAGAAAAAGAGATAACAAAAATCAAAAGCAA 14186
Qy 2204 GTCAATCATATATAGCCGACTTGAAGAAAAACAGTCCCTTTTCAGAAAAATCAAAACGA 2263
Db 14187 AACTCAAACTTTGTACTGAAAAATCTAATAAACTGACTAAATTTATAGAAAAACCTAAGA 14246
Qy 2264 ATCTTTCTTTAGGATCTGAAATATCCGTTTATATGCAAGAACCATACAGATACCGATAT 2323
Db 14247 AACTCATATCAATAAAAAATTT---TAATATGAGAGAACCATATATGACACCTTTCT 14303
Qy 2324 CAGATATATGCCGAAGAGCATATAATAGAAAGTAAATCACCCCTGATTTTATTCAGAAACCG 2383
Db 14304 GCCAATATATTTGAAAAACAGATAAATAGGATTTTATTGTTAGAAATTTGGTCAAGAAAGAAATG 14363
Qy 2384 ATTTCTTTGGTTAATGGATAAAGTGAAAAAATGATTTATTCGGTGAAAGAAAAATTT 2442
Db 14364 AAATACTTGGTTGATGAATAACAGTTTACAGAAATTCATTGCAATTTAAAAAATAAATTT 14422

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RESULT 7
US-10-750-185-56105
; Sequence 56105, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 56105
; LENGTH: 1423
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-56105

Query Match 1.4%; Score 39.4; DB 6; Length 1423;
Best Local Similarity 52.1%; Pred. No. 1.7;
Matches 88; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

Qy 2325 AGAATATGCCGAGAGCATATAATATAGAAAGTAAATCACCCTGATTTTATTCAGAAACCGA 2384
Db 1043 AAACTTTCCCTAGAGCCCTCCATATCACTGCCAACCTTGACTTTAGCTTACAGAGACCCA 1102
Qy 2385 TTTCTTTGCGTTAATGGATAAAGTGAATAAATGATTTATTCGGTGAAAGAAAAATTTA 2444

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Db 1103 TTTCAGACTTCTCATCTTTAGAACTGTAGAGAAATATAATTTGGTTCAAGTCAACACGTT 1162
 Qy 2445 TGCGCAATGGAGGTTAAAGTTTATCATGATTTTAAAAAATAAACAAATCA 2493
 Db 1163 TGTCGCAATTTGTACAGCAGCAATAGGGAACCTGATACATATGCACACA 1211

RESULT 8
 US-11-117-187-197/c
 ; Sequence 197, Application US/11117187
 ; Publication No. US20050266560A1
 ; GENERAL INFORMATION:
 ; APPLICANT: PREUSS, DAPHNE
 ; APPLICANT: COPENHAVER, GREGORY
 ; TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
 ; FILE REFERENCE: ARCD:309US
 ; CURRENT APPLICATION NUMBER: US/11/117,187
 ; CURRENT FILING DATE: 2005-04-28
 ; PRIOR APPLICATION NUMBER: US/09/531,120
 ; PRIOR FILING DATE: 2000-03-17
 ; PRIOR APPLICATION NUMBER: 60/125,219
 ; PRIOR FILING DATE: 1999-03-18
 ; NUMBER OF SEQ ID NOS: 212
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 197
 ; LENGTH: 151828
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-11-117-187-197

Query Match 1.4%; Score 39; DB 7; Length 151828;
 Best Local Similarity 44.1%; Pred. No. 26;
 Matches 162; Conservative 0; Mismatches 205; Indels 0; Gaps 0;
 Qy 2282 AATATCCGGTTATATGGCAAGAACCATACAGATACGATATCAGAAATATGCCGAGAGC 2341
 Db 49305 AAAATATAATAATAAGTTTGTGTCATATCATAAACCAATTTTAAATAATAGTATACCTAAT 49246
 Qy 2342 ATAAATATAGAACTATCAACCTGATTTTATTCAGAAACCGATTTCTTTGGCTTAATGG 2401
 Db 49245 TAAAAATTAAATAGTTTATCATGTTTAAACATAATAAAAAATATCATGTACATAT 49186
 Qy 2402 ATAAAGTGAAGAAATATATTCGGTGAAGAAATTTATGCGCAATGGAGGTTA 2461
 Db 49185 AAAAAAGACATTTATATATATGTCATCAAAAAAGATAGTTAAAAATAGAAAGATTTCT 49126
 Qy 2462 AGTTTATCATGATTTAAAAAATAAACATCAAGATTCATGTCACATATGCAATGGCCCC 2521
 Db 49125 TGCTACAAAAATTTACATATCTTATATTCACAAATCTTTTTTTTCTATATAAAGAT 49066
 Qy 2522 ATCCCTATACGCAATGAGTAATGAAGAAAGCGCTGTGCAAGAAACAGAACCCGCTA 2581
 Db 49065 AAATAAGTTGTCATATATTTTTCATCTATTTTTCACCATATAATAAATAATTT 49006
 Qy 2582 TTGCAATAGATAGAGATATAATTTCAAAGGTTTGGCAAAATTCCTGACAAATGAAAGCAA 2641
 Db 49005 TTGTTCAAAAATTTAAAAAATCTTTGTAACCAATCATCCAAAGAAAGGACATAGCGTCAT 48946
 Qy 2642 TTAAGAA 2648
 Db 48945 TTTAACA 48939

RESULT 9
 US-10-750-185-25909
 ; Sequence 25909, Application US/10750185
 ; Publication No. US20050260603A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MMI GENOMICS, INC.
 ; APPLICANT: DENISE, Sue K.
 ; APPLICANT: KERR, Richard
 ; APPLICANT: ROSENFELD, David
 ; APPLICANT: HOLM, Tom

; APPLICANT: BATES, Stephen
 ; APPLICANT: FANTIN, Dennis
 ; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
 ; FILE REFERENCE: MM1100-2
 ; CURRENT APPLICATION NUMBER: US/10/750,185
 ; CURRENT FILING DATE: 2003-12-31
 ; PRIOR APPLICATION NUMBER: US 60/437,482
 ; PRIOR FILING DATE: 2002-12-31
 ; NUMBER OF SEQ ID NOS: 64922
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 25909
 ; LENGTH: 1306
 ; TYPE: DNA
 ; ORGANISM: Bovine 19866880625794
 US-10-750-185-25909
 Query Match 1.4%; Score 38.2; DB 6; Length 1306;
 Best Local Similarity 55.7%; Pred. No. 3.4;
 Matches 73; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
 Qy 1953 AAGAAATATCTGTGAGTTTACAAGATGAAAAATGGATTAGCGCCAGAAAAAGGGAAATA 2012
 Db 546 ATGGTATGTTCTGGCTCTTTACAAGAAGATCACTCTCTCTCCCTATTGTGGAGCTA 605
 Qy 2013 TACCAAGAGGTAAATTTCTTTGATGAATTAATAATTCAAATTTGGCAGCCAAAGATTACA 2072
 Db 606 TAGAATTGAATGCAATTTCTTTTGAATGTAATAATGAAATTTGTACTGTAAATATGCATA 665
 Qy 2073 TGTGTCAAAT 2083
 Db 666 TCTGGTGAAT 676
 RESULT 10
 US-11-117-187-207/c
 ; Sequence 207, Application US/11117187
 ; Publication No. US20050266560A1
 ; GENERAL INFORMATION:
 ; APPLICANT: PREUSS, DAPHNE
 ; APPLICANT: COPENHAVER, GREGORY
 ; TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
 ; FILE REFERENCE: ARCD:309US
 ; CURRENT APPLICATION NUMBER: US/11/117,187
 ; CURRENT FILING DATE: 2005-04-28
 ; PRIOR APPLICATION NUMBER: US/09/531,120
 ; PRIOR FILING DATE: 2000-03-17
 ; PRIOR APPLICATION NUMBER: 60/125,219
 ; PRIOR FILING DATE: 1999-03-18
 ; NUMBER OF SEQ ID NOS: 212
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 207
 ; LENGTH: 82596
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-11-117-187-207
 Query Match 1.4%; Score 38; DB 7; Length 82596;
 Best Local Similarity 50.0%; Pred. No. 34;
 Matches 95; Conservative 0; Mismatches 95; Indels 0; Gaps 0;
 Qy 2231 AAAACAGCTCCCTTTTCAGAAAAATCAAAACGAATCTTTCTTTAGGATCTGAAATATCCG 2290
 Db 70938 AGAGTAGATGTTTTTAAATTTAGATCATGAATGAAATATATCTTATTACTAGAGAAAATCT 70879
 Qy 2291 GTTATATGCAAGAACCATACAGATACATATCAGAAATATGCCGAGAGCATATAATA 2350
 Db 70878 CACGCAACTTTTGAATTAATAATAATCAATCAACATTTTGTGGCTAAGCATACATATC 70819
 Qy 2351 GAAGTAATCACCTGATTTTTTATTCAGAAACCGATTTCTTTGCGTTAATGGAATAAAGTG 2410
 Db 70818 AAATTAATTAATTTATTTTCTTACTTAATTTTTTCTTAAATTTTTTCTTTAGTATTTATGAATTA 70759
 Qy 2411 AAAAAAATGA 2420

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Db 70758 TGATAAATTA 70749
|||||
Query Match 1.4%; Score 37.8; DB 6; Length 1624;
Best Local Similarity 45.7%; Pred. No. 4.9;
Matches 132; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

RESULT 11
US-11-117-187-211
; Sequence 211, Application US/11117187
; Publication No. US20050266560A1
; GENERAL INFORMATION:
; APPLICANT: PREUSS, DAPHNE
; APPLICANT: COPENHAVEN, GREGORY
; TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
; FILE REFERENCE: ARCD-309US
; CURRENT APPLICATION NUMBER: US/11/117,187
; CURRENT FILING DATE: 2005-04-28
; PRIOR FILING DATE: US/09/531,120
; PRIOR APPLICATION NUMBER: 2000-03-17
; PRIOR FILING DATE: 60/125,219
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 211
; LENGTH: 1082144
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-117-187-211

Query Match 1.4%; Score 38; DB 7; Length 1082144;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 95; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

Qy 2231 AAAACAGTCCCTTTCAGAAAATCAAAACGAATCTTCTTTAGGATCTGAAATATCCG 2290
Db 937718 AGAGTAGATGTTTAAATAGATCATGAATGAATATATCTTTATTAAGAGAAAATCT 937777

Qy 2291 GTTATATGGCAAGAACCATACAGATATCAGATATGCGCAAGAGCATAAATATA 2350
Db 937778 CACGCACTTGAATTAATATAATATCATGCAACATTTGTGCTAAGCATACATATC 937837

Qy 2351 GAAGTAATACCCCTGATTTTATTCAGAAACCGATTTCTTTGCGGTTAATGATAAAAGTG 2410
Db 937838 AAATTAATTAATTAATTTCTTACTTAAATTTTGTCTTAGTATTTATGAATTTAAATA 937897

Qy 2411 AAAAATGA 2420
Db 937898 TGATAAATTA 937907

RESULT 12
US-10-750-185-29572/c
; Sequence 29572, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR FILING DATE: US 60/437,482
; PRIOR APPLICATION NUMBER: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 29572
; LENGTH: 1624
; TYPE: DNA
; ORGANISM: Bovine 19866880413136
US-10-750-185-29572

Query Match 1.4%; Score 37.6; DB 6; Length 1908;
Best Local Similarity 49.0%; Pred. No. 6;
Matches 100; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

Qy 2397 AATGATAAAAGTCGAAAATATGATTTCCGGTGAAGAAAAATTTATCGGCAATGGA 2456
Db 715 AATGGCATATGATATACTGAATCATTTTACTGCCACAGAAAATTTAACACACATTTGT 774

Qy 2457 GGTTAAGGTTTATCATGATTTAAAAATAAACAATACAGAAATACATGTCACATGCAATT 2516
Db 775 AATCAACTGTAITTCATTTAAAAATAAATAAATAATGTAATCTCACTTCACTACTCTGA 834

Qy 2517 GGCCCATCCCTATACGCAATGAGTAATGAAGAAGAGCGCTGTTGCAAGAAACAGAAC 2576
Db 835 GGCACATGCATTTTGGAAAGAGGGTACCTGAAAAAATCACCATCTCCAGTTGGCAGAA 894

Qy 2577 CGCTATTGCAATAGATAGAAATA 2600
Db 895 CCACAAATAAATGGTGGTGA 918

US-10-750-185-59339
; Sequence 59339, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR FILING DATE: US 60/437,482
; PRIOR APPLICATION NUMBER: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 59339
; LENGTH: 1908
; TYPE: DNA
; ORGANISM: Bovine 19866880404878
US-10-750-185-59339

Query Match 1.4%; Score 37.6; DB 6; Length 1908;
Best Local Similarity 49.0%; Pred. No. 6;
Matches 100; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

Qy 2397 AATGATAAAAGTCGAAAATATGATTTCCGGTGAAGAAAAATTTATCGGCAATGGA 2456
Db 715 AATGGCATATGATATACTGAATCATTTTACTGCCACAGAAAATTTAACACACATTTGT 774

Qy 2457 GGTTAAGGTTTATCATGATTTAAAAATAAACAATACAGAAATACATGTCACATGCAATT 2516
Db 775 AATCAACTGTAITTCATTTAAAAATAAATAAATAATGTAATCTCACTTCACTACTCTGA 834

Qy 2517 GGCCCATCCCTATACGCAATGAGTAATGAAGAAGAGCGCTGTTGCAAGAAACAGAAC 2576
Db 835 GGCACATGCATTTTGGAAAGAGGGTACCTGAAAAAATCACCATCTCCAGTTGGCAGAA 894

Qy 2577 CGCTATTGCAATAGATAGAAATA 2600
Db 895 CCACAAATAAATGGTGGTGA 918

US-10-750-185-59339
; Sequence 59339, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR FILING DATE: US 60/437,482
; PRIOR APPLICATION NUMBER: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 59339
; LENGTH: 1908
; TYPE: DNA
; ORGANISM: Bovine 19866880404878
US-10-750-185-59339

Query Match 1.4%; Score 37.8; DB 6; Length 1624;
Best Local Similarity 45.7%; Pred. No. 4.9;
Matches 132; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

Qy 2000 AAAAGGGAAATATACAAAGAGGTAAATTTCTTTGATGAATTAATAATTCRAATTCGCAG 2059
Db 733 AAAATAGGAAATATGATCACAATGCTTATTTATTTTAGGAAAAAAGCCCTACTTTCAGATT 674

Qy 2060 CCAAAAGTTTCATGTTGTCAAATGGAACGAGAGAGAGCAGTTATACAAAAATAAAT 2119
Db 673 AAATATGTTTAAATTTTATATACTAATAAATAAATAAATTTCTAAATTTTAAAAAT 614

Qy 2120 CATTTGAAAGTGGTTCGTGTCGGTGATTCGATCCGTCGGGTTTATTTGCTAAAGCCACGAAG 2179
Db 613 ACCCACTAATTAATCTTTTGGAGTTTCAGATTTATAAATACATTTCTAAGACAAACAAA 554

Qy 2180 AGTTACTAAAGGTATAGAAAAAGTCAAAATCATATATATAGCCGACTTTGAAGAAAAACAGCT 2239
Db 553 ATCCTATAAAACATTCGACTATAAAGAGATACATTTCTAGTTTATTTAAAAATTTATTCA 494

Qy 2240 CCCTTTTCAGAAAATCAAAAACGAATCTTTCTTTAGGATCTGAAATATC 2288
Db 493 GAATTTTATTAGTAAGAAATACAGACTCTGTCTTCATTATAAATATATC 445

RESULT 13
US-10-750-185-59339
; Sequence 59339, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR FILING DATE: US 60/437,482
; PRIOR APPLICATION NUMBER: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 59339
; LENGTH: 1908
; TYPE: DNA
; ORGANISM: Bovine 19866880404878
US-10-750-185-59339

Query Match 1.4%; Score 37.6; DB 6; Length 1908;
Best Local Similarity 49.0%; Pred. No. 6;
Matches 100; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

Qy 2397 AATGATAAAAGTCGAAAATATGATTTCCGGTGAAGAAAAATTTATCGGCAATGGA 2456
Db 715 AATGGCATATGATATACTGAATCATTTTACTGCCACAGAAAATTTAACACACATTTGT 774

Qy 2457 GGTTAAGGTTTATCATGATTTAAAAATAAACAATACAGAAATACATGTCACATGCAATT 2516
Db 775 AATCAACTGTAITTCATTTAAAAATAAATAAATAATGTAATCTCACTTCACTACTCTGA 834

Qy 2517 GGCCCATCCCTATACGCAATGAGTAATGAAGAAGAGCGCTGTTGCAAGAAACAGAAC 2576
Db 835 GGCACATGCATTTTGGAAAGAGGGTACCTGAAAAAATCACCATCTCCAGTTGGCAGAA 894

Qy 2577 CGCTATTGCAATAGATAGAAATA 2600
Db 895 CCACAAATAAATGGTGGTGA 918

US-10-750-185-59339
; Sequence 59339, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR FILING DATE: US 60/437,482
; PRIOR APPLICATION NUMBER: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 59339
; LENGTH: 1908
; TYPE: DNA
; ORGANISM: Bovine 19866880404878
US-10-750-185-59339

Query Match 1.4%; Score 37.8; DB 6; Length 1624;
Best Local Similarity 45.7%; Pred. No. 4.9;
Matches 132; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

Qy 2000 AAAAGGGAAATATACAAAGAGGTAAATTTCTTTGATGAATTAATAATTCRAATTCGCAG 2059
Db 733 AAAATAGGAAATATGATCACAATGCTTATTTATTTTAGGAAAAAAGCCCTACTTTCAGATT 674

Qy 2060 CCAAAAGTTTCATGTTGTCAAATGGAACGAGAGAGAGCAGTTATACAAAAATAAAT 2119
Db 673 AAATATGTTTAAATTTTATATACTAATAAATAAATAAATTTCTAAATTTTAAAAAT 614

Qy 2120 CATTTGAAAGTGGTTCGTGTCGGTGATTCGATCCGTCGGGTTTATTTGCTAAAGCCACGAAG 2179
Db 613 ACCCACTAATTAATCTTTTGGAGTTTCAGATTTATAAATACATTTCTAAGACAAACAAA 554

Qy 2180 AGTTACTAAAGGTATAGAAAAAGTCAAAATCATATATATAGCCGACTTTGAAGAAAAACAGCT 2239
Db 553 ATCCTATAAAACATTCGACTATAAAGAGATACATTTCTAGTTTATTTAAAAATTTATTCA 494

Qy 2240 CCCTTTTCAGAAAATCAAAAACGAATCTTTCTTTAGGATCTGAAATATC 2288
Db 493 GAATTTTATTAGTAAGAAATACAGACTCTGTCTTCATTATAAATATATC 445
```

Matches 123; Conservative 0; Mismatches 124; Indels 1; Gaps 1;	
QY	2249 AAAAAACAAAAACGAATCTTTCTTTAGGATCTGAAATATCCGGTTATATGGCAAGAACCA 2308
Db	
QY	14717 AATTATATATTTAAATTTAGAAATTCCTAAATCCAAATTTCTGATTTTAAATCCAAACCC 14658
Db	
QY	2309 TACAAGATACGATATCAGAAATATGCGAAGAGCATAAATATAGAGTAATACCCCTGATT 2368
Db	
QY	14657 TATATTTATAAATTTCTAAAGTTTTTAACTTTTGCTCAACTTAAAAATTTAAATCATAAAAAT 14598
Db	
QY	2369 TTTATTCAGAAACCGATTCTTTTGGTTAATCGATAAAAGTCAAAAAATGATTATTCG 2428
Db	
QY	14597 TTTAATGGCATCTAATTTTTTTTCACTCCCTATTTAAATTTGTCAGAACTAAA-ATTTGG 14539
Db	
QY	2429 GTGAAAGAAAAATTTATGCGCAATGGAGGTTTAAAGTTTATCATGATTTTAAAAAATAAAC 2488
Db	
QY	14538 GCGAAACAATAATAGACAATAAAATGTTCTTAAATCTTTTGGCTACTTTTGAATATATAC 14479
Db	
QY	2489 AATCAGAA 2496
Db	
QY	14478 ATGAAGCA 14471
Db	

Search completed: December 14, 2005, 06:50:56
Job time : 939 secs

Matches 123; Conservative 0; Mismatches 124; Indels 1; Gaps 1;	
QY	2249 AAAAAACAAAAACGAATCTTTCTTTAGGATCTGAAATATCCGGTTATATGGCAAGAACCA 2308
Db	
QY	14717 AATTATATATTTAAATTTAGAAATTCCTAAATCCAAATTTCTGATTTTAAATCCAAACCC 14658
Db	
QY	2309 TACAAGATACGATATCAGAAATATGCGAAGAGCATAAATATAGAGTAATACCCCTGATT 2368
Db	
QY	14657 TATATTTATAAATTTCTAAAGTTTTTAACTTTTGCTCAACTTAAAAATTTAAATCATAAAAAT 14598
Db	
QY	2369 TTTATTCAGAAACCGATTCTTTTGGTTAATCGATAAAAGTCAAAAAATGATTATTCG 2428
Db	
QY	14597 TTTAATGGCATCTAATTTTTTTTCACTCCCTATTTAAATTTGTCAGAACTAAA-ATTTGG 14539
Db	
QY	2429 GTGAAAGAAAAATTTATGCGCAATGGAGGTTTAAAGTTTATCATGATTTTAAAAAATAAAC 2488
Db	
QY	14538 GCGAAACAATAATAGACAATAAAATGTTCTTAAATCTTTTGGCTACTTTTGAATATATAC 14479
Db	
QY	2489 AATCAGAA 2496
Db	
QY	14478 ATGAAGCA 14471
Db	

Query Match 1.4%; Score 37.6; DB 7; Length 50959;
Best Local Similarity 49.6%; Pred. No. 34;
Matches 123; Conservative 0; Mismatches 124; Indels 1; Gaps 1;

Matches 123; Conservative 0; Mismatches 124; Indels 1; Gaps 1;	
QY	2249 AAAAAACAAAAACGAATCTTTCTTTAGGATCTGAAATATCCGGTTATATGGCAAGAACCA 2308
Db	
QY	14717 AATTATATATTTAAATTTAGAAATTCCTAAATCCAAATTTCTGATTTTAAATCCAAACCC 14658
Db	
QY	2309 TACAAGATACGATATCAGAAATATGCGAAGAGCATAAATATAGAGTAATACCCCTGATT 2368
Db	
QY	14657 TATATTTATAAATTTCTAAAGTTTTTAACTTTTGCTCAACTTAAAAATTTAAATCATAAAAAT 14598
Db	
QY	2369 TTTATTCAGAAACCGATTCTTTTGGTTAATCGATAAAAGTCAAAAAATGATTATTCG 2428
Db	
QY	14597 TTTAATGGCATCTAATTTTTTTTCACTCCCTATTTAAATTTGTCAGAACTAAA-ATTTGG 14539
Db	
QY	2429 GTGAAAGAAAAATTTATGCGCAATGGAGGTTTAAAGTTTATCATGATTTTAAAAAATAAAC 2488
Db	
QY	14538 GCGAAACAATAATAGACAATAAAATGTTCTTAAATCTTTTGGCTACTTTTGAATATATAC 14479
Db	
QY	2489 AATCAGAA 2496
Db	
QY	14478 ATGAAGCA 14471
Db	

Matches 123; Conservative 0; Mismatches 124; Indels 1; Gaps 1;	
QY	2249 AAAAAACAAAAACGAATCTTTCTTTAGGATCTGAAATATCCGGTTATATGGCAAGAACCA 2308
Db	
QY	14717 AATTATATATTTAAATTTAGAAATTCCTAAATCCAAATTTCTGATTTTAAATCCAAACCC 14658
Db	
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Best Local Similarity 49.6%; Pred. No. 41;
Matches 123; Conservative 0; Mismatches 124; Indels 1; Gaps 1;

Search completed: December 14, 2005, 06:50:56
Job time : 939 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 23:36:00 ; Search time 1950 Seconds
(without alignments)

11640.740 Million cell updates/sec

Title: US-10-647-956A-5

Perfect score: 2745

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Scoring table: IDENTITY NUC

Gapop 10'0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2745	100.0	2745	3 US-09-817-514A-5	Sequence 5, Appli
2	2653.8	96.7	2748	7 US-10-609-113-45	Sequence 45, Appl
3	1442.2	52.5	2817	7 US-10-609-113-48	Sequence 48, Appl
4	1440.6	52.5	2817	7 US-10-706-424-15	Sequence 15, Appl
5	1440.6	52.5	2817	8 US-10-754-115-57	Sequence 57, Appl
6	1004.6	36.6	2883	7 US-10-706-424-11	Sequence 11, Appl
7	1004.6	36.6	2883	7 US-10-609-113-46	Sequence 46, Appl
8	1004.6	36.6	2883	8 US-10-754-115-46	Sequence 46, Appl
9	962	35.0	3132	6 US-10-282-794A-60	Sequence 60, Appl
10	962	35.0	3132	7 US-10-609-113-44	Sequence 44, Appl
11	962	35.0	3132	8 US-10-754-115-25	Sequence 25, Appl
12	957.2	34.9	2850	7 US-10-706-424-13	Sequence 13, Appl
13	957.2	34.9	2850	7 US-10-609-113-47	Sequence 47, Appl
14	730.8	26.6	2889	8 US-10-754-115-50	Sequence 50, Appl
15	730.8	26.6	2889	10 US-11-020-848-3	Sequence 3, Appli
16	730.8	26.6	2947	10 US-10-754-115-53	Sequence 53, Appl
17	730.8	26.6	2947	10 US-11-020-848-8	Sequence 8, Appli
18	730.8	26.6	7508	8 US-10-754-115-54	Sequence 54, Appl
19	730.8	26.6	7508	10 US-11-020-848-9	Sequence 9, Appli
20	666	24.3	3048	8 US-10-753-901-15	Sequence 15, Appl
21	666	24.3	3048	8 US-10-754-115-15	Sequence 15, Appl
22	666	24.3	3051	7 US-10-609-113-21	Sequence 21, Appl
23	666	24.3	39005	8 US-10-753-901-6	Sequence 6, Appli

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	25	599	21.8	38258	6	US-10-365-319-1	Sequence 1, Appli
	26	368.4	13.4	2793	7	US-10-609-113-12	Sequence 12, Appl
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	30	216.2	7.9	2823	6	US-10-365-742-63	Sequence 63, Appl
	31	148.6	5.4	858	7	US-10-609-113-40	Sequence 40, Appl
	32	57.4	2.1	7442	7	US-10-221-714A-409	Sequence 409, App
	33	53.8	2.0	6419	6	US-10-311-455-240	Sequence 240, App
	34	53.6	2.0	1062	8	US-10-425-115-120013	Sequence 120013,
	35	52.4	1.9	3673778	6	US-10-312-841-2	Sequence 2, Appli
	36	51.8	1.9	6292	7	US-10-221-714A-461	Sequence 461, App
	37	51.6	1.9	11745	6	US-10-240-453-206	Sequence 206, App
	38	51.4	1.9	14006	6	US-10-311-455-1931	Sequence 1931, Ap
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	41	51	1.9	11745	6	US-10-240-453-205	Sequence 205, App
	42	50.8	1.9	3683	8	US-10-473-126-339	Sequence 339, App
	43	50	1.8	573	4	US-09-925-065A-23123	Sequence 23123, A
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ALIGNMENTS

RESULT 1
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; Sequence 5, Application US/09817514A
; Patent No. US20020078478A1
; GENERAL INFORMATION:
; APPLICANT: ffrench-Constant, Richard
; APPLICANT: Bowen, David
; APPLICANT: Rocheleau, Thomas
; APPLICANT: Waterfield, Nicholas
; TITLE OF INVENTION: DNA SEQUENCES FROM PHOTORHABDUS LUMINESCENS
; FILE REFERENCE: 61645
; CURRENT APPLICATION NUMBER: US/09/817,514A
; CURRENT FILING DATE: 2000-03-26
; PRIOR APPLICATION NUMBER: US 60/191806
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 2745
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2745)
US-09-817-514A-5

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Db 1861 TACGGTTATCGTTATTACCAACCGTGGCGGGCAGATGGTTAAGCGCGAACCCGCGCAGGA 1920
QY 1921 ACATTTGATGGCTGAATCTATACCGAATGGTAAGAAATTAATCTGTGAGTTTACAGAT 1980
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; Sequence 45, Application US/10609113			
; Publication No. US20040110184A1			
; GENERAL INFORMATION:			
; APPLICANT: Bintrim, Scott			
; APPLICANT: Bevan, Scott			
; APPLICANT: Zhu, Baolong			
; APPLICANT: Merlo, Donald J.			
; TITLE OF INVENTION: Pesticidally Active Proteins and Polynucleotides Obtainable from			
; FILE REFERENCE: DAS-101XC2			
; CURRENT APPLICATION NUMBER: US/10/609,113			
; CURRENT FILING DATE: 2003-06-27			
; PRIOR APPLICATION NUMBER: US 60/392,633			
; PRIOR FILING DATE: 2002-06-28			
; PRIOR APPLICATION NUMBER: US 60/441,647			
; PRIOR FILING DATE: 2003-01-21			
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; SOFTWARE: PatentIn version 3.2			
; SEQ ID NO 45			
; LENGTH: 2748			
; TYPE: DNA			
; ORGANISM: Photorhabdus strain W14			
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Qy	721	GCTATGATGTGGCGGGGAGCTTAAAGGGAGTTGTTAACTCAACTCAAGGTGAGGGCGAA	780
Db	721	GCTACGAGTAGCGGGGAGCTTAAAGGCTGTTGGTTGACACTCAAGGTGAGGGCGAG	780
Qy	781	CAGGTGATTATCAAAATCGCTAACTACTCCGCGCGCGGCAAAATTTACGTGAAGAGCAC	840
Db	781	CAAGTGATTATCAAAATCGCTGACTACTCCGCGCGCGGCAAAATTTACGCGAAGAGCAC	840
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Qy 1441 TACGACAGCAACGGCATGAGACAACTGAAAGTGAAGTGAAGCAAGCAACCCAGAACTACTACG 1500
Db 1441 TACGACAGCAACGGCATGAGACAACTGAAAGTGAAGTGAAGCAAGCAACCCAGAACTACTACG 1500
Qy 1501 CAGCAACAAACGGGTAATCTATTTGCGCGGACTGAGCTAGCCACAAACCCAGAGCAAGCC 1560
Db 1501 CAGCAACAAACGGGTAATCTATTTGCGCGGACTGAGCTAGCCACAAACCCAGAGCAAGCC 1560
Qy 1561 ACAACAAACGGAAGTGTACAGGTTATCACCTCGGTGAAGCGGTGCGCGCACAGGTACGG 1620
Db 1561 ACAACAAACGGAAGTGTACAGGTTATCACCTCGGTGAAGCGGTGCGCGCACAGGTACGG 1620
Qy 1621 GTGTGCACTGGGAGAGCGGTAAAGCCAGAGAGATGTCAACAAATATCAACTACGTTACAGC 1680
Db 1621 GTGTGCACTGGGAGAGCGGTAAAGCCAGAGAGATGTCAACAAATATCAACTACGTTACAGC 1680
Qy 1681 TACGATAATCTGATCGGCTCAGCCAGCTTGAACCTGACAAACCAAGCAAAATTTATCAGC 1740
Db 1681 TACGATAATCTGATCGGCTCAGCCAGCTTGAACCTGACAAACCAAGCAAAATTTATCAGC 1740
Qy 1741 GAGGAAGAGTATTATCCATTTGGCGGACAGCGCTGTGGGAGCAACAGCAACCAAGCA 1800
Db 1741 GAGGAAGAGTATTATCCATTTGGCGGACAGCGCTGTGGGAGCAACAGCAACCAAGCA 1800
Qy 1801 GCCAGCTATAAACGATTTCGCTATTTCGGGCAAGAACGAGATGCCACCGGTTGTATTAT 1860
Db 1801 GCCAGCTATAAACGATTTCGCTATTTCGGGCAAGAACGAGATGCCACCGGTTGTATTAT 1860
Qy 1861 TACGGTTATCGTTATACCAACCGTGGCGGCGAGATGGTTAAGCGGCGGACCGCGGAGGA 1920
Db 1861 TACGGTTATCGTTATACCAACCGTGGCGGCGAGATGGTTAAGCGGCGGACCGCGGAGGA 1920
Qy 1921 ACCATTGATGGCTGAATCTATACCGAATGTAAGAAATATCTCTGTGAGTTTACAAGAT 1980
Db 1921 ACCATTGATGGCTGAATCTATACCGAATGTAAGAAATATCTCTGTGAGTTTACAAGAT 1980
Qy 1981 GAAATGGATTAGCGCCAGAAAAAGGGAATATATACCAAGAGGTAAATTTCTTTGATGAA 2040
Db 1981 GAAATGGATTAGCGCCAGAAAAAGGGAATATATACCAAGAGGTAAATTTCTTTGATGAA 2040
Qy 2041 TTAATAATTCAAATTTGGCGCCAAAGTTTCAATGTTGTCAAATGGAACGGAAGAGAGC 2100
Db 2041 TTAATAATTCAAATTTGGCGCCAAAGTTTCAATGTTGTCAAATGGAACGGAAGAGAGC 2100
Qy 2101 AGTTATACAAAAATAAATCAATTCGAGTGGTTCGTTGCGGTGATTCGATCCGTCGGGT 2160
Db 2101 AGTTATACAAAAATAAATCAATTCGAGTGGTTCGTTGCGGTGATTCGATCCGTCGGGT 2160
Qy 2161 TATTTGCTAAGCCACGAGAGTTACTAAAAGGTATAGAAAAAGTCAAATCATATATAGC 2220
Db 2161 TATTTGCTAAGCCACGAGAGTTACTAAAAGGTATAGAAAAAGTCAAATCATATATAGC 2220
Qy 2221 CGACTTGAAGAAAAACAGCTCCCTTTTCAAAAAATCAAAAAAGTCTTTCTTTTAGGATCT 2280
Db 2221 CGACTTGAAGAAAAACAGCTCCCTTTTCAAAAAATCAAAAAAGTCTTTCTTTTAGGATCT 2280
Qy 2281 GAAATATCCGGTTATATGGCAAGAACCATACAAGATACGATATCAGATATGCGGAAGAG 2340
Db 2281 GAAATATCCGGTTATATGGCAAGAACCATACAAGATACGATATCAGATATGCGGAAGAG 2340
Qy 2341 CATAAATATAGAAGTAATCACCTGATTTTATTCAGAAAAAGTCTTTCTTTGCGTTAATG 2400
Db 2341 CATAAATATAGAAGTAATCACCTGATTTTATTCAGAAAAAGTCTTTCTTTGCGTTAATG 2400
Qy 2401 GATAAAGTGAAAAAATGATTTTCCGGTGAAGAAAAAATTTATGCGGCAATGGAGTT 2460
Db 2401 GATAAAGTGAAAAAATGATTTTCCGGTGAAGAAAAAATTTATGCGGCAATGGAGTT 2460
Qy 2461 AAGGTTTATCATGATTTTAAAAAATAAACAATCAGAAATTTACATGTCAACTATGCAATTGGCC 2520

Db 2461 AAGGTTTATCATGATTTTAAAAAATAAACAATCAGAAATTTACATGCTCAACTATGCAATTGGCC 2520
Qy 2521 CATCCCTATACGCAATTTGAGTAATGAAGAAAGCGCTGTTGCAAGAAACAGAACCGCT 2580
Db 2521 CATCCCTATACGCAATTTGAGTAATGAAGAAAGCGCTGTTGCAAGAAACAGAACCGCT 2580
Qy 2581 ATTGCAATAGATAGAGAAATATAATTTCAAAGGTTGTTGGCAAAATTCCTGACAAATGAAAGCA 2640
Db 2581 ATTGCAATAGATAGAGAAATATAATTTCAAAGGTTGTTGGCAAAATTCCTGACAAATGAAAGCA 2640
Qy 2641 ATTAAAAAATCAATGAAAGACATAAAATTAATTAAGATATCAACAGAGGCTATTATATT 2700
Db 2641 ATTAAAAAATCAATGAAAGACATAAAATTAATTAAGATATCAACAGAGGCTATTATATT 2700
Qy 2701 CGCTCTGCGGCTATCCCTGAGAAATTTAGGAATGCGGAGAACTTCA 2745
Db 2701 CGCTCTGCGGCTATCCCTGAGAAATTTAGGAATGCGGAGAACTTCA 2745

RESULT 3
US-10-609-113-48
; Sequence 48, Application US/10609113
; Publication No. US20040110184A1
; GENERAL INFORMATION:
; APPLICANT: Bintrim, Scott
; APPLICANT: Bevan, Scott
; APPLICANT: Zhu, Baolong
; APPLICANT: Merlo, Donald J.
; TITLE OF INVENTION: Pesticidally Active Proteins and Polynucleotides Obtainable from
; TITLE OF INVENTION: Paenibacillus Species
; FILE REFERENCE: DAS-101XC2
; CURRENT APPLICATION NUMBER: US/10/609,113
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US 60/392,633
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/441,647
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 48
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Photorhabdus strain W14
US-10-609-113-48

Query Match 52.5%; Score 1442.2; DB 7; Length 2817;
Best Local Similarity 82.9%; Pred. No. 0;
Matches 1664; Conservative 0; Mismatches 328; Indels 15; Gaps 1;

Qy 21 AATTGACCAAAAGACCCCTCGATTAAAGTTAGATTAACAGGAAATTAATATGTTACGTAC 80
Db 21 ACTTTATCACCATACGCTTACCGTCACTAGTTTCACGATAACCGTGGACTAGCTATCCGTAA 80
Qy 81 TTTAGAATATCTACGCACTCAAGCTGACGAAAAACAGTGAATTAATTTACGTTCTATGA 140
Db 81 TATTAGTTTTCACGCACTACCGCAGAGAAATACCGATACCGGTATTACCGCCATCA 140
Qy 141 GTTCAATATTCCGGGATTTTCAGGTAAAGCAACGATTCCTCGTA-----A 185
Db 141 ATATAATGCCGGGATATTTTGAACCAAGCAATTTGATTCCTCGCTGTATGACGCCAAACA 200
Qy 186 AATAAAAAACAGAGCGGCCCAATTTTCATTCGTGCTTTAAATCTTCGCGTCAAGTTTT 245
Db 201 GACTTAACAAACGCTGTACAACCGAAATTTTATCTGCGGACATAATTTGACCGCAATATCCT 260
Qy 246 ACGTGAAGAAAGTGTTCATGCGCGTTCGACTATTACCTCAATGATATTGAAAGTCGCCC 305
Db 261 GCGAACAGAGGCGTCGATGCCGTCGACGATTTACCTCAACGATATTGAAGSCGCC 320
Qy 306 GGTGTTGATCATCAATGCAACCGGTGTCGCGCAAAACCATTCGTTTATGAAGATACACCT 365
Db 321 GGTGTTGACCATCAATGCAGCGGTGTCCGCGCAAAACCATTCGCTACGAGATACACCT 380

366 TCCGGTCTGCTGCTATACCGAAACAGTACAGGAGGAGAGAAACGACCGAAGC 425
Db
381 GCCGGTCTGCTGCTATACGAAACAGGAGGAGAGAAACGACCGAAGC 440
Qy
426 TCTTATCGGCGCGCAATACGCGCAAGAAAGATTACAACTCGCGGTCAGTGTGT 485
Db
441 CCTTATCGGCGCGCAATACGCGCAAGAAAGATTACAACTCGCGGTCAGTGTGT 500
Qy
486 CCGCATACGATACGCGGAGCTTACTCACTCAATAGCGCTTCTTGCGCTGCGTGT 545
Db
501 CCGCATACGATACGCGGAGCTTACTCACTCAATAGCGCTTCTTGCGCTGCGTGT 560
Qy
546 GCTATCAATCTCAACAACTGTTACCGTAACACGAGTCCGAGTGGACAGGTGAGA 605
Db
561 TCTATCAATCTCAACAACTGTTACCGTAACACGAGTGGACAGGTGAGA 620
Qy
606 CCGAGGCTCTGGCAACAAACCTGAGTGTGTCTATATCAACCAAGATTAACACTGA 665
Db
621 CCGAGGCTCTGGCAACAAACCTGAGTGTGTCTATATCAACCAAGATTAACACTGA 680
Qy
666 TCGCACCGGCGCTTACTGACCGAGCGATGCGAAAGCAATTCAGCGGCTGCGCTA 725
Db
681 TCGCACCGGCGCTTACTGACCGAGCGATGCGAAAGCAATTCAGCGGCTGCGCTA 740
Qy
726 TGATGTGGCGGCGAGCTAAAGGGAGTGTGTTAACTCAAGAGTCAAGCGGAACAGT 785
Db
741 TGATGTGGCGGCGAGCTAAAGGGAGTGTGTTAACTCAAGAGTCAAGCGGAACAGT 800
Qy
786 GATTATCAATCGTAACTACTCCGCGCGCGGCAAAATTAAGTGAAGAGCACGGTAA 845
Db
801 GATTATCAATCGTAACTACTCCGCGCGCGGCAAAATTAAGTGAAGAGCACGGTAA 860
Qy
846 CGGATGTCACTGAATACAGCTACGAAACCGGAAACCAACGGCTTATCGCATTAAC 905
Db
861 CGGATGTCACTGAATACAGCTACGAAACCGGAAACCAACGGCTTATCGCATTAAC 920
Qy
906 TCGCGCTTCAATACAGCGCAAGTGTGCAAGACCTACGCTCAATATGACCCAGTAG 965
Db
921 TCGCGCTTCAATACAGCGCAAGTGTGCAAGACCTACGCTCAATATGACCCAGTAG 980
Qy
966 CAATGTCAATTAATCGTAACTGCGAAGCACTCGCTTTTGGCGCAATCAGAAAGT 1025
Db
981 CAATGTCAATTAATCGTAACTGCGAAGCACTCGCTTTTGGCGCAATCAGAAAGT 1040
Qy
1026 AGCCCGGAGAAATAGCTATACCTACGATCCCTGTATCAGCTTATCAGCGCAACCGGCG 1085
Db
1041 AGCCCGGAGAAATAGCTATACCTACGATCCCTGTATCAGCTTATCAGCGCAACCGGCG 1100
Qy
1086 CGAAATGGCGCAATATCGGTGAGCAAAACCAACCACTTCCCTCCCTGCGCTACCTTCTGA 1145
Db
1101 CGAGATGGCGCAATATCGGTGAGCAAAACCAACCACTTCCCTCCCTGCGCTACCTTCTGA 1160
Qy
1146 CAACAATACCTACACTAATATATCTCGAGCTACGATGATGATGATGATGATGATGATGAT 1205
Db
1161 TAAACAATACCTACACTAATATATCTCGAGCTACGATGATGATGATGATGATGATGATGAT 1220
Qy
1206 GCAAAATTCGCGCACAGTTCGCGAGTACCCAGAAACCACTACCGTGGCTATCACCTCTC 1265
Db
1221 GAAATTCGACATAGTTCACCGCGCGGCAAAATTAACACGAGATTAACGTTTC 1280
Qy
1266 AAACCGCAGCAATCGGGGTGTTCTAGTACGTTAAACCAACCGATCCAAATCAAGTGGATAC 1325
Db
1281 AAATCGCAGCAATCGGGGTGTTCTAGTACGTTAAACCAACCGATCCAAATCAAGTGGATAC 1340
Qy
1326 GTTGTGTTGATCGGGGTGTTCTAGTACGTTAAACCAACCGATCCAAATCAAGTGGATAC 1385
Db
1341 CTTATTGATGCGGGAGGCGCATCAACACGCTTGTATCGGCGCAAGTCTTAACCTGGAC 1400
Qy
1386 ACCACGAGGAGGTAAAGCAGGTGTTAAATGCGCGGAAATGAGTGGTACCGTACCA 1445
Db
1401 ACCCGAGGCGAATGAAACAGCCCAATATAGCGGAGGAAATGAGTGGTATCGCTACCA 1460
Qy
1446 CAGCAACGGCATGAGCAAACTGAAAGTGTGAAACGCAACCCAGCAATATCTACGAGCA 1505

Db
1461 TAGCAACGGCATACGCCAGCTAAAGTGAATGAACAACTCAGATATATCCCGCAACA 1520
Qy
1506 ACAACGGGTAAATCTATTTTCGGGAGCTGGAGCTACGACAAACCCAGAGCAACCCCAAC 1565
Db
1521 ACAACGGGTAACTTATCTACCGGGCTGGAAATACGTACAAACCCAGCAACCCCAAC 1580
Qy
1566 AACGGAGAGTTACAGCTTATCACACTCGGTGAGAGCGGTGCGGCAACAGGTACGGGTGT 1625
Db
1581 AACAGAGAGTTACAGCTTATCACACTCGGTGAGAGCGGTGCGGCAACAGGTACGGGTGT 1640
Qy
1626 GCACTGGGAGAGCGGTAAAGCCAGAGATCTCAACAAATATCAACTACGTTTACAGCTACGA 1685
Db
1641 GCATTGGGAGAGCGGTAAACAGAGATATTAATCAATACGTTTACAGCTACGA 1700
Qy
1686 TAATCTGATCGGCTCCAGCCAGCTTGAATCTGACCAACCAAGGACAAATATATCAAGCGAGGA 1745
Db
1701 TAATCTTATGCTCCAGCCAACTTCAATAGATAGCGAGCAAAATATATCAAGTGAAGA 1760
Qy
1746 AGAGTATTAATCAATTTGGCGGAGACGCTGTGGGAGCAAAACAGCAACAGAAAGCCAG 1805
Db
1761 AGAATATTAATCAATTTGGTGTGACAGCGCTGTGGGAGCAAAACAGCAACAGAAAGCCAG 1820
Qy
1806 CTATATAACGATTCGCTATTTCCGGCAAAACAGAGATGCCACGGGTGCTGTTATTATACGG 1865
Db
1821 CTATATAACGATTCGCTATTTCCGGCAAAACAGAGATGCCACGGGTGCTGTTATTATG 1880
Qy
1866 TTATCTGATTAATCAACACCGTGGCGGAGATGCTTAAAGCGGAGCCCGGAGGAAACCAT 1925
Db
1881 CTACCGTATTAATCAACACCGTGGCGGAGATGCTTAAAGCGGAGCCCGGAGGAAACCAT 1940
Qy
1926 TGATGGCTGATTAATCAATCAAGATGTAAGAAATTAATCTGTGAGTTTCAAGATGAAA 1985
Db
1941 TGATGGCTGATTAATCAATCAAGATGTAAGAAATTAATCTGTGAGTTTCAAGATGAAA 2000
Qy
1986 TGGATTAGCGCCAGAAAGGGAATA 2012
Db
2001 GGGATTATCACCGGCAACAGAAACAGA 2027

RESULT 4
US-10-706-424-15
; Sequence 15, Application US/10706424
; Publication No. US20040103455A1
; GENERAL INFORMATION:
; APPLICANT: ffrench-Constant, Richard
; APPLICANT: Waterfield, Nicholas
; TITLE OF INVENTION: DNA Sequences from tcd Genomic Region of Photorhabdus luminescens
; FILE REFERENCE: 62878
; CURRENT APPLICATION NUMBER: US/10706,424
; CURRENT FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2814)
US-10-706-424-15

Query Match 52.5%; Score 1440.6; DB 7; Length 2817;
Best Local Similarity 82.9%; Pred. No. 0;
Matches 1663; Conservative 0; Mismatches 329; Indels 15; Gaps 1;
Qy 21 AATTGACCAAAAGACCCCTCGATTAAGGTATTAGATAACAGGAAATTAATATGTAGTAC 80
Db 21 ACTTTATCACCATAACGCTACCGTTCAGTGTTCACGATAACCGTGGACTAGCTATCCGTAA 80
Qy 81 TTTAGAAATATACGCACTCAAGCTGACGAAACAGTGTGATGAATTAATACGTTCTATGA 140
Db 81 TATTAGTTTTCACCGCACTACCGCAAGCAAAATACCGATACCCGCTATTATCCCGCATCA 140

QY 141 GTTCAATATTCGGGATTTTCAGGTAAAGACACCGATCCTCGTA-----A 185
Db 141 ATATAATTCGGCGGATTAATTTGAACCAAGACATGATCCTCGCTGTATACGCCAAACA 200
QY 186 AAATAAAACACAGAGCGGCCAAATTTCAATTCGTGTCTTTAAATCTTGCCTGCAAGTTTT 245
Db 201 GACTAACACCGCTGTACACCGAATTTATCTGGGACATAATTTTGACCGCAATATCCT 260
QY 246 ACGTGAAGAAGTTGTGATGCGCGTCCGACTTATTTACCCCTCAATGATATTGAAGTTCGCC 305
Db 261 GCGAACAGAGAGGCTGATGCGCGTCCGAGGATTTACCCCTCAACGATATTGAAGCGCGCC 320
QY 306 GGTGTTGATCATCAATCGAACCGGTGTCGCCAAACCATCTGTTATGAAGTAAACACCT 365
Db 321 GGTGTTGACCATCAATGACGCGGTGTCGCCAAACCATCTGTTACGAAGTAAACACCT 380
QY 366 TCCCGGTCTGCTCGCTATCACCGAACAAAGTACAGGACGAGAGAAACCGACCGAACG 425
Db 381 GCCCGTCCGCTGCTCGCTATCAGCGAACAAAGGACGCGAGAGAAACCGACCGAGCG 440
QY 426 TCTTATCTGGGCCCGGCAATACGCCGCAAGAAAGATTAACAACCTCGCGGTCTAGTGTGT 485
Db 441 CCTTATCTGGGCCCGGCAATACGCCGCAAGAAAGACCAACCTTTCGCGGTCTAGTGTGT 500
QY 486 CCGCATTTACGATACCGGGACTTACTCACTCAATAGCTTTCTCTGCTGCGTCCGT 545
Db 501 CCGCATTTACGATACCGGAGACTTACTCACTCAACAGCCCTTCCCTGACCGCGCGCT 560
QY 546 GCTATCAATCTCAACAACTGCTTACCGATAACAGGATGCCGACTGGACAGGTGAAGA 605
Db 561 TCTATCAATCTCAACAACTGCTTACCGATAACAGGATGCCGACTGGACAGGTGAAGA 620
QY 606 CCAGAGCCTCTGGCAACAAACAACTGAGTGTGTCTATATCAACCAAGTAAACCTGA 665
Db 621 CCAGAGCCTCTGGCAACAAACAACTGAGTGTGTCTATATCAACCAAGTAAACCTGA 680
QY 666 TGCCACCGGGCTTTACTGACCCAGACCGATGCCAAGGCAACATTCAGCGCTGGCCTA 725
Db 681 TGCCACCGGGCTTTACTGACCCAGACCGATGCCAAGGCAACATTCAGCGCTGGCCTA 740
QY 726 TGATGTGCGCGGACGCTTAAAGGGAGTTGGTTAACTCAAGGTCAAGCGGCAACAGGT 785
Db 741 TGATGTGCGCGGACGCTTAAAGGGAGTTGGTTAACTCAAGGTCAAGCGGCAACAGGT 800
QY 786 GATTATCAAAATCGCTAACTACTCCGCGCGGCAAAATTAACGTAAGACGCGTAA 845
Db 801 GATTATCAAAATCGCTAACTACTCCGCGCGGCAAAATTAACGTAAGACGCGTAA 860
QY 846 CCGGATTTGCTGATGATACGCTAGACCGGAAACCAACGGCTTATCGGCATTTACCAC 905
Db 861 CCGGATTTGCTGATGATACGCTAGACCGGAAACCAACGGCTTATCGGCATTTACCAC 920
QY 906 TCGCGTCCATCAGACGCAAGGTGTGCAAGACCTACGCTATCAATATGACCCAGTAGG 965
Db 921 TCGCGTCCATCAGACGCAAGGTGTGCAAGACCTACGCTATCAATATGACCCAGTAGG 980
QY 966 CAATGTCTAATATTCGGTAAATGATGCGGAAGCCACTCGCTTTTGGCGCAATCAAGAGT 1025
Db 981 CAATGTCTAATATTCGGTAAATGATGCGGAAGCCACTCGCTTTTGGCGCAATCAAGAGT 1040
QY 1026 AGCCCGGAGATAGCTATACCTAGATTCCTGTATCAGCTTATCAGCGCCACCGGGCG 1085
Db 1041 AGCCCGGAGATAGCTATACCTAGATTCCTGTATCAGCTTATCAGCGCCACCGGGCG 1100
QY 1086 CGAATGCGCAATATCTGGTCAAGAAACAAACCACTTCCCTCGGCTGCTACCTTCTGA 1145
Db 1101 CGAGATGCGCAATATCTGGTCAAGAAACAAACCACTTCCCTCGGCGCTACCTTCTGA 1160
QY 1146 CAACAAATACCTACCTAATCTATCTCGAGCTTACAGCTATGATCACTAGTGTATCTGAC 1205
Db 1161 TAACAAATACCTACCAACTATCTCGCACTTATCTTATACCTGCGGCAATTTTGAC 1220

QY 1206 GCAAAATTCGCGCACAGCTGCCACAGCTACCCAGAACAACTACACCGTGGCTATCACCCCTCTC 1265
Db 1221 GAAATTCAGCATAGTTTACACGCGCGCAAAATAACTACACGAGGATATAACCGTTTC 1280
QY 1266 AAACGCGACCAATCGGGGTGTTCTCAGTACGCTACACCAGCTCCAAATCAAGTGGATAC 1325
Db 1281 AAATCGCACCAACCGCGCGTACTCAGCACATTTAGCCGAGATCCAACTCAAGTCCATGC 1340
QY 1326 GTTGTGTTGATCGCGTGGTTCACCAACACAGTTTATTTACCCGCGACAGACACTTATCTGGAC 1385
Db 1341 CTTATTTGATCGGAGGCCATCAACACAGCTTGTATTCGCGCAAGTTCTAACTTGGAC 1400
QY 1386 ACCACGAGGAGGTTAAAGCAGGTTAATAATCGCCCGGAAATGAGTGTGTAACGCTACGA 1445
Db 1401 ACCGCGAGCGAATTGAAACAAAGCCAAATAAGCGCAGGAAATGAGTGTGTAACGCTACGA 1460
QY 1446 CAGCAACGCGATGAGCAAACTGAAAGTGTGAAAGCCAAACCCAGAAATCTACGCGAGA 1505
Db 1461 TAGCAACGCGATACGCGCAGCTAAAGTGAATGAACAAACAACTCAGAAATATCCGCAACA 1520
QY 1506 ACAACGGGTAAATCTATTTGCGGACTGGAGCTACGCACAACCCAGAGCAACGCCCAAC 1565
Db 1521 ACAAGGGTAACTTATCTACCGGGCTGGAATACGTACAAACCCAGAACAAACGCCCAAC 1580
QY 1566 AACGGAAGGTTTACAGCTTATCACACTCGGTGAAGCCGCTCGCGCACAGGTACGGGTGT 1625
Db 1581 AACAGAAGGTTTACAGCTTATCACACTCGGTGAAGCCGCGCGCGCAAGTCCGAGTAT 1640
QY 1626 GCACTGGGAGAGCGTTAAGCCAGAGATGTCAACAATATCAACTACACTACGTTACAGCTACGA 1685
Db 1641 GCATTCGGGAGAGCGGTAAACCCAGAGATATTAATAACAATCAACTCAGCTTCGTTACAGCTACGA 1700
QY 1686 TAATCTGATCGGCTCCAGCCAGCTTCAACTGGCAACCAAGGACAAATATCAAGCGAGGA 1745
Db 1701 TAATCTTATTTGGCTCCAGCCAACTTCAATTAGTAGCAGGACAAATATCAAGTGAAGA 1760
QY 1746 AGAGTATTATCCATTTTGGGGGACAGCGCTGTGGGCGAGCAAAACAGCAAAACAGAACCCAG 1805
Db 1761 AGAATATTATCCATTTTGGTTACAGCGCTGTGGGCGCAAGGAATCAAAACCGAAGCCAG 1820
QY 1806 CTATAAAACGATTCGCTATTTCCGGCAAGAAACGAGATGCCACCGGGTGTATTTATACGG 1865
Db 1821 CTATAAAACCATTCGTTATTTCTGTTAAAGAGCGGGATGTTTACCGGGCTGTATTTATATGG 1880
QY 1866 TTATCGTTATTACCAACCGTGGCGGCGAGATGTTTAAAGCGCGGACCCCGGCGAGAACCAT 1925
Db 1881 CTACCGTTATTACCAACCGTGGCGGCGAGATGTTTAAAGTGCAGACCCCGGCGAGAACCAT 1940
QY 1926 TGATGGCTGAATCTATACCGAATGGTAAAGAAATAATCTCTGTGAGTTTACAAGATGAAA 1985
Db 1941 TGATGACGTGAATTTATATCGCATGGTGAGAAATAAACCCGGTGACGCAATTTGATGTTCA 2000
QY 1986 TGAATTAGCCCGCAAGAAAGGGAATA 2012
Db 2001 GGGATTATCACCGGCCAACAGAACAGA 2027

RESULT 5
US-10-754-115-57
; Sequence 57, Application US/10754115
; Publication No. US20040208907A1
; GENERAL INFORMATION:
; APPLICANT: Hey, Timothy
; APPLICANT: Schleper, Amanda
; APPLICANT: Bevan, Scott
; APPLICANT: Bintim, Scott
; APPLICANT: Mitchell, Jon
; APPLICANT: Li, Ze Sheng
; APPLICANT: Ni, Weiting
; APPLICANT: Zhu, Baolong
; APPLICANT: Merlo, Don
; APPLICANT: Apel-Birkhold, Patricia
; APPLICANT: Meade, Thomas

;
; TITLE OF INVENTION: Mixing and Matching TC Proteins for Pest Control
; FILE REFERENCE: DAS-104XCI
; CURRENT APPLICATION NUMBER: US/10/754,115
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US 60/441,723
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens strain W14
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1)..(2817)
US-10-754-115-57

Query Match 52.58; Score 1440.6; DB 8; Length 2817;
Best Local Similarity 82.94; Pred. No. 0;
Matches 1663; Conservative 0; Mismatches 329; Indels 15; Gaps 1;

Qy	21	AAATTGACAAAGACCCCTCGATTAAAGGTATTAGATAACAGGAAATTAATGTACGTAC	80
Db	21	ACTTTATCACCATACGCTACGTCAGTGTTCAGGATTAACCGTGGACTAGCTATCCGTAA	80
Qy	81	TTTAGAATATCTACGCACTCAAGCTGACGAAACAGTGATGAATTAATTACGTTCTATGA	140
Db	81	TAATTAGTTTTCACCGCACTACCGCAGAGCAATACCGATACCGTATTAACCGCCATCA	140
Qy	141	GTTCAATATTCCGGGATTTAGGTAAAGACCGGATCTCTGTA-----A	185
Db	141	ATATAATGCCGGCGGATTTTGAACCAAGCATTTGATCTCTCGCTGTATGACGCCAACA	200
Qy	186	AAATAAAACACAGAGCGGCCAAATTTTCATTTCGTGTCTTTAAATCTTCCCGGTCAAGTTT	245
Db	201	GACTAACAGCTGTACAAACCGAATTTTATCTGGCGACATAATTTGACCGGCAATATCCT	260
Qy	246	ACGTGAAGAAAGTTGTGATCCGCTCGGACTATTACCTCAATGATATTGAAAGTCCGCC	305
Db	261	CGAAACAGAGAGCGTGCATCCGCTCGGACGATTAACCTCAACGATATTGAAGCGGCC	320
Qy	306	GGTGTGATCATCATGCAACCGGTGTCCGCCAAACCATCTGTTATGAAGATTAACCCCT	365
Db	321	GGTGTGACCATCAATGACGCGGTGTCCGCCAAACCATCTGCTACGAAGATAACCCCT	380
Qy	366	TCCGGTCTGCTGCTCTATACCGAAACAGTACAGCAGGAGAGAAACGACCGAACG	425
Db	381	GCCCGTCCGCTGCTCTCTATACGGAACAGGACAGGACAGAGAAACGACCGAGCG	440
Qy	426	TCATTATCTGGCCCGGCAATACGCCGAAGAAAGATTACAAACCTCCCGGTTCAGTGTGT	485
Db	441	CTTTATCTGGCCCGGCAATACGCCGAAGAAAGATTACAAACCTTCGCGGTTCAGTGTGT	500
Qy	486	CCGCAATTAAGATACCGCGGACTTACTCAATCAATAGCTTTCTCTGCTGCGGTGCT	545
Db	501	CCGCCAATTAAGATACCGCGGACTTACTCAATCAACAGCTTTGCCCCCTGACCGCGCT	560
Qy	546	GCTATCAATCTCAACAACTGCTTACCGATACCGGATCCGACTGGACAGGTGAAGA	605
Db	561	TCATATCAATCTCAACAACTGCTTACCGATACCGGATCCGACTGGACAGGTGAAGA	620
Qy	606	CCAGAGCTCTGGCAACAAACCTGAGTAGTGTCTATATCACCCAAAGTAAACACTGA	665
Db	621	CCAGAGCTCTGGCAACAAACCTGAGTAGTGTCTATATCACCCAAAGTAAACACTGA	680
Qy	666	TGCCACCGGGCTTTACTGACCCAGCCGATGCGCAAGGCAACATTCAGCGGTGCGCTTA	725
Db	681	TGCCACCGGGCTTTACTGACCCAGCCGATGCGCAAGGCAACATTCAGCGGTGCGCTTA	740
Qy	726	TGATGTCCCGGCGAGCTAAAGGGAGTTGGTTAACTCAAGGTCAGGCGGAACAGGT	785
Db	741	TGATGTCCCGGCGAGCTAAAGGGAGTTGGTTAACTCAAGGTCAGGCGGAACAGGT	800

Qy	786	GATTATCAAAATCGCTAACCTACTCCGCCCGCGGCAAAAATTAAGTGAAGACGCGTAA	845
Db	801	GATTATCAAAATCGCTAACCTACTCCGCCCGCGGCAAAAATTAAGTGAAGACGCGTAA	860
Qy	846	CGGGATTGTCACTGAATACAGCTACGAACCGGAAACCCAAACGGCTTATCGGCATTACCAC	905
Db	861	CGGGATTGTCACTGAATACAGCTACGAACCGGAAACCCAAACGGCTTATCGGCATTACCAC	920
Qy	906	TGCCCGTCCATCAGACGCCAAGGTGTGCAAGACCTACGCTATCAATATGACCCAGTAGG	965
Db	921	TGCCCGTCCATCAGACGCCAAGGTGTGCAAGACCTACGCTATCAATATGACCCAGTAGG	980
Qy	966	CAATGTCATTAATATCCGTAATGATCGGAAAGCCACTCGCTTTTGGGCGCAATCAGAAAGT	1025
Db	981	CAATGTCATTAATATCCGTAATGATCGGAAAGCCACTCGCTTTTGGGCGCAATCAGAAAGT	1040
Qy	1026	AGCCCCGGGAGATAGCTATACCTTACGATTCCTCTGATCAGCTTATCAGGCGCACCGGCG	1085
Db	1041	AGCCCCGGGAGATAGCTATACCTTACGATTCCTCTGATCAGCTTATCAGGCGCACCGGCG	1100
Qy	1086	CGAAATGGGCAATATCGGTACGAAACCAACCAACTTCCCTCCCTCGCTACCTTTCTGA	1145
Db	1101	CGAGATGGGCAATATCGGTACGAAACCAACCAACTTCCCTCTCGGCGCTACCTTTCTGA	1160
Qy	1146	CAACAATACCTACATACTACTCGAGCTACAGCTATGATCAGAGTGTATCTGAC	1205
Db	1161	TAACAATACCTACATACTACTCGAGCTTATCTATGACCGTGGCGCAATTTGAC	1220
Qy	1206	GCAAAATTCGGCAGCTCGCCAGTACCCAGAACACTACACGCTGGCTATCACCTCTC	1265
Db	1221	GAAAAATTCAGCATAGTTTACCAGCGCGCAAAATAACTACAGCAGGATATAACGGTTTC	1280
Qy	1266	AAACCCGAGCAATTCGGGGTGTCTCAGTACGCTTAAACACCGATCCAAATCAAGTGGATAC	1325
Db	1281	AAATCGAGCAACCGCGCGGTACTCAGACATTTGACCGGAGATCCAACTCAAGTCGATGC	1340
Qy	1326	GTGTTTGTATGCGGTGTGTACCAAAACCGAGTTTATACCGGAGACAGACTTATCTGGAC	1385
Db	1341	CTTATTTGATGCGGGAGGCGCATCAAAACCGAGTTGTTTATCGGCGCAAGTTCTAACTTGGAC	1400
Qy	1386	ACCACGAGGAGTTAAAGCAGTTTAAATGCCCCGGGAAATGAGTGTACCGCTACGA	1445
Db	1401	ACCGGAGGCGAATTAAGAAACAGCCCAATAGCGGAGGAAATGAGTGTATCGCTACGA	1460
Qy	1446	CAGCAACCGCATGAGACAACTGAAAGTGAAGTGAACCAACCCAGAAATACTACGAGCA	1505
Db	1461	TAGCAACGCGATACGCGCAGTAAAGTGAATGAACAACTCAGANATATCCGCGNACA	1520
Qy	1506	ACAAACGGGTAATCTATTTGCCGGACTGAGCTTACGACAAACCCAGAGCAACGCCAACAC	1565
Db	1521	ACAAAGGTAATCTATCTACCGGGGTGGAAATACGTAACAAACCCAGAAACAAACGCCAACAC	1580
Qy	1566	AACGGAAGAGTTACAGTTTATCAGCTCGGTGAGCGGTGCGGCAACAGGTACGGGTGTT	1625
Db	1581	ACAGAAAGTTTACAGTTTATCAGCTCGGTGAGCGGTGCGGCAACAGGTACGGGTGTT	1640
Qy	1626	GCACTCGGAGAGCGGTAAAGCAGAGTGTCAACAATAATCAACTACGTTTACAGCTACGA	1685
Db	1641	GCATTCGGAGAGCGGTAAACAGAGATATTAATAAATCAGCTTCTGTTTACAGCTACGA	1700
Qy	1686	TAACTGATCGGCTCCAGCCAGCTTGAACCTGGCAACCAAGGCAAAATTAATCAGCGAGGA	1745
Db	1701	TAACTTATTTGGCTCCAGCCAACTTCAATTTAGATAGCGGCAAAATTAATCAGTGAAGA	1760
Qy	1746	AGAGTATTAATCCATTTTGGGGGAGACAGCTGTGGGAGCAACAGCCAAACAGAACCCAG	1805
Db	1761	AGAATATTAATCCATTTTGGTGTACAGCGTGTGGGGGCAAGGAATCAAAACCGAAGCCAG	1820
Qy	1806	CTATAAAACGATTCGCTTATTTCCGGCAAGAAACGAGATGCCACCGGTGTGTTATTATCGG	1865
Db	1821	CTATAAAACGATTCGCTTATTTCTGTTAAAGCGGGATGTTTACCGGCTGTATTATTATGG	1880
Qy	1866	TTATCGTTTATTAACAACCGGTGGGCGGAGATGTTTAAAGCGGAGCCCGGAGAACCAT	1925

Db 1881 CTACCGTTATTACCAACCGTGGCGGCAGATGTTAGGTGCAGACCGCGCAGGAACCAT 1940
Qy 1926 TGATGGCGCTGATCTATACCGAATGGTAAGAAATAATCCTGTGAGTTTACAAGATGAAA 1985
Db 1941 TGATGSACTGAATTTATATCGCATGGTGAGAAATAACCCCGGTGACGCAATTTGATGTTCA 2000
Qy 1986 TGGATTAGCGCCAGAAAAGGGAATA 2012
Db 2001 GGGATTATACCGGCCCAACAGACAGA 2027

RESULT 6
US-10-706-424-11
; Sequence 11. Application US/10706424
; Publication No. US20040103455A1
; GENERAL INFORMATION:
; APPLICANT: french-Constant, Richard
; APPLICANT: Waterfield, Nicholas
; TITLE OF INVENTION: DNA Sequences from tcd Genomic Region of Photorhabdus luminescens
; FILE REFERENCE: 62878
; CURRENT APPLICATION NUMBER: US/10706.424
; CURRENT FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 2883
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) .. (2880)
US-10-706-424-11

Query Match 36.6%; Score 1004.6; DB 7; Length 2883;
Best Local Similarity 69.3%; Pred. No. 1.4e-250;
Matches 1433; Conservative 0; Mismatches 594; Indels 42; Gaps 3;
Qy 1 ATGAGCAGTTACAATTCTGCATTTGACCAAAAGACCCCTCGATTAGGTATTAGATAAC 60
Db 1 ATGAAAAACATGATGATCCCAAACTTTATCAAAAAACCCCTACTGTGAGGTTTACGATAAC 60
Qy 61 AGGAAATTAATGATGACGTACTTTAGAAATATCTAGCACTCAAGCTGACGAAACACAGTGAT 120
Db 61 CGTGGTCTGAATAATCCGTAAACATCGATTTTCATCGTACTACCGCAATGGTGATCCCGAT 120
Qy 121 GAATTAATAGCTTCTATGAGTTCAATATTCGGGATTTACGGATTTACGATTAAGACCGATCCT 180
Db 121 ACCGGTATTACCGGCCATCAATAGATATTACGGACACCTTAAATCAAAATCAAAATCGATCCG 180
Qy 181 CGTAAATATAAACCA-----GAGCGGCCCAAAATTTTCATTCGTGCTTT 225
Db 181 CGCTATATGAAGCAAGCAACCAACCAATACGATCAAAACCAATTTTCITTTGGAGTAT 240
Qy 226 AATCTTGGCGGTCAAGTTTACGTGAAGAAAGTTGTATGCGGTGCGGACTATTACCCCTC 285
Db 241 GATTTGACGGGTATCCCTATATGACAGAGACATTTGATGAGTGCAGCTGTACCTTG 300
Qy 286 AATGATATTGAAGTCGCCCGGTGTGATCAATCAATGCAACCGGTGTCGCCCAAAACCAT 345
Db 301 AATGATATTGAAGCGGTGCGCTACTAACGGTACTGCAACAGGGGTTTATACAAATCGA 360
Qy 346 GTTATGAAGATAACACCCCTTCCCGTCTGCTCGTATCACCGAACAAGTACAGGCA 405
Db 361 CAATATGAACCTTCTTCCCTCCCGGTGCTGTGTTATCTGTTGCGGAACAAACACCCGAG 420
Qy 406 GGAGAGAAA-----ACGACCGAACGCTTATCTGGGCGCGCAATACGCCCAAGAAAAA 459
Db 421 GAAAAACATCCCGTATCACCGAACGCTGATTTGGGCTGCGAATACCGAAGCAGAGNAA 480
Qy 460 GATTACAACTCGCGGTGAGTGTGTCGCGCAATTACGATACCGGGGACTTACTCAATC 519
Db 481 GACCATAACCTTGGCGGCAGTGGCGGTCACTATGACACGGCGGAGTTTACCCGGTTA 540

Qy 520 AATAGCCTTTCTCTGGCTGGCGTCTGCTATCACAATCTCAACAACTGCTTACCGATAAC 579
Db 541 GAGAGTTTATCACTGACCGGTACTGTTTATCTCAATCCAGCCAACCTATTGATCGACACT 600
Qy 580 CAGATGCGGACTGGAAGACAGAGAGCTCTGGCAACAAACAACTGAGTAGTAT 639
Db 601 CAAGAGCAAACTGGACAGGTGATAACGAAACCGTCTGGCAAAACATGCTGGTGTATGAC 660
Qy 640 GTCTATATCAACCAAGTAACACTGATGCCACCGGGCTTTACTGACCCAGACCGATGCC 699
Db 661 ATCTACACAACTGAGCACTTTCGATGCGACCGGTGCTTTACTGACTCAGACCGATGCG 720
Qy 700 AAAGGCAACATTCAGCGCTGGCTATGATGTGCGCGGCGAGCTAAAGAGGAGTTGGTTA 759
Db 721 AAAGGCAACATTCAGAGACTGGCTTATGATGTGCGCGGCGAGCTAAAGGAGTGGCTA 780
Qy 760 AACTCAAAAGGTGAGCGGAAACAGGTGATTAATAATCGCTAACCTACTCTCGCGCGCGG 819
Db 781 AACTCAAAAGGCGAGCGGAAACAGGTGATTAATAATCGCTAACCTACTCTCGCGCGCGG 840
Qy 820 CAAAATTTAGTGAAGACAGCGTAACGGGATTTGCTCACTGAATACAGCTACGAAACCGGAA 879
Db 841 CAAAATTTAGTGAAGACAGCGTAACGGGATTTGCTCACTGAATACAGCTACGAAACCGGAA 900
Qy 880 ACCCAACGGCTTATCGGCATTACCACTCGCGCTCCATCAGACGCCAAGGTGTTGCAAGAC 939
Db 901 ACCCAACGGCTTATCGGCATTACCACTCGCGCTCCATCAGACGCCAAGGTGTTGCAAGAC 960
Qy 940 CTACGCTATCAATATACCGCAGTAGCAATGTCATTAATATCGGTAAATGATGCGGAAGCC 999
Db 961 CTGGCTATGAATATGACCGGTAGGCAATGTCATGAGTATCGGTAAATGATGCGGAAGCC 1020
Qy 1000 ACTCGCTTTGGCGCAATCAGAAAGTAGCCCGGAGATAGCTATACCTACGATTCCTCG 1059
Db 1021 ACCCGCTTTGGCGCAATCAGAAAGTAGTCGCGGAAACACTTATACCTACGATTCCTCG 1080
Qy 1060 TATCAGCTTATCAGCGCCACCGCGGCAATGGCCAATATCGGTGAGCAAAACCAACCA 1119
Db 1081 TATCAGCTTATCAGCGCCACCGCGGCAATGGCCAATATAGGTGAGCAAAACCAACCA 1140
Qy 1120 CTTCCCTCCCTCGCTTCTCTGACAAACAACTACCTACCTAATATCTCGCAGGTAC 1179
Db 1141 TTTCCCTCACCGCTCTACCTCTGATACAAACAACTATACCACTATACCGGTACTTAT 1200
Qy 1180 AGTATGATCAGAGTGTATCTGACGCAATTTGGCGACAGCTCGCAGCTACCCAGAC 1239
Db 1201 ACTTATGACCGTGGCGCAATCTGACCAAAATCCAGCACAGTTCCACGGCGAGCAAAAC 1260
Qy 1240 AACTACACCGTGGCTATCACCTCTCAAAACCGCAGCAATCGGGGTGTTCTCAGTACGCTA 1299
Db 1261 AACTACACCACTATACCGGTTTCAATTCGCAACCCGCGCAGTACTCAGCACATTG 1320
Qy 1300 ACCACCGATCCAAATCAAGTGGATAGTGTGTTGATGCGCGGTGCTACCAAAACAGTTTA 1359
Db 1321 ACCGAGATCCGCGCAAGTAGATGCTTTGATGCGAGCGGACATCAGAACACCTTG 1380
Qy 1360 TTACCGGACAGACATTTATCTGACACCAAGGAGAGTTAAGCAGGTTAATAATGGC 1419
Db 1381 ATATCAGGACAAAACCTGAACTGGAATCTCGTGGTGAACCTGCAACAAAGTAACTCGTT 1440
Qy 1420 CCGGAAATCAG-----TGGTACCGCTACGACAGCAACCGCATG 1458
Db 1441 AAACGGGACAAAGGCGCAATGATGCGGAATGGTATCGTTATAGCGGTGACGGAAGA 1500
Qy 1459 AGCAACTGAAAGTGAAGTGAACAGCCAAACCGAATACTACGCAAGCAACACCGGTAACT 1518
Db 1501 AGGATGTTAAATCAATGAACAGCAGCGCCAGCAACAAACGCTCAAAACAAACGCTGACT 1560
Qy 1519 TATTTCCGGGACTGAGCTACGCAACACCGAGGCAACCCCAACAAACGAGAGCTTA 1578
Db 1561 TATTTCCGGAACCTTAGAATCTCGTTAAACAAACAGCAGCGGCCCAACCGAAGATTTG 1620

QY 1579 CACGTTATCACATCGGTGAAGCGGTCCGCGCACAGGTACGGGTGTTCACCTCGGAGAGC 1638
Db 1621 CAAGTTATATCCCGTAGCGAAGCGGCGCGGCGCACAGGTACGAGTATTTACATTCGGGAGAGC 1680
QY 1639 GGTAAAGCCAGAAGATGTCACCAATATCACTACGTTTACAGCTACGATATCTGATCGGC 1698
Db 1681 GGTAAACCGGAAGATTCGCAATATCACTGCGGTATAGTTACGATATCTTATCGGT 1740
QY 1699 TCAGCCAGCTTGAATCGGACCAACCAAGGACAAATATATCAGCGAGGAAGATTAATCCA 1758
Db 1741 TCCAGTCAACTTGAATAGATAGCAAGGACAAATATCACTAGTGAAGAAGATTAATCCC 1800
QY 1759 TTTGSCGGGACAGCGTGTGGGCGAGCAACAGCAGCAACAGACCCAGCTATAAAGCAAT 1818
Db 1801 TATGGTGGAAACAGCATTTATGGGCGCGCAGGAATCAGACAGAACCCAGTTATAAAGCATC 1860
QY 1819 CGCTATTTCCGGGCAAGAAAGAGATGCCACCGGTGTGTTATTTATACGTTATCGTTATTAC 1878
Db 1861 CGTTATTCAGCAAGAGCGGGATGCCACCGGCTATTTACTACGGCTATCGGTATTAC 1920
QY 1879 CAACCGTGGCGGCGAGATGGTTAAGCGGACCCCGGAGAACCAATTTGATGGGCTGAAT 1938
Db 1921 CAACCGTGGATAGACGGTGGTTAAGCTCCGATCCGCGAGAACCAATCGATGGGCTGAAT 1980
QY 1939 CTATACCGAATGTGAAGAAATATCTGTGAGTTTACAGATGAATAATGGAATTAGCGCCA 1998
Db 1981 TTATATCGGATGTGAGGAATATCCAGTTACCTCTCTGATCCTGATGATGATTAATGCCA 2040
QY 1999 GAAAAGGGAATATACCAAGAGGTAAA 2027
Db 2041 ACAATTGCAGAACGATAGCAGCACTAAA 2069

RESULT 7
US-10-609-113-46
; Sequence 46, Application US/10609113
; Publication No. US20040110184A1
; GENERAL INFORMATION:
; APPLICANT: Bintrim, Scott
; APPLICANT: Bevan, Scott
; APPLICANT: Zhu, Baolong
; APPLICANT: Merlo, Donald J.
; TITLE OF INVENTION: Pesticidally Active Proteins and Polynucleotides Obtainable from
; FILE REFERENCE: DAS-101XC2
; CURRENT APPLICATION NUMBER: US/10/609,113
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US 60/392,633
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/441,647
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
; LENGTH: 2883
; TYPE: DNA
; ORGANISM: Photorhabdus strain W14
US-10-609-113-46

Query Match 36.6%; Score 1004.6; DB 7; Length 2883;
Best Local Similarity 69.3%; Pred. No. 1.4e-250;
Matches 1433; Conservative 0; Mismatches 594; Indels 42; Gaps 3;
QY 1 ATGAGGAGTTACAAATCTGCAATTCACCAAGACCCCTCGATTAAAGTATTAGATAC 60
Db 1 ATGAAAAACATTGATCCCAACCTTTATCAAAAAACCCCTACTGTCAGCGTTACGATAAC 60
QY 61 AGCAATTAATGATGCTACTTTAGAAATATCTACGCACTCAAGCTCAACGAAACAGTGAT 120
Db 61 CGTGGTCTGATATCCGTAACATCGATTTTCATCGTACTACCGCAATATGGTGTCCCGAT 120
QY 121 GAATTAATACGTTCTATGAGTTCAATATTTCCGGGATTTTCAGGTAAAAAGCACCGATCCT 180

Db 121 ACCCGTATTATCCCGCCCATCAATACGATATTACGGACACCTAAATCAAAGCATCGATCCG 180
QY 181 CGTAAAAATAAAACCA-----GAGCGGCCCCAAATTTCAATTCGTGTCTTT 225
Db 181 CGCTATATGAAGCCAAGCAAAACCAACATACGATCAAAACCCAAATTTCTTTGGCAGTAT 240
QY 226 AATCTTGGCGGTCAAGTTTACGTGAAGAAAGTTGTATGATGCCGTCGGGATTTACCCCTC 285
Db 241 GATTTGACCGGTAAATCCCTTATGTACAGAGAGCATTTGATGCAAGTCCGCACTGTCACTTG 300
QY 286 AATGATATTGAAAGTCGCCCGGTGTTGATCATCAATGCAACCGGTGTCCGCCAAAAACCAT 345
Db 301 AATGATATTGAAAGCGCTCCGCTACTAAACCGGTGACTGCAACAGGGGTATACAAACTCGA 360
QY 346 CGTTATGAAGATAAACCCCTTCCCGTCTGCTCTGCTATCAACCGAACAAGTACAGGCA 405
Db 361 CAATATGAAACTTCTTCCCTGCCCGGTCTGTTATCTGTTGCCGCAACAAACACCCGAG 420
QY 406 GGAGAGAAA-----ACGACCGGAACGCTCTTATCTGGGCGGCAATACGCGGCAAGAAAAA 459
Db 421 GAAAAAACATCCCGTATACCGGAACCGCTGATTTGGGCTGGCAATACCGAAGCAGAGAA 480
QY 460 GATTACAACCTCGCCGTCAGTGTGTCGCCATTACGATACCGCGGACTTTACTCAACTC 519
Db 481 GACCATAACTTTGCCCGCCAGTCGTCGCTACTATGACACAGCGGGAGTTTACCCGGTTA 540
QY 520 AATAGCCTTTCTCTGGCTGGCGTCTGCTATCACAACTCTCAAACTGCTTACCGATAAC 579
Db 541 GAGAGTTTATCACTGACCGGTACTGTTTATCTCAATCCAGCCAATATTGATCGACACT 600
QY 580 CAGGATGCGGACTGGAACAGGTGAAGACAGAGCTCTCGGCAACAAAACTGAGTAGTGAT 639
Db 601 CAAGAGCAAACTGGACAGGTGATACGAAACCGTCTGGCAAAACATGCTGGCTGATGAC 660
QY 640 GTCTATATCACCCAAAGTAACACTGATGCCACCGGGGCTTTACTGACCCAGACCGATGCC 699
Db 661 ATCTACAACTCTGAGCACCTTCGATGCCCGGTGCTTTACTGACTCAGACCGATGCG 720
QY 700 AAAGCAACATTCAGCGGTGGCTATGATGTCGGCGGCGAGCTAAAGAGGAGTTGGTTA 759
Db 721 AAAGGGAACATTCAGAGACTGCTTATGATGTGGCGGCGAGCTAAACGGGAGCTGGCTA 780
QY 760 ACACCTAAAGGTGAGCGGAAACAGGTGATTAATAATCGCTAACCTACTCTCCGCGCGGG 819
Db 781 ACACCTAAAGGCGCAGACGGAACAGGTGATTAATAATCGCTAACCTACTCTCCGCGCGGA 840
QY 820 CAAAAATTACGTGAAGACGCGTAACGGGATGTCTACCTGATATACAGCTACGACGCGGA 879
Db 841 CAAAAATTACGTGAGGAACACGCGCAATGATTTATCACCAGATACAGTTTATGAACCGGAA 900
QY 880 ACCCAACGGCTTATCGGCATTACCACTCGCCGCTCCATCAGACGCCAAGGTGTGCAAGAC 939
Db 901 ACCCAACGGCTGATCGGTATCAAAACCCCGCTCCGTGACAGACATAAGTGTACAGAC 960
QY 940 CTACGCTATCAATATGACCCAGTAGGCAATGCTTAATAATCGTAAATGATGCGGAAGCC 999
Db 961 CTGCGCTATGAATATGACCCGCTAGGCAATGTATCAGCATCGTAAATGACGCGGAAGCC 1020
QY 1000 ACTCGCTTTTGGGCAATCAGAAAGTAGCCCGGAGAAATAGCTATACCTACGATTCCTTG 1059
Db 1021 ACCCGCTTTTGGCAAAATCAGAAAGTAGTCCCGGAAAAACACTTTATACCTACGATTCCTTG 1080
QY 1060 TATCAGCTTATCAGCGCCACCGGCGGAAATGGCCAATATCGGTGAGCAAAACACCA 1119
Db 1081 TATCAGCTTATCAGCGCCACCGGCGGAAATGGCGAATATAGTTCACAAAGTCAACCA 1140
QY 1120 CTTTCCCTCCCTGCGCTACTCTTGACAACTACCTACACTATATCTCGAGCTAC 1179
Db 1141 TTTTCCCTCACCCTCTACTCTTGATAACACACCTATACCACTATACCCGCTACTTAT 1200
QY 1180 AGCTATGATCAGATGTTAATCTGACGCAAAATTCGCGCAGCTCGCCAGCTACCCAGAAC 1239
Db 1201 ACTTATGACCGTGGCGCAATCTGACCAAAATCCAGCACAGTTTCAACCGCGAGCAAAAC 1260

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Qy 1240 AACTACACCGTGGCTATCACCCCTCTCAACCGCAGCAATCGGGTGTCTCAGTAGCCTA 1299
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1261 AACTACACCAACCAATATCACGGTTTCANATCGCAGCAACCGCGAGTACTCAGCACATTG 1320
Qy 1300 ACCACCGATCAAAATCAAGTGGATACGTTGTTGATCCCGGTGTCTACCAAAACAGTTTA 1359
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1321 ACCGAGATCGGGCGCAAGTAGATGCTTTGTTGATCGAGCGGACATCAGAACACCTTG 1380
Qy 1360 TTACCCGGACAGACATTTATCTGGACACCAAGGAGAGTTAAGCAGGTTAATAATGGC 1419
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1381 ATATCAGACAAAACCTGAATCTGGAATACTCGTGTGAATCTGCAACAAAGTAACACTGGTT 1440
Qy 1420 CCGGGAATCAG-----TGGTACCGCTACGACAGCAACGCGCATG 1458
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1441 AAACGGGACAGGCGCCATATGATGATCGGGAATGGTATCGTTATAGCGGTAGCGGAAGA 1500
Qy 1459 AGACAACTGAAAGTGAAGTGAACAGCCCAACCCAGCAATATCTACGCAACCAACCGGTAAATC 1518
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1501 AGGATGTTAAATCAATGAACAGCAGCGCCAGCAACACGCTCAAAACACAAACGTTGACT 1560
Qy 1519 TATTGCGGGAATCGGAGCTACGCACAAACCCAGAGCAACCGCCACAAACGGAAGAGTTA 1578
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1561 TATTGCGGAATCTAGAACTTCGTCTAACACAAACAGCAGCGCCACAAACGGAAGATTG 1620
Qy 1579 CAGGTTATCACACTCGGTGAAGCGGTGCGGCACAGGTACGGGTGTTGCACTGGGAGAGC 1638
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1621 CAAGTTATACCGGTAGCGGAAGCGGGCGGGGCAAGGTACAGTATACATTTGGGAGAGC 1680
Qy 1639 GGTAAAGCAGAAAGATGTCACAAATCAACTACGTTTACAGCTACGATATCTGATCGGC 1698
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1681 GGTAAACCGGAGATATCGCAATATCACTGTTGCTTATAGTTACGATATCTTATCGGT 1740
Qy 1699 TCCAGCAGCTTGAACTGGACAAACCAAGGACAAATATACAGCGAGGAAGATATTATCCA 1758
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1741 TCCAGTCAACTTGAATTAGATAGCGAAGGACAAATATCAGTGAAGGAAGATATTATCCC 1800
Qy 1759 TTTGGCGGACAGCGTCTGGGACAGCAACAGCCAAACAGAGCCAGCTATAAACCATTT 1818
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1801 TATGGTGAACAGCATTTATGGGCGCCAGGAATCAGACAGAGCCAGTTATAAACATATC 1860
Qy 1819 CGCTATTTCGGCAAGAACAGAGATGCCACCGGTTGTATTATTACGGTTATCGTTATTAC 1878
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1861 CGTTATTTCAGCAAGAGCGGATGCCACCGGCTATATTACTACGGCTATCGGTATTAC 1920
Qy 1879 CAACCGTGGCGGCGAGATGTTAAGCGCGGACCCCGGAGAACCATTTGATGGCTGAAT 1938
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1921 CAACCGTGGATAGACCGGTGTTAAGCTCCGATCCGCGAGGAACAATCGATGGGCTGAAT 1980
Qy 1939 CTATACCGAATGTTAAGAAATAATCCTGTGAGTTTACAAGATGAATGGATTAGCGCCA 1998
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1981 TTATATCGATGGTGAGGAATAATCCAGTTTACCCTCTTGTATCTGTGATTAATGCCA 2040
Qy 1999 GAAAAGGGAATATATCCAAAGAGTAAA 2027
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2041 ACAATTGCAGAACGCATAGACACTAAA 2069
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RESULT 8
US-10-754-115-46
; Sequence 46, Application US/10754115
; Publication No. US20040208907A1
; GENERAL INFORMATION:
; APPLICANT: Hey, Timothy
; APPLICANT: Schleper, Amanda
; APPLICANT: Bevan, Scott
; APPLICANT: Bintrim, Scott
; APPLICANT: Mitchell, Jon
; APPLICANT: Li, Ze Sheng
; APPLICANT: Ni, Weiting
; APPLICANT: Zhu, Baolong
; APPLICANT: Merlo, Don
; APPLICANT: Apel-Birkhold, Patricia
```

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; APPLICANT: Meade, Thomas
; TITLE OF INVENTION: Mixing and Matching TC Proteins for Pest Control
; FILE REFERENCE: DAS-104XC1
; CURRENT APPLICATION NUMBER: US/10/754,115
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US 60/441,723
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
; LENGTH: 2883
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2880)
; US-10-754-115-46
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Query Match 36.6%; Score 1004.6; DB 8; Length 2883;
Best Local Similarity 69.3%; Pred. No. 1.4e-250;
Matches 1433; Conservative 0; Mismatches 594; Indels 42; Gaps 3;
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Qy 1 ATGAGCAGTTACAAATCTGCAATTGACAAAGACCCCTCGATTAAAGTTATTAGATAAC 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 ATGAAAAACATTTGATCCCAAACTTTTATCAAAAAACCCCTACTGTCAGCGTTTACGATAAC 60
Qy 61 AGGAATTTAAATGTAGCTACTTTTAGAATATCTACGCACTCAAGCTGACGAAAAACAGTGAT 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 CGTGGTCTGATATCCGTAACATCGATTTTTCATGTAATACCGCAATGGTGATCCCGAT 120
Qy 121 GAATTAATTAAGTTCTTATGAGTTTCAATATTTCCGGGATTTTCAGGTAAAAAGCACCGATCT 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 ACCGTTATTACCGCCCATCAATACGATATTTACGGGACACCTAAATCAAGCATCGATCCG 180
Qy 181 CGTAAAAATAAAACCA-----GAGCGGCCCAATTTTCATTCGTGTCCTTT 225
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
181 CGCTATATGAAGCCAAAGCAAAACCAACATACGATCAAAACCAATTTTCTTTGGCAGTAT 240
Qy 226 AATCTTGGCGGTCAAGTTTACGTGAAGAAAGTTGATGCGCGTCCGACTATTACCGCTC 285
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
241 GATTTGACCGGTAAATCCCTTATGTACAGAGAGCATTTGATGACAGTGCATCTGCACCTTG 300
Qy 286 AATGATATTGAAAGTCCCGGTGTTGATCATCAATGCAACCGGTGTCCGCCAAAAACCAT 345
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
301 AATGATATTGAAAGCGCGTCCGCTACTAAACGCTGACTGCAACAGGGGTTATACAAACTCGA 360
Qy 346 CGTTATGAAGATAACACCTTCCCGGTGCTGCTGCTATCACCGAACAAAGTACAGGCA 405
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
361 CAATATGAAACTTCTTCCCTGCGCGTCTGTTATCTGTTCCGCAACAAACACCCGAG 420
Qy 406 GGAGAGAAA-----ACGACCGGAACGCTTTATCTGGCGCGCAATACGCCCAAGAAAAA 459
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
421 GAAAAAACATCCCGTATCCCGGAACCGCTGATTTGGCTGGCAATACCGAAGCAGAGAA 480
Qy 460 GATTACAAACCTCCCGGTCAAGTGTGTCGCGCATTTACGATACCGGGGACTTTACTCAATC 519
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
481 GACCAATAACCTTCCCGGCCAGTGGTGGCTGCTATGACACGCGGGAGTTACCGGTTA 540
Qy 520 AATAGCCTTTCTCTGGCTGGCGTCTGCTGATATCAATCTCAACAACTGCTTACCGATAAC 579
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
541 GAGAGTTTATCACTGACCGGTACTGTTTATCTCAATCCAGCCAACTATTGATCGACACT 600
Qy 580 CAGGATGCCGACTGGACAGGTGAAGACACGAGCTCTGGCAACAAACAACTGAGTAGTAT 639
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
601 CAAGAGGCAAACTGGACAGGTGATAAGAAACCGTCTGGCAAAACATCTGGCTGATGAC 660
Qy 640 GTCTATATCAACCAAAAGTAACTGATGCCACCGGGCTTTTACTGACCCAGACCGATGCC 699
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
661 ATCTACACAACTTGACACCTTCGATGCCACCGGTCTTTTACTGACTCAGACCGATGCG 720
Qy 700 AAAGGCAACATTACGCGGCTGGGCTATGATGTGCGCGGCGAGCTAAAGAGGAGTTGTTA 759
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
721 AAAGGGAACATTACAGAGACTGGCTTATGATGTGCGCGGCGAGCTAAACGGGAGCTGGCTA 780
```

QY 760 ACACTCAAGGTGAGCGGAAAGAGTATTAATCAAAATCGTAACTACTCCGCGCGGG 819
DB 781 ACACTCAAGGTGAGCGGAAAGAGTATTAATCAAAATCGTAACTACTCCGCGCGGG 840
QY 820 CAAAAATACGTGAAGAGACAGGTACGGGATGTCAGTGAATACAGCTACGAAACGGAA 879
DB 841 CAAAAATACGTGAAGAGACAGGTATGATGTTATCAGCGAAATACAGTATGAAACGGAA 900
QY 880 ACCCAAGCGCTTATCGGCTTACCACTCGCGGTCATCAGACCCAAAGGTGTCAGAAC 939
DB 901 ACCCAAGCGCTGATCGGTATCAAAACCGCGGTCGTCAGACACTAAAGTGTACAGAAC 960
QY 940 CTACGCTTATCAATATACCCAGTAGGCAATGTCATTAATATCCGTAAATGATCGGAAGCC 999
DB 961 CTGCGCTATGATATGACCGGTAGGCAATGTCATCAGCATCGTAAATGACCGGAAGCC 1020
QY 1000 ACTCGCTTTTGGGCAATCAGAAAGTAGCCCGGAGAAATAGTATACCTACGATTCCTTG 1059
DB 1021 ACCCGCTTTTGGCACAATCAGAAAGTAGTCCCGGAAACACTTTATACCTACGATTCCTTG 1080
QY 1060 TATCAGCTTATCAGCGCCACCGGCGGAAATGCGCAATATCGTTCAGCAAAACCAACAA 1119
DB 1081 TATCAGCTTATCAGCGCCACCGGCGGAAATGCGCAATATAGTTCAGCAAAAGTCAACAA 1140
QY 1120 CTTCCCTCCCTGCGCTACCTCTGACAAACAAATACCTACACTAATATATCTCGCAGCTAC 1179
DB 1141 TTTCCCTCACCGCTCTACTCTTGATACACACCTATACCACTATACCCGTACTTAT 1200
QY 1180 AGTATGATCAGAGTGTATCTGACGCAAAATTCGGGACAGCTCGCCAGTACCCAGAAC 1239
DB 1201 ACTTATGACCGTGGCGCAATCTGACCAAAATCCAGCAGAGTTCACCGCGAGCGCAAAAC 1260
QY 1240 AACTACACGTGCTATCACTCTCAAAACCGCAGCAATCGGGTGTCTCAGTACGCTA 1299
DB 1261 AACTACACCAATATCAGGTTTCAAAATCGCAGCAACCGCGCAGTACTCAGCACAATTG 1320
QY 1300 ACCACCGATCCAAATCAAGTGAATAGTGTGTTGATCGCGGTGTCACCAAAACAGTTTA 1359
DB 1321 ACCGAAGATCCGCGCAAGTAGATGCTTTGTTGATCGCGGACATCAGAACACCTTG 1380
QY 1360 TTACCCGAGCAGACACTTATCTGACACCAAGAGAGGTAAAGCAGGTAAATATGCG 1419
DB 1381 ATATCAGGCAAAACCTGAATCTGCTGTAATCTGCTGTAATCTGCTGTAATCTGCTGTT 1440
QY 1420 CCGGGAATGAG-----TGGTACCGCTACACAGCAGCAGCGCATG 1458
DB 1441 AAACGGGCAAGGGCGCCAAATGATGATCGGGAATGTTATCGTTATAGCGGTGACGGAAGA 1500
QY 1459 AGACAACTGAAGTGAAGTGAAGCAAGCCAACTACGAGCAACCAAGGGAATC 1518
DB 1501 AGGATGTTAAATCAATGACAGAGGCGGCAAGCAACGCTCAACACACAGTGTGACT 1560
QY 1519 TATTTCCGGGACTGAGCTACGCAACACCGAGCAAGCCCAACCAAGGGAAGTTA 1578
DB 1561 TATTTCCGAACTTAGAACTTCTCTAAACAAACAGCAGCGCCCAACCGGAAGATTG 1620
QY 1579 CAGTTTATCACACTCGGTGAGCGGTGCGGACAGGTACGGGTGTTGCACTGGGAGAGC 1638
DB 1621 CAAAGTTATCACCGTAGCGAAGCGGCGCGGCAAGGTACGATGTTATACATGGGAGAGC 1680
QY 1639 GGTAAAGCAGAAGATGTCAACAAATCAACTACGTTACAGCTACGATTAATCTGATCGGC 1698
DB 1681 GGTAAACCGGAAGATTCGACAAATATCAGTTGCGTTATAGTACGATTAATCTTATCGGT 1740
QY 1699 TCAGCCAGCTTGAATCGGCAACCAAGGCAAAATATACGAGGAGGAGGATTAATCCA 1758
DB 1741 TCAGTCAACTTGAATTAGATAGCGAAGGCAAAATATCAGTGAAGGAATATATCCC 1800
QY 1759 TTTGGCGGAGCAGCGCTGTGGGAGCAACAGCAGCAACAGCAGCCAGCTTAATAACGATT 1818
DB 1801 TATGGTGAACAGCATTTATGGCGCGCGGGAATCAGACAGAGCCAGTTATTAACACTATC 1860

QY 1819 CGCTATTCGGCAAAAGACGAGATGCCACCGGTTGTTATTTATTCAGGTTATTCGTTATTAC 1878
DB 1861 CGTTATTCAGGCAAAAGAGCGGATGCCACCGGCTATATTTACTACGGCTATTCGTTATTAC 1920
QY 1879 CAACCGTGGCGGCGAGATGGTTAAGCGCGGACCGGCGAGGAAACCAATTGATGGGCTGAAT 1938
DB 1921 CAACCGTGGATAGGACGGTGGTTAAGCTCCGATCCGCGAGGAAACAATCGATGGGCTGAAT 1980
QY 1939 CTATACCGAATGGTAAAGAAATTAATCCTGTGAGTTTACAAGATGAAATCGATTAGCGCCA 1998
DB 1981 TTATATCGGATGGTGAAGAAATTAATCCAGTTACCTCTCTCTGATCGCTGATGATGATGCA 2040
QY 1999 GAAAAGGGAATATATACCAAGAGGTAAA 2027
DB 2041 ACAATTGCAGAACGCATAGCAGCACTAAA 2069

RESULT 9

US-10-262-794A-60
; Sequence 60, Application US/10262794A
; Publication No. US20030207806A1
; GENERAL INFORMATION:
; APPLICANT: Ensign, Gerald C
; APPLICANT: Bowen, David J
; APPLICANT: Petell, James
; APPLICANT: Fatig, Raymond
; APPLICANT: Schoonover, Sue
; APPLICANT: French-Constant, Richard
; APPLICANT: Rocheleau, Thomas A.
; APPLICANT: Blackburn, Michael B.
; APPLICANT: Hey, Timothy D.
; APPLICANT: Merlo, Donald J.
; APPLICANT: Orr, Gregory L.
; APPLICANT: Roberts, Jean L.
; APPLICANT: Strickland, James A.
; APPLICANT: Guo, Lining
; APPLICANT: Ciche, Todd A.
; APPLICANT: Sukhapinda, Kitisri
; TITLE OF INVENTION: Insecticidal Protein Toxins From Photorhabdus
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dow Agrosciences Patent Department
; STREET: 9330 Zionville Road
; CITY: Indianapolis
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/262,794A
; FILING DATE: 02-OCT-2002
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,567
; FILING DATE: 05-MAY-1997
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/063,615
; FILING DATE: 18-MAY-1993
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/395,497
; FILING DATE: 28-FEB-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 60/007,255
; FILING DATE: 06-NOV-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/608,423
; FILING DATE: 28-FEB-1996
; PRIORITY APPLICATION DATA:

RESULT 10
US-10-609-113-44
; Sequence 44, Application US/10609113
; Publication No. US20040110184A1
; GENERAL INFORMATION:
; APPLICANT: Bintrim, Scott
; APPLICANT: Bevan, Scott
; APPLICANT: Zhu, Baolong
; APPLICANT: Merlo, Donald J.
; TITLE OF INVENTION: Pesticidally Active Proteins and Polynucleotides Obtainable from
; FILE REFERENCE: DAS-101XC2
; CURRENT APPLICATION NUMBER: US/10/609,113
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US 60/392,633
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/441,647
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44
; LENGTH: 3132
; TYPE: DNA
; ORGANISM: Photorhabdus strain W14
US-10-609-113-44

Query Match 35.0%; Score 962; DB 7; Length 3132;
Best Local Similarity 72.2%; Pred. No. 1.8e-239; Mismatches 470; Indels 39; Gaps 4;
Matches 1323; Conservative 0;

QY	205	CCAAATTTTCATTCGTGCTTTAATCTTTCGCGGTCAAGTTTTCGTGAAGAAAGTGTGAT	264
DB	220	CTTAATTTTCTGCGCAGCATGATCTGCCGGTCATGCCCTCGGACAGAGTGTGAT	279
QY	265	GCCGGTGGCAATTAACCTCAATGATATTGAAGTGCGCCGTGTTGATCATCAATGCA	324
DB	280	GCTGGTGTACTGTGCAATTTGAATGATATTGAAGTGTGTTGCGTAATGCAATGCG	339
QY	325	ACCGGTGTCGCCAAACCATCGTATGAGATAACACCTTCCCGTGTCTGCTCGCT	384
DB	340	ACCGGTGTTCTGTCAGACCCGTCCTATGAAAGGCAACACCTTGCCCGTGTGTTATCT	399
QY	385	ATCACCGAAACAGT-----ACAGGAGGAGAGAGAAACGACCAAGTCTTATCTGGGC	438
DB	400	GTGAGCGGAGAGTTTCAACCAAGAGAGTGTAAAGTGACAGCGCTTTATCTGGCT	459
QY	439	GGCAATAACCGCCGAGAAAGATTACAACTCGCCGGTCAGTGTGTCGCCCAATACGAT	498
DB	460	GGGAATACAACTCGGAGAAAGATATAACCTCTCCGGTCTGTGTATACGCCACTACGAC	519
QY	499	ACCGCGGACTTACTCAACTCAATAGCTTCTCTGCGTGGCGTGTCTATCAATCT	558
DB	520	ACAGCGGGAGTGACCGGGTGTGATGAGTCACTGCGCGGCCCATGCTATCCCAATCT	579
QY	559	CAACAACCTGCTTACCGAATACCAAGATGCGAGTGAAGAGGTGAAGACAGAGCCTCTGG	618
DB	580	CACCAATTGCTGCGGAGAGGCGAGGAGGCTAACTGGAGCGGTGACACGAACTGTCTGG	639
QY	619	CAACAAAACTGATGATGATGCTATATACCCAAAGTAACTGATGCCACCGGGCT	678
DB	640	CAGGGAATGCTGCAAGTGAAGTCTATACGACACAAAGTACCACCTAATGCCATCGGGCT	699
QY	679	TTACTACCCAGACCGATGCCAAGGCAATTCAGCGGTGCGCTATGATGTGGCGGG	738
DB	700	TTACTGACCCAAACCGATGCCAAGGCAATTAATTCAGCGTGTGCTTATGACATTCGCGGT	759
QY	739	CAGCTAAAGGGAGTGTGTTTAACTCAACACTCAAGAGGTGAGCGGAAACAGGTGATTCAATCG	798
DB	760	CAGTAAAGGGAGTGTGTTTGAACGGTGAAGGCGCAGAGTGAAACAGGTGATTGTTAAGTCC	819
QY	799	CTAACCTTACTCCCGCGCGGCAAAATTAACGTGAAGAGCACCGGTAAACGGGATGTCACT	858

DB	820	CTGAGCTGTGTCAGCCGCGCATATAAATTGCGTGAAGAGACGGTAACGGCGTGGTTACG	879
QY	859	GAATACAGCTACGAACCGGAAACCCAAACGGCTTATCGGCATTACCACTACGCC-----	910
DB	880	GAGTACAGTTATGAGCGGGAACCTCAACGCTCTGATAGGTATCACCACCGCGGTGCGAA	939
QY	911	----GTCCATCAGACGCCCAAGGTGTTCGAAGACCTTACGCTATCAATATGACCCAGTAGGC	966
DB	940	GGGAGTCAATCAGGAGCCAGAGATTTCAGGAGTATACGCTATAAGTATGATCCGGTGGG	999
QY	967	AATGTCATTAAATATCGTAAATGATCGGAAGCCACTCGCTTTTGGCGCAATCAGAAGTA	1026
DB	1000	AATGTTATCAGTATCCATTAATGATCCGAAGCTACCCGCTTTTGGCGTAAATCAGAAGTG	1059
QY	1027	GCCCCGAGATAGCTATATACCTACGATTCCTGTATCAGCTTATCAGCGCACCGGCGC	1086
DB	1060	GAGCCGAGAAATCGCTATGTTTATGATTCTCTGTATCAGCTTATGATGCGACAGGCGT	1119
QY	1087	GAATGGCCAAATATCGGTGAGCAAAACAAACCAACTTCCTCCCTG-----CGCTACCT	1140
DB	1120	GAATGGCTAATATCGGTGAGCAAAACCAACTTCCTCCCTCACCCTTATACCTGTCTCT	1179
QY	1141	TCTGACAAATACCTTACCTAATCTCTCCGAGCTACAGCTATGATACAGTGTGTAAT	1200
DB	1180	ACTGACGACAGCATTTATACCAATTAACCTTCGTACCTATATCTTATGACCGTGGCGTAAT	1239
QY	1201	CTGACGCAAAATTCGCGACAGCTCGCCAGCTACCCAGAAACATACACCGTGGCTATCAC	1260
DB	1240	TGGTTCAAATTCGACACAGTTTACCCGCGACTCAAAATAGTTTACACACAGATATCAC	1299
QY	1261	CTCTAAACCGCAGCAATCGGGGTGTTCTCAGTACGCTAACCAACCGATCCAAATCAAGTG	1320
DB	1300	GTTCACGCGCAGTAACCGGCGGTATTGAGTGACATAACGACAGATCCAAACCGAGTG	1359
QY	1321	GATACGTTTGTGTCGCGTGTTCACCAACCGAGTTTATACCCGCGACAGACATATATC	1380
DB	1360	GATGCGCTATTGATTTCCGCGCGTCTATCAGAAGATGTTAATACCGGGGCAAAATCTGGAT	1419
QY	1381	TGACACCAACGAGGAGATTAAAGCAGGT-----TAATATGCGCCGGGA	1425
DB	1420	TGGAATATTCGGGTGAAATTGCACGAGTCAACCGGTGACCGTGAATAATAGCAGTGAC	1479
QY	1426	AATGAGTGTGTCGCTTACGACAGCAACGGCATGAGCAAACTGAAAGTGTGAGTAACGCCA	1485
DB	1480	AGTGAATGTATGCTATAGCAGTGATGCGCTGCTAAAGTGTGAGTGAACAGCAG	1539
QY	1486	ACCGAATATCTACGACAGCAACCGGTAATCTATTTCGCGGACTGAGGCTACGCACA	1545
DB	1540	ACGGGCAACAGTACTCAAGTACAAACGGGTGACTTATCTGCGGGATTAGAGCTACGGACA	1599
QY	1546	ACCGAGCAACCGCCACAAACGGAAGATTACAGTTATCACCTCGGTGAAGCGGT	1605
DB	1600	ACTGGGGTTGCAAGTAATAAACCCGAGATTTGCGAGTGAATACGGTAGTGAAGCGGT	1659
QY	1606	CGCGCACAGTACGGGTGTGCACTGGGAGAGCGGTAAAGCCAGAAAGTGTCAACAATAT	1665
DB	1660	CGCGCACAGTAAAGGTTATTCACCTGGGAAAGTGTGTAAGCCGACAGATATTGACAAAT	1719
QY	1666	CAACTAGCTTACGCTACGATTAATCTGATCGGCTCCAGCCAGCTTGAACCTGGACAACAA	1725
DB	1720	CAGGTGCGCTACAGCTACGATTAATCTGTTGGTCCAGCCAGCTTGAACCTGGATAGCGAA	1779
QY	1726	GGACAAATTTACGCGGAGGAAGTATTATCCATTTTGGGGGACAGCGCTGCGGACGA	1785
DB	1780	GGCAGATTCTCAGTCAGGAAGAGTATTATCCGTATGGCGGTACGGCGATATGGCGGCG	1839
QY	1786	AACAGCAACCAAGACCGCTATATAAAGTATTCGCTATTTCGGCAAAAGAACGAGATGCC	1845
DB	1840	AGAAATCAGACAGAGCCAGCTACAAATTTATTCGTTACTCCGGTAAAGACCGGATGCC	1899
QY	1846	ACCGGTTGTATTATTCAGGTTATCGTTATACCAACCGTGGCGGCGAGATGTTAAGC	1905
DB	1900	ACTGGATTGTTATTTACGCTACCGTATTATCAACCTTGGGTGGGTGCGATGCTTGA	1959

QY 1666 CAACTACGTTACAGCTACGATATCTGATCGGCTCCAGCGAGCTTGAACTGGCAACCAA 1725
Db 1720 CAGGTGGCTACAGCTACGATATCTGCTGGCTCCAGCGAGCTTGAACTGGATAGCGAA 1779
QY 1726 GGAACAATATACAGCGAGGAGGATATATCCATTTTGGCGGACAGCGCTGGCGCAGCA 1785
Db 1780 GGGCAGATTCTCAGTCAGGAGGAGGATATATCCGATATGGCGGTACGCGGATATGGCGCGG 1839
QY 1786 AACAGCAAAACAGAACGACGCTATATAAAGATTTCGCTATTTCCGGCAAAAGAACAGATGCC 1845
Db 1840 AGAATCAGACAGAACGACGCTACAAATTTATTCGTTACTCCGGTAAAGAGCGGGATGCC 1899
QY 1846 ACCGGTTGTTATTAACGTTATCGTTATACCAACCGTGGCGCGGACAGATGGTTAAGC 1905
Db 1900 ACTGGATTGTTATTAACGCTACCGCTTATTAATCAACCTTGGGTGGTCCGATGGTTGAGT 1959
QY 1906 GCGGACCGCGCAGAACCAATGATGGCTGGAATCTATACGAATGGTGAAGAAATATCCT 1965
Db 1960 GCTGATCCGCGCGGAACCGTGGATGGCTGAATTTGTACCGAATGGTGAAGAAATACCCC 2019
QY 1966 GTGAGTTTACAGATGAAATGATGATTAGCGCC 1997
Db 2020 ATCAGATTGACTGACCATGACGATGACACC 2051

RESULT 12
US-10-706-424-13
; Sequence 13, Application US/10706424
; Publication No. US20040103455A1
; GENERAL INFORMATION:
; APPLICANT: ffrrench-Constant, Richard
; APPLICANT: Waterfield, Nicholas
; TITLE OF INVENTION: DNA Sequences from tcd Genomic Region of Photorhabdus luminescens
; FILE REFERENCE: 62878
; CURRENT APPLICATION NUMBER: US/10/706,424
; CURRENT FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 2850
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2847)
US-10-706-424-13

Query Match 34.9%; Score 957.2; DB 7; Length 2850;
Best Local Similarity 68.6%; Pred. No. 3.1e-238;
Matches 1398; Conservative 0; Mismatches 598; Indels 42; Gaps 4;
QY 21 AATTGACCAAGACCCCTCGATTAAAGTTATGATTAACAGGAAATTAATGTCGTAC 80
Db 21 ACTTTATCAATACAGCCCAACCGTTAAAGTCTACGATAACCGTGGCTGACCAATCGTAA 80
QY 81 TTTAGAAATCTACGCACTCAAGCTCAGCAAAACAGTGATGAATTAATACGTTCTATGA 140
Db 81 CATCGACTTTCACCGTGACGTCGCGGAGCGGATACAGATCTCGTTATACCGCCACCA 140
QY 141 GTTCAATATTCGGGATTTTCAGTAAAGAACCGATCTCTCGTA-----A 185
Db 141 ATATGATACCCGAGGACACTTGAGCCAAAGCAATGATCCACGGCTGTATGACGCCAAACA 200
QY 186 AAATAAAACAGAGCGGCCAAATTTTCATCTGTCTTTAATCTTGGCGGTCAAGTTT 245
Db 201 AACCAATACTCAGCAAAACCCCAACTCTCTCGGCAATACAACTCTCACCGGCACACTT 260
QY 246 ACCTGAAGAAAGTTGATCGCGGTGGACTATTTACCTCAATGATATTGAAAGTCGCC 305
Db 261 GCGACAGAAAGTGTGATCGCGCGGCTACCGTAGCCCTCAATGATATTGAAGCGCTCA 320
QY 306 GGTGTTGATCATCAATGCAACCGGTGTCCGCCAAACCATCGTTATGAAGATAACCCCT 365

Db 321 AGTGTGATTGTAAACCGCAACCGCGGCCATTTCAGACCCGACCAATATGAAGCCAATACCT 380
QY 366 TCCCGGTCTGCTGCTGCTATCACCGAAACAAGTACAGGCGAGGAGAAAC-----GAC 419
Db 381 GCCCGGTCTGCTATTTATCGTAAAGTGAACAAGCCCGGAGAACAGACTCCCGCGCTTAC 440
QY 420 CGAAACGCTTTATCTGGCGCGCAATACGCGCGCAAGAAAGATTACAACTTCGCCCGGTCA 479
Db 441 TGAGCATTTTATTTGGGCTGGTAAATACACAGCGCGGAGAAAGATCATATCTTTGCCGCGCA 500
QY 480 GTGTGTCGCCATTAAGTATACCGCGGACTTACTCAACTCAATAGACTTTCTCTGCTGCTG 539
Db 501 GTATGTCGCCACTACGACACAGAGGAGTACGCAACTGGAAAGCCTGTCTATTGACAGA 560
QY 540 CGTGTGCTATCACAACTCTCAACACTGTCTTACCAGATAACCCAGGATGCCGACTGGACAGG 599
Db 561 AAACATCTTATCTCAATCCCGTCAGTTATTACCGCGCTCAGGAAGCAGACTGGACAGG 620
QY 600 TGAAGACAGAGCCTCTGGCAACAAAACTGAGTAGTGTCTATATACCCCAAAGTAA 659
Db 621 TAAAGATGAACCTCTCTGGCAGACCAAACTCAATAGCGAAACTTACACGACACAAAGCAC 680
QY 660 CACTGATGCCACCGGGCTTTACTGACCCAGACCGATGCCAAGGCCAAACATTCAGCGGCT 719
Db 681 CTTTGATGCTACCGCGCTTTGCTGACCCAAACCGGATGCAAAAGGCCAAATGCAACGCTCT 740
QY 720 GGCCTATGATGTGGCGCGGCGAGCTAAAGGGAGTTGGTTAAACACTCAAAGGTTCAGCGGA 779
Db 741 GGTTCACACGTGGCAGGACCAATTACAGGTAGTGGCTGACATTTGAAAACCAAGTGA 800
QY 780 ACAGGTGATTATCAATCGCTAACTCTCCCGCGCGCGGCAAAAATTCGTGAAGAGCA 839
Db 801 GCAAGTCAATTGCAATCCCTGACCTATTCCCGCGCAGCGCCAGAAATTCGCGTGAAGACA 860
QY 840 CGGTAAAGGATGTCTACGTAATACAGCTACGAAACCGGAACCCCAAGCGCTTATCGGCAT 899
Db 861 CGGTAAAGGCTTATCAGTGAATACAGCTATGAACCGGAACCTCTACGATTTGATCGGTAC 920
QY 900 TACCCTCGCCGCTCAATCAGAGCGCAAGGTGTGCAAGACCTACGCTATCAATATGACCC 959
Db 921 CACTACTCGCGCTCAATCAGATAGCAGAGGTGTTACAGATCTACGCTATGACATGATCC 980
QY 960 AGTAGCAATGTCAATTAATATCCGTAATGATGCGGAAGCCACTCGTTTGGCGCAATCA 1019
Db 981 TGTAGGGAATATTTAGTGTCCGTAATGATGCAAGAGCCACCCGCTTCTGGCGCAATCA 1040
QY 1020 GAAAGTAGCCCGGAGATAGCTATACCTACGATTCCTGTTCCCTGTATCAGCTTATCAGCCAC 1079
Db 1041 GAAATATAGTCCCTGAAAATACCTACACCTACGATTCCTGTTATCAGCTTATCAGTCAAC 1100
QY 1080 CGGGCGGAAATGGCCCAATATCGGTGAGCAAAACCAACCACTTCCCTCCCT-----TGC 1133
Db 1101 AGACGTGAGATGGCTAAACATCGGCAGCAAGCAACCAACTTCTTCGCAATCATCCC 1160
QY 1134 GGTACCTCTGACCAACAATACCTTACATACTATCTCGCAGCTACAGCTATGATCAGAG 1193
Db 1161 TCTTCCTACTGATGAAACTCATATACCAACTATATCTCGCAGCTATAATTTACGATCGCG 1220
QY 1194 TGGTAATCTGACGCAAAATTCGGCAGACAGCTCGCCAGCTACCCAGAAACAACTACACCGTGC 1253
Db 1221 CGGCAATTTGGTTCAATCCGGCAGACTTCCCGCGCGCCCAAAATTAACCTACACCAACA 1280
QY 1254 TATCACCTCTCAAAACCGCAGCAATCGGGGTGTCTCAGTACGCTAACCAACCGATCCAA 1313
Db 1281 TATCCCGTTTGAATCGCAGTAAACCGGCAAGTGTGAGTTGCTGATCTCAGACCCAC 1340
QY 1314 TCAAGTGGATAGCTGTTTGTATCGCGGTGGTCAACCAACAGTTTATTTACCGGACAGAC 1373
Db 1341 ACAGGTGGAGGCACGTGTTGATCGCGCGGACATCAACAAATTTCTTTACCGGGCAAGA 1400
QY 1374 ACTTATCTCGACACCAAGGAGGTTAAAGCAGGTTA-----ATAATGG 1418

Db 1401 GCTGAGTTGGAATACACGAGGTGAACATAAAGAGGTAAAGCCAGTCAAGTCGCGAGAGCGC 1460
Qy 1419 CCCEGGAAATGAGTGGTACCGCTACGACAGCAACGCGCATGAGACAACCTGAAAGTGAGTGA 1478
Db 1461 CAGCGATCGGGAATGGTATCGTTACCGCAACGACGCGCATCGACGGTTAAAGGTCAAGTGA 1520
Qy 1479 ACAGCCAAACCCAGAAATCTACGACAGCAACACCGGTAATCTATTGCGCGGACTGGAGCT 1538
Db 1521 GCAACAGACTGGCAAGCAGCAGCAGCAAGCAAGCAAGTAACTTATCTCCGATCTGGAGCT 1580
Qy 1539 ACACCAACCCAGAGCAACGCCCAACCAACAGCAAGAGTATACAGTATACACCTCGGTGA 1598
Db 1581 ACGTACAACAACAAATGGGACTACTACATCAGAGAGCTGCTGATCTATTACCGTGGAGC 1640
Qy 1599 AGCGGTGGCGACAGGTACGGGTGGTGGCTGGAGAGCGGTAAAGCCAGCAAGATGTCAA 1658
Db 1641 AGCAGGCCACGCAACAGTGGGAGTTCTACACTGGGAACACTACGCCACACCGCGGTATCAA 1700
Qy 1659 CAATAATCAACTAGCTTACAGCTACGATAATCTGATCGGTCCAGCCAGCTTGAACCTGGA 1718
Db 1701 TAACAATCAGCTTCGCTATAGCTATGATTAATTTGATTTGGTTCAGTCAACTTGAACCTGGA 1760
Qy 1719 CAACCAAGGCAAAATATACGCGAGGAGAGTATTAATCCATTTGGCGGACAGCGCTGTG 1778
Db 1761 TAACGAGGACAAATATCAGTCAGGAAGAGTATTAATCCATTTGGCGGACAGCATTTATG 1820
Qy 1779 GGCAGCAACAGCAACAGAGCCAGCTATAAAGCAATTCGCTATTCGCGCAAGAACG 1838
Db 1821 GGCAGCAAGAAACCAATAGAGCCAGCTACAAATCCCTCGTTACTCAGGTAAAGAACG 1880
Qy 1839 AGATGCCACCGGTGTGATTATTAATACGGTTATCGTTATTATCCAAACCGTGGCGGCGCAGATG 1898
Db 1881 CGATGCTACCGGCTCTATTATACGGCTACCGCTATTATACCGGCTGGGTGGTGGTGGT 1940
Qy 1899 GTTAAGCGCGGACCGCGCAGGAAACATTGATGGGCTGAATCTATACCGCAATGGTAAGAAA 1958
Db 1941 GTTAAGCGCGGATCCGCTGGAACAACTGATGGACTGAATCTATACCGGATGGTGAAGAA 2000
Qy 1959 TAATCCTGTGAGTTTACAAGTGAATGAATGATAGCCGCAAGAAAGGGAATATACC 2016
Db 2001 TAATCCGTCACACTGGTTGATATTTCTGGGCTTGACACTACGAAATACAAATATTCCTCC 2058

RESULT 13

US-10-609-113-47
; Sequence 47, Application US/10609113
; Publication No. US20040110184A1
; GENERAL INFORMATION:
; APPLICANT: Bintrim, Scott
; APPLICANT: Bevan, Scott
; APPLICANT: Zhu, Baolong
; APPLICANT: Merlo, Donald J.
; TITLE OF INVENTION: Pesticidally Active Proteins and Polynucleotides Obtainable from
; TITLE OF INVENTION: Paenibacillus Species
; FILE REFERENCE: DAS-101XC2
; CURRENT APPLICATION NUMBER: US/10/609,113
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US 60/392,633
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/441,647
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47
; LENGTH: 2850
; TYPE: DNA
; ORGANISM: Photorhabdus strain W14
US-10-609-113-47

Query Match 34.9%; Score 957.2; DB 7; Length 2850;
Best Local Similarity 68.6%; Pred. No. 3.1e-238;
Matches 1398; Conservative 0; Mismatches 598; Indels 42; Gaps 4;

Qy 21 AATTGACCAAGACCCCTCGATTAAAGTATTAGATAAAGAGGAAATTAATGTACGTAC 80
Db 21 ACTTTATCAACATACGCCACCGTTAAACGCTTACGATTAACCGTGGCTGACCAATTCGTAA 80
Qy 81 TTTAGAAATATCTACGCACCTCAAGCTGACGAAACAGTGATGAATTAATATACGTTCTATGA 140
Db 81 CATCGACTTTACCGTGACGCTGCGGGAGCGATACAGATACTCGTATTACCGGCCACCA 140
Qy 141 GTTCAATATTCGGGATTTTCAGGTAAAGACCCGATCTCTGTA-----A 185
Db 141 ATATGATACCCGAGGACACTTGAGCCAAAGCATTTGATCCACGGCTGTATGACGCCAAACA 200
Qy 186 AAATAAAACACAGCGCGCCAAATTTCAATTCGTGCTTTAAATCTTGGCGGTCAAGTTTT 245
Db 201 AACCAATTAATCGAACAACCCCACTTCTCTGGCAATACATCTCACCGGCGACACTTT 260
Qy 246 ACGTGAAGAAAGTTGTTGATCGCGGTCCGACTATTACCCCTCAATGATATTGAAAAGTCGCC 305
Db 261 GCGGACAGAAAGTGTGATGCGCGGTACCGTAGCCCTCAATGATATTGAAAGCCGTCA 320
Qy 306 GGTGTTGATCATCAATGCAACCGGTCTCGGCCAAACCATCGTTATGATAGATTAACACCT 365
Db 321 AGTGTGATTTGTAACCGCAACCGCGCCCAATTCAGACCCGCAATATGAAAGCCAATACCT 380
Qy 366 TCCCGGTGCTGCTCGCTATCACCGAAACAAGTACAGGAGGAGAGAAAC-----GAC 419
Db 381 GCCCGGTGCTTATTATCGTAAAGTGAACAAGCCCCGGGAGACAGACTCCCGCGCTTAC 440
Qy 420 CGAACGCTTTATCTGGCGCGCAATACGCGCAAGAAAGAAAGATTACAACCTCCCGCGTCA 479
Db 441 TGAGCATTTTATTTGGCTGGTAAATACACAGGCGGAGAAAGATCATATAATCTTCCGCGCA 500
Qy 480 GTGTGCGGCATTACGATACCGCGGACTTACTCAACTCAATAGCTTTCTCTGCGTGG 539
Db 501 GTATGTCGCGCACTACGACACAGCAGGAGTGACCAACTGGAAAGCCTGTGATTGACAGA 560
Qy 540 CGTGTGCTATCACAATCTCAACAACTGCTTACCGATTAACAGGATGCGGACCTGGACAGG 599
Db 561 AAACATCTTATCTCAATTCGGTCAGTTTATAGCCGAGCGGTGAGGAGCAGCTGGACAGG 620
Qy 600 TGAAGACCAAGAGCTCTGGCAACAAAGAACTGATGATGTCTATATATCAACCAAGTAA 659
Db 621 TAACGATGAACCCCTCTGCGAGACCAAACTCAATAGCGAAACTTACAGCACACAAAGCAC 680
Qy 660 CACTGATGCCACCGCGGCTTTACTGACCCAGACCGATGCCAAGGCAACATTCAGCGCT 719
Db 681 CTTTGTGTCACCGCGCTTTGCTGACCCAAACCGATGCAAAAGGCAACATGCAACGCTCT 740
Qy 720 GGCCTATGATGTCGCGGCGAGCTAAAGGGAGTGTGTTAACTCAAAAGCTCAGGCGGA 779
Db 741 GGCTTACAGCTGGCAGGACAAATTACAGGTAGCTGGCTGACATTTGAAAACCAAGTGA 800
Qy 780 ACAGGTGATTATCAAAATCGCTAACTTACCTCGCGCGCGGCAAAAAATACGTGAAGACA 839
Db 801 GCAAGTCATTGTCAAATCCCTGACCTATTCCCGCGGAGCCAGAAATTTGGGTGAAGAAC 860
Qy 840 CGGTAAACGGGATTTGCTCACTGAATACAGCTACGAAACCGGAAACCAACCGGCTTATCGCAT 899
Db 861 CGGTAAATGGGTTTATCACTGAATACAGCTATGAAACCGGAAACCTCTACGATTTGATCGGTAC 920
Qy 900 TACCACTCGCGCTCCATCAGACCCCAAGGTGTTGCAAGACCTACGCTATCAATATGACCC 959
Db 921 CACTACTCGCGCTCAATCAGATAGCAGGTGTTACAAGATCTACGCTATGACATGATATCC 980
Qy 960 AGTAGGCAATGTCAATTAATATCGTAAATGATGCGGAAGCCACTCGCTTTTGGGCGCAATCA 1019
Db 981 TGTAGGGAATATTATTAGTGTCTCGTAAATGATGAGAAAGCCACCGCTTCTGGGCGCAATCA 1040
Qy 1020 GAAAGTAGCCCGGAGAAATAGCTATACCTACGATTCCTGTATCAGCTTATCAGCGCCAC 1079
Db 1041 GAAAAATAGTCCCTGAAAAATACCTACACCTACGATTCCTGTATCAGCTTATCAGTGAAC 1100
Qy 1080 CGGGCGGAAATGGCCAAATATCGTTCAGCAAAAAACAACCAACTTCCCTCCCC-----TGC 1133

Db 1101 AGGACGTGAGTGGCTAAACATCGCGCAGCAAGCAACCAACTTCCTTCGCGCAATATCCC 1160
Qy 1134 GCTACCTTCTGACAAACAATACCTACACTAATCTACTCGCAGCTACAGCTATGATCACAG 1193
Db 1161 TCTTCCTACTGATAAATCTATATACCACTATATCTCGCAGCTAATATACGATCGCG 1220
Qy 1194 TGGTAATCTGACGCAATTCGGCAGCTCGCCAGCTACCGAGAACAACTACACCGTGGC 1253
Db 1221 CGGCAATTTGGTTCAAAATCGGCACAGTTTCCCGCGCGCCAAATAAATCTTACACCA 1280
Qy 1254 TATCACCTCTCAACCGCAGCAATCGGGTGTCTCAGTACGCTAACCAACCGATCCAA 1313
Db 1281 TATCACCGTTTGAATCGCAGTAACCGGCGAGTGCTGAGTTGCTTAACCTCAGACCCA 1340
Qy 1314 TCAAGTGGATACCTGTTGATCCCGTGGTCAACAAACAGTTTATTTACCCGACAGAC 1373
Db 1341 ACAGTGGAGCACTGTTGATCCCGCGGACATCAACAAATTTGTACCGGGCAAGA 1400
Qy 1374 ACTTATCTGGACACCGAGGAGTTAAAGCAGTTA-----ATAATGG 1418
Db 1401 GCTGAGTTGAATACACGAGGTGAACCTTAAACAGGTAAACGCCAGTCAGTCGCGAGAGCGC 1460
Qy 1419 CCCGGGAATGAGTGTACCGCTACGACAGCAACGCGCATGAGACAACTGAAAGTGATGA 1478
Db 1461 CAGCGATCGGGAATGTTATCGTTACGGCAACGACGCGCATGCGAGCTTAAAGTCAGTGA 1520
Qy 1479 ACAGCCAAACCCAGAACTACTACGAGCAACAAACGGGTAATCTATTTCGCGGACTCGAGCT 1538
Db 1521 GCAACAGACTGGCAACGACGAGCAGCAACAGTAATCTTCTCCGATCTGAGCT 1580
Qy 1539 ACGCAACACCCAGAGCAACGCCCAACAAACGGAAGATTTACAGTTATCACTCGGTGA 1598
Db 1581 ACGTACAAACAAATGGGACTACTACATCAGAAGACCTGCTATTTACCGTGGAGC 1640
Qy 1599 AGCGGTGGGCAAGTACGAGTACGGGTGTTGACTGGGAGCGGTAAAGCCAGAAATGCAA 1658
Db 1641 AGCAGGCCACGCAAGTGGAGTTCTACACTGGGAAACTACGCCACCGCGGTATCAA 1700
Qy 1659 CAATAATCAACTACGTACAGTACGATATCTGATCGGCTCCAGCGAGCTTCAACTGGA 1718
Db 1701 TAACAATCAGCTTCGCTATAGCTATGATAATTTGATTTGTTGCTCAGTCAACTGACTGGA 1760
Qy 1719 CAACCAAGGACAAATATACGAGGAGGAGTATATCCATTTGGCGGACAGCGCTGTG 1778
Db 1761 TAACGAGGACAAATATCAGTCAGGAGAGTATATCCATTTTGGCGGACACGATATG 1820
Qy 1779 GGAGCAACAGCCAAACAGAACGCGAGCTATAAACGATTCGCTATTCGGGAAAGACG 1838
Db 1821 GGCAGCAAGAAACCAATAAGCCAGCTACAAATCTCTCCGTACTCAGGTAAAGAACG 1880
Qy 1839 AGATGCCACCGGTGTTATTTATACGTTATCGTTATTTATCAACCGTGGCGGCGAGATG 1898
Db 1881 CGATGCTACCGGCTCTATTATTTACGCTACCGCTATTATTCAGCGTGGGTTGTTAGGTG 1940
Qy 1899 GTTAAGCGCGGACCGGACGAGAACATTGATGGGCTGAATCTATACCGAATGTTAAGAAA 1958
Db 1941 GTTAAGCGCGGATCGGCTGGAACATCGATGAGTGAATCTATACCGGATGTTGAGAAA 2000
Qy 1959 TAATCTGTGAGTTTACAGATGAATAATGAGTTAGCGCCAGAAAAGGGAATAATACC 2016
Db 2001 TAATCCGTCAACACTGTTGATATTTCTGGGCTTGCACTACGAAATACAAATATTTCC 2058

RESULT 14

US-10-754-115-50
; Sequence 50, Application US/10754115
; Publication No. US20040208907A1
; GENERAL INFORMATION:
; APPLICANT: Hey, Timothy
; APPLICANT: Schleper, Amanda
; APPLICANT: Bevan, Scott
; APPLICANT: Bintrim, Scott

; APPLICANT: Mitchell, Jon
; APPLICANT: Li, Ze Sheng
; APPLICANT: Ni, Weiting
; APPLICANT: Zhu, Baolong
; APPLICANT: Merlo, Don
; APPLICANT: Apel-Birkhold, Patricia
; APPLICANT: Meade, Thomas
; TITLE OF INVENTION: Mixing and Matching TC Proteins for Pest Control
; FILE REFERENCE: DAS-104XCI
; CURRENT APPLICATION NUMBER: US/10/754,115
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US 60/441,723
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50
; LENGTH: 2889
; TYPE: DNA
; ORGANISM: Xenorhabdus bovienii
; US-10-754-115-50

Query Match 26.6%; Score 730.8; DB 8; Length 2889;
Best Local Similarity 63.9%; Pred. No. 3.5e-179;
Matches 1170; Conservative 0; Mismatches 632; Indels 30; Gaps 3;

Qy 235 GGTCAAGTTTTACGTGAAGAAAGTTGATGTCGGCTCGGACTATTACCTCAATGATATT 294
Db 247 GGTGATGTCTACGGACAGAGAGTGTGGATGCGCGACAAACTGTCTATTTTGTAGTGACATC 306
Qy 295 GAAAGTCGCGCGGTGTTGATCATCAATGCAACCGGTGTCGCCAAACCATCGTTATGAA 354
Db 307 GAAGTGTGTCGCTTACTGAATATCAGTGGATGGGTGTCGTCAAACACTGGCAANTATGAA 366
Qy 355 GATAACACACCTTCCCGTCTGCTGCTATCACCGAAC-----AAGTACAGGAGCA 408
Db 367 GAGAGTACATTGCGGGGCGCTTGTCTGCTGTCAGTGAACGGGAAGATGAGGCTTCAACA 426
Qy 409 GAGAAACGACCGAAGCTTTATCTGGGCGGCAATACGCGGCAAGAAAAGATTACAAC 468
Db 427 CCCAAATATTGACCGGTTTATTTGTGCGGAAATAGCCCATCAGAAAAAGATCACAAT 486
Qy 469 CTGCGCGTCAAGTGTGTCGCCCATACGATACCGCGGACTTACTCAACTCAATAGCCTT 528
Db 487 TTGGCGGAAAAATATCTTCGTATATGATATACCGCGGATTAACACAGCTTAATGCTGTG 546
Qy 529 TCTCTGCTGGGCTCGCTGCTATCACAACTCTCAACAACTGCTTACCGATACAGGATGCC 588
Db 547 TCTCTGACAGCGTGTGATCTCTACAACTCCCGTCACTTATTCAGGATGATGTCACAGCA 606
Qy 589 GACTGGACAGGTGAAGACCGAGAGCTCTGGCAACAAAACTGATGATGATGCTATATC 648
Db 607 GATTGAGCGGAAGTGAAGTCCAGTGGAGACGCACTGAGTAACGACATATTCACA 666
Qy 649 ACCCAAGTAACTGATGATGCCCGGGCTTTACTGACCGACCGGCTGCGCAAGCAAC 708
Db 667 ACCGAAATCACCGCTCACTGCGTGGCAATTTCTGACTCAGAAATGATGCGCAAAAGCAAC 726
Qy 709 ATTACGCGCTGGCTTATGATGCGCGGCGAGCTAAAAGGGAGTTGGTTAAACACTCAAA 768
Db 727 CAGCAACGATTGCTTATGATGCGGAGGAGTAAAGGCAAGCTGGCTGACGNTAAAA 786
Qy 769 GGTTCAGCGGAAACAGGTGATTAATCAAACTCGTTAACTTCTCCCGCGCGGCAAAATTA 828
Db 787 GGCCAGATGAGCAGGTGATGTTAACTCCCTGACTTACTCCCGCGCGGAGGAACTG 846
Qy 829 CGTGAAGACGCGTAAACGGGATGTCAGTCAAGTACAGTACGAAACCGGAAACCAACGG 888
Db 847 CGTGAAGAGCAGGTTAACCGGTTGTCTCTGAAATCTCTCTATGAAGCACAACCTCGCGT 906
Qy 889 CTTATCGGCAATACCACTCGCGTCCATCAGACCGCAAGGTGTTGCAAGACCTTACGCTAT 948
Db 907 TTGATAGGTGTAACGGCTTACCCTGCTCAGTCAAGTAAAAAAGATTGCAAGGATCTTGTCTAT 966

Qy 949 CAATATGACCCAGTAGGCAATGTCTTAATATCGTAATGATCGGAAGCCACTCGCTTT 1008
Db |||||
Qy 967 AACTATGATCGGTGCGTAATCTCTGTAATTCGCAATATCGAGAGCAACCCGTTTC 1026
Db |||||
Qy 1009 TGGCGCAATCAGAAAGTAGCCCGAGAAATAGCTATACCTACGATTCCTGTATCAGCTT 1068
Db |||||
Qy 1027 TGGCGTAATCAGATAGTAGAACACAGAGAACCACTATGCTTATGACTCGCTTATCAACTC 1086
Db |||||
Qy 1069 ATCAGGCCACCGGGCGGAAATGGCCAATATCGGTGAGCAAAACAACCACTTCCCTCC 1128
Db |||||
Qy 1087 ATCAGTCTAGTGTGTCAGAAATCGCCAGTATCGGTGAGCGGCGCGCTGCCTGTA 1146
Db |||||
Qy 1129 CC-----TGGCTTACCTTCTGACAAACAATACCTACACTAACTATCTCGCAGCTACAGC 1182
Db |||||
Qy 1147 CCGATTATCTCTTCTGCAATGACGATGTTTATCTGCTACACCCGCAATATCAC 1206
Db |||||
Qy 1183 TATGATCACAGTGTGTAATCTGACCAAAATTCGGCACAGCTCGCCAGCTACCCGAAACAAC 1242
Db |||||
Qy 1207 TATGATCGCGTGGAAATCTCTGCCAGATCGGCATTTGGCTCCTGTACAGATAATAAG 1266
Db |||||
Qy 1243 TACACCGTGGGTATCACCTCTCAACCGCAGCAATCGGGGTGTTCTCAGTACGCTAAC 1302
Db |||||
Qy 1267 TACACCAAAAGATCACCGTATCGAATCGTAGTAATCGTGCAGTATGGGATACCTTGACC 1326
Db |||||
Qy 1303 ACCGATCCAAATCAAGTGGATACGTTGTTGATCGCGGTGTCAACAAACCAAGTTTATTA 1362
Db |||||
Qy 1327 ACAGATCCGCCAAAGTGGATACCTCTGTTTATCATGAGGGGCATCACTTCAACTCCAG 1386
Db |||||
Qy 1363 CCCGACAGACACTTATCTGTGACACCAACGAGGAGGTTAAAGCAGGTTA----- 1411
Db |||||
Qy 1387 TCAGGCCAGACTTATGTTGGAACCTATCGGGTGAACCTACAGCAAAATAACAAGATACAG 1446
Db |||||
Qy 1412 -----ATAATGCCCGGAAATAGAGTGTTACCGCTACGACAGCAACGGCATGAGACAA 1464
Db |||||
Qy 1447 CGTGACGAAAACCCGAGATAAAGAGCGGTATCGCTATGTTGTTGGGCTGCGCGGGTC 1506
Db |||||
Qy 1465 CTGAAAGTGAAGTGAACAGCCAAACCCAGAAATACTACGAGCAACACCGGTAATCTATTG 1524
Db |||||
Qy 1507 GTGAAATATCAGCACAGCAGCGGGGGAAGCAGCCATGTGCAGCGTGTGTTTATCTG 1566
Db |||||
Qy 1525 CCGGCACTGGAGCTACGCAACACCCAGAGCAACGCCCAACAACCGGAGAGTTACAGTT 1584
Db |||||
Qy 1567 CCGGGTTGGAATCTACGCAACACTCAGCATGATGGACATTAATCGAAGACTTACAGGTG 1626
Db |||||
Qy 1585 ATCACTCGGTGAAGCGCGTGGCGCAGGTACGGGTGTTGCACTGGGAGAGCGGTAA 1644
Db |||||
Qy 1627 ATATATGTTGAGTGAAGCAGGACGTCTCAGGTACGCGTACTTCAATGGGAAATACCACCA 1686
Db |||||
Qy 1645 CCAGAAGATGTCAACAATAATCAACTAGTTTACAGCTACGATAATCTGATCGGCTCCAGC 1704
Db |||||
Qy 1687 CCGGTAATCTTAACAATGACTACTGCGTTACAGCTACGATAGTTGATGGGTTCCAGT 1746
Db |||||
Qy 1705 CAGCTTGAATCGCAACAAGGCAAAATATACGCGAGGAAGATATTAATCCATTTGGC 1764
Db |||||
Qy 1747 CAGCTTGAATGGATGGAGCGGCAGATTATACGCGAGGAAGATACTACCCCTATGGA 1806
Db |||||
Qy 1765 GGGACAGCGCTGTGGGCAAGCAACAGCCAAACAGAGCCAGCTATAAAACGATTCGCTAT 1824
Db |||||
Qy 1807 GGTACAGCAATATGGCGGCAAGAAACAGACCCGAAGCCAAATTACAAACCAATTCGCTAC 1866
Db |||||
Qy 1825 TCCGCGAAGAACGAGATGCCACCGGTTGATTATTACGGTATTCGTTATTACCAACCG 1884
Db |||||
Qy 1867 TCCGCGAAGAGCGTATGCGACGGGGCTTTATTACTACGGGCACCGTTATTATCAGCCG 1926
Db |||||
Qy 1885 TGGCGGGCAGATGGTTAAGCGCGGACCCCGCAGGAACCAATTGATGGGCTGAATCTATAC 1944
Db |||||
Qy 1927 TGGCTAGGCGCTGTTGAGCGCAGATCCCGCGGAACCGTGGAGCGACTGAATCTATAT 1986
Db |||||
Qy 1945 CGAATGTAAGAAATAATCTCTGTGAGTTTACAAGATGAATAATGGAATTAGCCCGCAAAAA 2004
Db |||||
Qy 1987 CGAATGTTGAGGAATAAACCCGATTACTTACCGGATGAGATGGGCTTGCCTCGATAGGC 2046
Db |||||
Qy 2005 GGGAAATATACCAAGAGGTAATTTCTTTGA 2036

Db 2047 GATAAGATCAGCGAAGGGATTTATGAGCCTGA 2078
|||

RESULT 15

US-11-020-848-3
; Sequence 3, Application US/11020848
; Publication No. US20050155104A1
; GENERAL INFORMATION:
; APPLICANT: Apel-Birkhold, Patricia
; APPLICANT: Hey, Timothy
; APPLICANT: Sheets, Joel
; APPLICANT: Meade, Tom
; APPLICANT: Li, Ze Sheng
; APPLICANT: Lira, Justin
; APPLICANT: Russell, Sean
; APPLICANT: Thompson, Robin
; APPLICANT: Mitchell, Jon
; APPLICANT: Pencill, Kristin
; TITLE OF INVENTION: Toxin Complex Proteins and Genes from Xenorhabdus bovienii
; FILE REFERENCE: DAS-114XC1
; CURRENT APPLICATION NUMBER: US/11/020,848
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: US 60/534,893
; PRIOR FILING DATE: 2004-01-07
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3
; LENGTH: 2889
; TYPE: DNA
; ORGANISM: Xenorhabdus bovienii
US-11-020-848-3

Query Match 26.8%; Score 730.8; DB 10; Length 2889;
Best Local Similarity 63.9%; Pred. No. 3.5e-179;
Matches 1170; Conservative 0; Mismatches 632; Indels 30; Gaps 3;

Qy 235 GGTCAAGTTTACGTGAGAAAGTGTGATCCGGTCCGACTATTACCTCAATGATATT 294
Db |||||
Qy 247 GGTGATGTCCTACGGACAGAGATGTGGATGCCGGAACAACCTGTCTATTTGAGTGACATC 306
Db |||||
Qy 295 GAAAGTCGCCCGGTGTTGATCAATGCAACCGGTGTCGCCCAAAACCAATCGTTATGAA 354
Db |||||
Qy 307 GAAGTCTGTCGTTACTGAATATCAGTCGATGGTGTGTCGTCAAACACTGCGCAATATGAA 366
Db |||||
Qy 355 GATAACACCCCTCCCGTCTGTCGCTATCACCGAAC-----AAGTACAGGCGGA 408
Db |||||
Qy 367 GAGAGTACATTGCGGGGCGCTTGTCTGCTGTCAAGTGAACGGAAGATGAGGCTTCAACA 426
Db |||||
Qy 409 GAGAAACGACCGAAGCTCTTATCTGGCGCGCAATACGCCCAAGAAAAAGATTACAAC 468
Db |||||
Qy 427 CCCCATAATTGGAACGGTTTATTTGTCGGGAATAGCCCATCAGAAAAGATCACAAT 486
Db |||||
Qy 469 CTGCGCGGTCAAGTGTGTCCGCCATTACGATACCGCGGACTTACTCAACTCAATAGCCTT 528
Db |||||
Qy 487 TTGCGGGAAAAATATCTTCTCATATGATATACCGCGGATTAACACAGCTTAATGCTGTG 546
Db |||||
Qy 529 TCTCTGCTGGGTGCTGTCTATCAATCTCAACAACTGCTTACCGGATACCGAGATGCC 588
Db |||||
Qy 547 TCTCTGACCAAGCGTGGATCTCTCACAAATCCCGTCAGTTATTGCAAGATGATGTCACAGCA 606
Db |||||
Qy 589 GACTGGACAGGTGAGAACCAAGAGCCCTCTGGCAACAAAACTGAGTAGTGTCTATATC 648
Db |||||
Qy 607 GATTGGAGCGGAAGTAGACGAATCCAGTGGGAAGACGGGACTGAGTAACGACATATTCACA 666
Db |||||
Qy 649 ACCCAAGTAACACTGATGCCACCGGGCTTTACTGACCCAGACCGATGCCAAAGGCAAC 708
Db |||||
Qy 667 ACCGAATCACCGTGTGATGCGGTTGGCAATTTCTTGAATCAGAATGATGCCAAAGCAAC 726
Db |||||
Qy 709 ATTACGGCGCTGGCCTTATGATGGCCGGCAGCTTAAAGGGAGTTGGTTAACTCAAA 768
Db |||||
Qy 727 CAGCAACGATGTCTCTATGATGGGAGGGGAGTTAAAGGCAAGCTGGCTGACGATAAA 786
Db |||||

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QY 769 GGTGAGCGGAAACAGGTGATTATCAATCGCTAACCTACTCCGCGCGCGGCAAAATTA 828
Db 787 GGCAGAAATCAGCAGGTGATAGTAACTCCCTGACTTACTCCGCGCGGCGAGAACTG 846
QY 829 CGTGAAGAGCACGGTAAACGGGATTGTCACTGAATACAGCTACGAACCGGAACCCCAACGG 888
Db 847 CGTGAAGAGCAGGTAAACGGGTTGTCACTGAATACCTTATGAGCACAACCTGGCGT 906
QY 889 CTTATCGGCATTAACCACTCGCGCTCCATCAGAGCCCAAGGTGTGGAAGACCTACGCTAT 948
Db 907 TTGATAGGTGTAACGGCTTACCGCTCAGTCAGATAAAAAAGATTGCAGGATCTTGTCTAT 966
QY 949 CAATATGACCCAGTACGCAATGTCATTAATATCCGTAATGATGGAGACCACTCCGCTTT 1008
Db 967 AACTATGATCCGGTCGGTAATCTCCTGAATATTCGCAATTAATGCAGAGCAACCCCGTTTC 1026
QY 1009 TGGCGCAATCAGAAAGTAGCCCGGAGAAATAGCTATACCTACGATCCCTGTATCAGCTT 1068
Db 1027 TGGCGTAATCAGATAGTAGAACACAGAGAACCACTATGCTTATGACTGCTTATCACTC 1086
QY 1069 ATCAGCGCCACCGGGCGGAAATGGCCAATATCGGTGAGCAAAACCAACTTCCCTCC 1128
Db 1087 ATCAGTGTCTAGTGTGAGAAATCGCCAGTATCGGTGAGCAGGCGAGCGGCTGCCTGTA 1146
QY 1129 CC-----TGGGCTACCTTCTGACACAACATACCTACACTAACTATCTGCGAGCTACAGC 1182
Db 1147 CCGATTATTCCTCTTCTGCAATGACGATGTTTATATCTCGCTACACCCGACATATCAC 1206
QY 1183 TATGATCACAGTGTGTAATCTGACGCAAAATTCGCGACAGCTCGCCAGTACCCAGAAACAAC 1242
Db 1207 TATGATCGCGGTGGAATCTCTGCCAGATCCGGATTCGGCTCTGCTACAGATATTAAG 1266
QY 1243 TACACCGTGGCTATACCCCTCTCAAAACCGCAGCAATCGGGGTGTTCTCAGTACGCTAAC 1302
Db 1267 TACACCAAAAGATCACCGTATCGAATCGTAGTAATCGTGCAGTATGGGATACCTTGACC 1326
QY 1303 ACCGATCCAAATCAAGTGGATAGTGTGTTGATCGCGGTGGTCAACCAACCACTTTATTA 1362
Db 1327 ACAGATCCCGCCAAAGTGGATACCCCTGTTTGTATCATGGAGGGCATCAACTTCAACTCCAG 1386
QY 1363 CCGGACAGACACTTATCTCGACACACAGGAGAGTTAAAGCAGGTTA----- 1411
Db 1387 TCAGGCCAGACTTATGTTGGAACTATCGGGGTGAACTACAGCAATTAACAAAGATACAG 1446
QY 1412 -----ATAATGGCCCGGGAATGAGTGTGTACCGCTACGACAGCAACCGCATGAGACAA 1464
Db 1447 CGTGACGAAAAACCCGACAGATAAAGAGCGGTATCGCTATGTTGGGCTGCGCGGTC 1506
QY 1465 CTGAAGTGTAGTGAACAGCCCAACCCAGATACTACGAGCAACAACGGGTAAATCTATTGG 1524
Db 1507 GTGAAAATCAGCACACAGCAGGCGGGGGAAGCAGCCATGTGACGCGTGTGTTTATCTG 1566
QY 1525 CCGGACTGGAGCTACGCAACCCAGAGCAACCCACACACCAACGGAAGTTACAGCTT 1584
Db 1567 CCGGGTTTGAACCTACGCAACCTCAGCATGTGCGACATTAATCGAAGACTTACAGGTG 1626
QY 1585 ATCACACTCGGTGAAGCGGTGCGCACAGGTACGGGTGTTGCACCTGGGAGAGCGGTAAAG 1644
Db 1627 ATTATCATGGTGAAGCAGACGTGCTCAGTACGCGTACTTCAATGGGNAATACCACCA 1686
QY 1645 CCAGAGATGTCAACATAATCAACTACGTTACGTTACGATACGATATCTGATCGGCTCAGC 1704
Db 1687 CCGGATAATCTTAACAATGACTCACTGCGTTTACAGCTACGATAGTTGATGGGTTCCAGT 1746
QY 1705 CAGCTTGAACCTGACACCAACCAAGGACAAATTCAGCGAGGAGAGTATTTCCATTGGC 1764
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QY 1825 TCCGGCAAGAACAGAGATGCCACCGGGTTGTATTATTAACGTTTATCGTTATTACCAACCG 1884
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QY 1885 TGGCGCGGCGAGATGGTTAAAGCGCGGACCCGGCAGGAACCAATTGATGGGCTGAAATCTATAC 1944
Db 1927 TGGCTAGGGCGCTGTTGAGCGCGAGATCCGCGCGGAACCGTGGACGACTGAATCTATAT 1986
QY 1945 CGAATGCTAAGAAATAATCTCTGTGAGTTTACAAGATGAAAAATGAGTTAGCGCCAGAAAAA 2004
Db 1987 CGAATGCTGAGGAATAAACCCGATTACTTACCGGGATGSCAGATGGGCTTGGCGCGATAGGC 2046
QY 2005 GGGAAATATACCAAGAGGTTAAATTTCTTTGA 2036
Db 2047 GATAAGATCAGCAAGGGATTTATAGCCTGA 2078
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Search completed: December 14, 2005, 06:35:20
Job time : 1965 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 19:24:31 ; Search time 497 Seconds
(without alignments)

9817.720 Million cell updates/sec

Title: US-10-647-956A-5

Perfect score: 2745

Sequence: 1 atgagcagttacaattctgc.....taggaatcgaggagaacttca 2745

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA.*

- 1: /cgn2_6/ptodata/1/ina/1 COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2745	100.0	2745	3	US-09-817-514A-5
2	1012.4	36.9	37948	3	US-09-251-645-11
3	962	35.0	3132	3	US-08-851-567B-60
4	56.2	2.0	1039	3	US-09-302-540-1280
5	56	2.0	7218	2	US-08-232-463-14
6	47.4	1.7	147382	3	US-09-949-016-14624
7	46.6	1.7	612	3	US-09-302-540-1357
8	45.6	1.7	314798	3	US-09-949-016-13539
9	45.2	1.6	582	3	US-09-949-016-61868
10	45	1.6	94987	3	US-09-949-016-12510
11	45	1.6	96987	3	US-09-949-016-14429
12	44.2	1.6	1141	3	US-09-806-708B-22
13	44.2	1.6	4005	3	US-08-956-171B-631
14	44.2	1.6	4005	3	US-08-781-986A-631
15	44	1.6	19124	2	US-08-487-826B-13
16	43.4	1.6	640681	3	US-09-790-988-1
17	43.2	1.6	3945	3	US-09-200-650B-6
18	42.6	1.6	1827	3	US-09-270-767-1308
19	42.6	1.6	1837	3	US-09-270-767-16590
20	42.4	1.5	168575	3	US-09-426-290-1
21	42.2	1.5	1676	3	US-09-009-443-1
22	41.6	1.5	601	3	US-09-949-016-37135
23	41.6	1.5	601	3	US-09-949-016-16112
24	41.6	1.5	1350	3	US-09-248-796A-4759

ALIGNMENTS

RESULT 1

US-09-817-514A-5
; Sequence 5, Application US/09817514A
; Patent No. 6639129
; GENERAL INFORMATION:
; APPLICANT: firench-Constant, Richard
; APPLICANT: Bowen, David
; APPLICANT: Rocheleau, Thomas
; APPLICANT: Waterfield, Nicholas
; TITLE OF INVENTION: DNA SEQUENCES FROM PHOTORHABDUS LUMINESCENS
; FILE REFERENCE: 61645
; CURRENT APPLICATION NUMBER: US/09/817,514A
; CURRENT FILING DATE: 2000-03-26
; PRIOR APPLICATION NUMBER: US 60/191806
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 5
; LENGTH: 2745
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2745)
US-09-817-514A-5

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Db	61	AGGAAATTAATAGTACGTACTTTAGAAATATCTACGCACCTCAAGCTGACGAAACACGTGAT	120		
QY	121	GAATTAATACGTTCTATCAGTTCAATATTCGGGATTTTCAGGTAAAGACCGATCCT	180		
Db	121	GAATTAATACGTTCTATCAGTTCAATATTCGGGATTTTCAGGTAAAGACCGATCCT	180		
QY	181	CGTAAATAAATAAACACGAGCGGCCCAAAATTTTCATTCGTGCTTTTAAATCTTTCGGGTCAA	240		
Db	181	CGTAAATAAATAAACACGAGCGGCCCAAAATTTTCATTCGTGCTTTTAAATCTTTCGGGTCAA	240		
QY	241	GTTTTACGTGAAGAAAGTGTGATGCCGGTTCGCGACTATTACCTCAATGATATTGAAAGT	300		

Db	241	GTTTACGTGAGAAAGTGTGATGCGCGTGGAGCTATTACCCCTCAATGATATTGAAGT	300
Qy	301	CGCCCGGTGTTGATCATCAATGCAACCGGTGTCCGCCAAACCAATCGTTATGAAGATAAC	360
Db	301	CGCCCGGTGTTGATCATCAATGCAACCGGTGTCCGCCAAACCAATCGTTATGAAGATAAC	360
Qy	361	ACCCCTCCCGGTGCTGCTGCTGCTATCACCGAACAGTACAGGCAGAGAGAAACGACC	420
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Qy	421	GAACGCTCTTATCTCGGCGCGCAATACCGCCGCAAGAAAAGATTACAACTCGCCGGTCAG	480
Db	421	GAACGCTCTTATCTCGGCGCGCAATACCGCCGCAAGAAAAGATTACAACTCGCCGGTCAG	480
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Db	481	TGTGTCCGCATTAAGATACCGCGGACTTACTCTCAATAGCCTTCTCTGGCTGGC	540
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Qy	601	GAAGACAGAGCCTCTGGCAACAAAACCTGAGTAGTGTCTATATCACCCAAAGTAAC	660
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Qy	661	ACTGATGCCACCGGGCTTTACTGACCCAGACCGATGCAAGGCAAACTTCAGCGGCTG	720
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Qy	721	GCCTATGATGTCGCGGCGAGCTAAAGGGAGTTGGTTACACTCAAGGTCAGGCGGAA	780
Db	721	GCCTATGATGTCGCGGCGAGCTAAAGGGAGTTGGTTACACTCAAGGTCAGGCGGAA	780
Qy	781	CAGGTGATTATCAAACTGCTTAACTCTCCCGCGCGGCAAAAATACGTGAAGAGCAC	840
Db	781	CAGGTGATTATCAAACTGCTTAACTCTCCCGCGCGGCAAAAATACGTGAAGAGCAC	840
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Db	841	GGTAACGGGATGTCATGAATACAGCTACGAAACGGAAACCCAAACGGCTTATCGGCATT	900
Qy	901	ACCACTCGCGCTCATCAGACCGCAAGGTGTGCAAGACCTACGCTATCAATATGACCCA	960
Db	901	ACCACTCGCGCTCATCAGACCGCAAGGTGTGCAAGACCTACGCTATCAATATGACCCA	960
Qy	961	GTAGGCAATGTCATTAAATATCCGTAATGATGCGGAAGCCACTCGCTTTTGGCGCAATCAG	1020
Db	961	GTAGGCAATGTCATTAAATATCCGTAATGATGCGGAAGCCACTCGCTTTTGGCGCAATCAG	1020
Qy	1021	AAAGTAGCCCGGAGAAATAGCTATACCTACGATTCCTGTTATGAGCTTATCAGCGCAC	1080
Db	1021	AAAGTAGCCCGGAGAAATAGCTATACCTACGATTCCTGTTATGAGCTTATCAGCGCAC	1080
Qy	1081	GGGCGGAAATGGCCAAATATCGGTGAGCAAAACCAACTTCCCTCCCTCGCGCTACCT	1140
Db	1081	GGGCGGAAATGGCCAAATATCGGTGAGCAAAACCAACTTCCCTCCCTCGCGCTACCT	1140
Qy	1141	TCTGACAACTATACCTAACTATATCTGCGAGCTACAGCTATGATCAAGTGGTAAT	1200
Db	1141	TCTGACAACTATACCTAACTATATCTGCGAGCTACAGCTATGATCAAGTGGTAAT	1200
Qy	1201	CTGACGCAAAATTCGGCAAGCTGCGAGCTACCCAGAACAACTACCGTGGCTATCAC	1260
Db	1201	CTGACGCAAAATTCGGCAAGCTGCGAGCTACCCAGAACAACTACCGTGGCTATCAC	1260
Qy	1261	CTCTCAACCGCAGCAATTCGGGGTGTCTCAGTAGCTTAACCAACCGATCCCAATCAAGTG	1320
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Db	1381	TGACACACCGAGAGAGTTAAAGCAGGTTAAATATGCGCCGGAATAGTGGTACCGC	1440
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Qy	1561	ACAACAAACGGAAGTTACAGTTATCACACTCGGTGAAGCCGGTCGCGCACAGGTACGG	1620
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Qy	1621	GTGTTGCACCTGGGAGAGCGGTAAAGCAGAGAGTGTCAACAATAATCAACTACGTTACAG	1680
Db	1621	GTGTTGCACCTGGGAGAGCGGTAAAGCAGAGAGTGTCAACAATAATCAACTACGTTACAG	1680
Qy	1681	TACGATAATCTGATCGGCTCCAGCCAGCTTGAACCTGGACAAACCAAGGACAAATTTATCAG	1740
Db	1681	TACGATAATCTGATCGGCTCCAGCCAGCTTGAACCTGGACAAACCAAGGACAAATTTATCAG	1740
Qy	1741	GAGGAAGAGTATTATTCATTTGGCGGACAGCCCTGTGGCAGCAACCAAGGACAAACAGAA	1800
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Qy	1801	GCAGCTTATAAAACGATTTCGCTATTCCGCAAAAGACGAGATGCCACCGGTTGTATTAT	1860
Db	1801	GCAGCTTATAAAACGATTTCGCTATTCCGCAAAAGACGAGATGCCACCGGTTGTATTAT	1860
Qy	1861	TACGTTATCGTTATTAACCAACCGTGGCGGCGAGATGGTTAAGCGCGGACCCGCGCAGGA	1920
Db	1861	TACGTTATCGTTATTAACCAACCGTGGCGGCGAGATGGTTAAGCGCGGACCCGCGCAGGA	1920
Qy	1921	ACCATTTAGTGGCTGATCTATACCGAATGGTAAGAAATTAATCTCTGAGCTTTACAGAT	1980
Db	1921	ACCATTTAGTGGCTGATCTATACCGAATGGTAAGAAATTAATCTCTGAGCTTTACAGAT	1980
Qy	1981	GAAATTTAGTGTAGCGGCAAAAGGAAATATACCAAGAGGTAAATTTCTTTGATGAA	2040
Db	1981	GAAATTTAGTGTAGCGGCAAAAGGAAATATACCAAGAGGTAAATTTCTTTGATGAA	2040
Qy	2041	TTAAATTTCAAAATTTGGCAGCCAAAAGTTCACTGTTGTCAAATGGAAACGAGAGAGC	2100
Db	2041	TTAAATTTCAAAATTTGGCAGCCAAAAGTTCACTGTTGTCAAATGGAAACGAGAGAGC	2100
Qy	2101	AGTTATACAAAATTAATTAATTTGAAAGTGGTTGCTGCTGCTGATTCGGTCCGCTG	2160
Db	2101	AGTTATACAAAATTAATTAATTTGAAAGTGGTTGCTGCTGCTGATTCGGTCCGCTG	2160
Qy	2161	TATTTGCTAAGCCACCAAGAGTTACTTAAAGGTATAGAAAAAGTCAAATCATATATAGC	2220
Db	2161	TATTTGCTAAGCCACCAAGAGTTACTTAAAGGTATAGAAAAAGTCAAATCATATATAGC	2220
Qy	2221	CGACTTTGAAAGAAACAGCTCCCTTTTTCAGAAAAATCAAATACTTTTCTTTAGGATCT	2280
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Qy	2281	GAAATATCCGGTTATATGCGCAAGAACCATACAGATACGATATCAGAAATATGCCGAGAG	2340
Db	2281	GAAATATCCGGTTATATGCGCAAGAACCATACAGATACGATATCAGAAATATGCCGAGAG	2340
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Qy	2401	GATAAAGTGAAGAAAAATGATTTATTCGGTGAAGAAAAATTTATGCGGCAATGGAGGTT	2460
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QY 2521 CATCCCTATACGAATTTAGTAAAGAAAGAGCGCTGTTCAAGAAACAGAACCCGCT 2580
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QY 2581 ATTGCAATAGATAGAGATATATATTTCAAAGGTTTGGCAAAATTCCTGACAAATGAAAGCA 2640
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RESULT 2

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US-09-251-645-11
; Sequence 11, Application US/09251645
; Patent No. 6281413
; GENERAL INFORMATION:
; APPLICANT: Kramer, Vance C.
; APPLICANT: Morgan, Michael K.
; APPLICANT: Anderson, Arne R.
; APPLICANT: Hart, Hope
; APPLICANT: Warren, Gregory W.
; APPLICANT: Dunn, Martha
; APPLICANT: Chen, Jeng S.
; TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
; TITLE OF INVENTION: AND NUCLEIC ACID SEQUENCES CODING THEREFOR
; FILE REFERENCE: CGC1963/A
; CURRENT APPLICATION NUMBER: US/09/251,645
; CURRENT FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 37948
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (15171)..(18035)
; OTHER INFORMATION: orf5
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (23768)..(31336)
; OTHER INFORMATION: hph2
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (31393)..(35838)
; OTHER INFORMATION: orf2
US-09-251-645-11
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Query Match 36.9%; Score 1012.4; DB 3; Length 37948;
Best Local Similarity 69.5%; Pred. No. 3.5e-287;
Matches 1414; Conservative 0; Mismatches 596; Indels 24; Gaps 2;

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QY 61 AGGAAATTAATGTACGTACTTTAGATATCTACGCACTCAAGCTGACGAAACAGTGT 120
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Db 15231 CGAGGTCTAACGATTCGTATACGACTTTACCGTACCACCGCAACCGCGATACCGAT 15290
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QY 1198 AATCTGACGCAATTCGGCACAGCTCGCCAGCTACCCAGACCAACCTACACCGTGGCTATC 1257
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Db 16371 AATTTGACTAAAAATCCAGCACAGTTTCCCGGGAGCGCAAAACAACTACACCAACAATC 16430
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Qy 1318 GTGATACGTTGTTTGTATCGCGTGGTCCACCAACCAAGTTTATTAACCGGACAGACACTT 1377
Db 16491 GTAGATGCTTTATTTGATGAGGGGACNTCAGACAGCTTGATATCAGACAAACCTG 16550
Qy 1378 ATCTGGAACACCGAGAGAGTTAAAGCAGGTTAATTAATGGCCCGGAAA----- 1427
Db 16551 AACTGGAATACACGCGGTGAATACAAATGTGACATTTGGTAAACCGGACAAAGGGCGCC 16610
Qy 1428 -----TGAGTGTTACCGTACGACAGCAACCGCATGAGACAACTGAAAGTGA 1476
Db 16611 AATGATGATCGGAATGGTATCGCTATAGTAGTGACGGGAGAGGATATTAATAATCAAT 16670
Qy 1477 GAACAGCAACCCAGAACTACTAGCAGCAACACCGGTAATCTATTTGCCGGGACTGGAG 1536
Db 16671 GAACAGCAGACGACGCAACTCTCAACACAGAGAATACTTATTTGCCGAGTTAGAA 16730
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Qy 1597 GAACCGGTCGCGCAGCAGGTACGGGTGTTGCACTGGGAGAGCGTAAAGCAGAGATGTC 1656
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Qy 1717 GACAACCAAGGACAAATTTATCAGCAGGAGAGATTTATCCATTTGGCGGACAGCGCTG 1776
Db 16911 GACAGCAAGGAGAAATTTATGTTAGGAGAGTACTATCCCTATGCGGACCGCATTA 16970
Qy 1777 TGGCAGCAACACCCCAACAGAGCCAGCTATTAAGAGATTCCTATTCGGCAAGAA 1836
Db 16971 TGGCAACAGAGAGCGGACAGAGCCAGTATTAAGAACCTATCCGTTATTCAGSTAAAG 17030
Qy 1837 CGAGATCCACCGGGTGTATTTATGAGTGTATCGTTATTTACCAACCGTGGCGGGCAGA 1896
Db 17031 CGGATGCGCAGCACTATTTATGCGTTACGATATTTATGAGCTTGGGTAGGACGA 17090
Qy 1897 TGGTTAAGCGCGGACCGGACGAGCAACCAATGATCGGCTGAATCTATACCGAATCGTAAGA 1956
Db 17091 TGGTTAAGTCGGATCCGGCAGGAAACAGTAGATGGTGTGAATTTATATCGGATGGTAAG 17150
Qy 1957 AATAATCTGTGAGTTTACAGATGAAATGGATTAGCGCCAGAAAAGGAAA 2010
Db 17151 AATAATCGGTTACTCTGCTTGTATCCTGATGGATTAATGCCAACAATTTGCAGAA 17204

RESULT 3

US-08-851-567B-60
; Sequence 60, Application US/08851567B
; Patent No. 6528484

GENERAL INFORMATION:

; APPLICANT: Ensign, Jerald C
; APPLICANT: Bowen, David J
; APPLICANT: Petell, James
; APPLICANT: Fatig, Raymond
; APPLICANT: Schoonover, Sue
; APPLICANT: French-Constant, Richard
; APPLICANT: Rocheleau, Thomas A.
; APPLICANT: Blackburn, Michael B.
; APPLICANT: Hey, Timothy D.
; APPLICANT: Merio, Donald J.
; APPLICANT: Orr, Gregory L.
; APPLICANT: Roberts, Jean L.
; APPLICANT: Strickland, James A.
; APPLICANT: Guo, Lining

; APPLICANT: Ciche, Todd A.
; APPLICANT: Sukhapingda, Kitiyari
; TITLE OF INVENTION: Insecticidal Protein Toxins From Photorhabdus
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dow Agrosciences Patent Department
; STREET: 9330 Zionsville Road
; CITY: Indianapolis
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,567B
; FILING DATE: 05-MAY-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/063,615
; FILING DATE: 18-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/395,497
; FILING DATE: 28-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/007,255
; FILING DATE: 06-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/608,423
; FILING DATE: 28-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/705,484
; FILING DATE: 28-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Seav, Nicholas J
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.93804
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3132 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-851-567B-60

Query Match 35.0%; Score 962; DB 3; Length 3132;
Best Local Similarity 72.2%; Pred. No. 5.8e-273;
Matches 1323; Conservative 0; Mismatches 470;

Qy 205 CCAATTTTCATTCGTCTTAACTTTCGCGGTCAAGTTTTCAGTGAAGAAAGTTTGAT 264
Db 220 CCTAATTTTCTGTCGGCAGCATGATCTGGCCGTCATGCCCTCGGACAGAGAGTTCAT 279
Qy 265 GCGGTCGGACTATTACCCCTCAATGATATTGAAAGTCGCCCGGTGTTGATCATCAATGCA 324
Db 280 GCTGGTCGTACTGTTGCATTTGAATGATATTGAAGTTCGTTGATGACAAATGAATGCG 339
Qy 325 ACCGGTGTCCGCCAAACCAATCGTTATGAAGATGAACCCCTTCCGGTGTCTGCTCGCT 384
Db 340 ACCGGTGTTCGTGAGACCCGTCGCTATGAAGGCAACACCTTGGCCGTCGCTTGTATCT 399
Qy 385 ATCACCAGCAAGT-----ACAGGAGGAGAGAAACGACCGCTCTTATCTGGGCC 438
Db 400 GTGAGCGGAGCAAGTTTTCACCAAGAGAGTGTCTAAAGTGAAGAGCCCTTATCTGGGCT 459
Qy 439 GGCAATACGCCGCAAGAAAAGATTACAACTCCCGGTCAGTGTGTGTCGCCCATACGAT 498

Db 460 GGAATACAACTCGGAGAAAGATATAACCTCTCCGGTCTGTGTATACGCCACTAGCAC 519
Qy 499 ACCCGGGAGTTACTCAACTCAATAGCCTTTCTCTGGCTGGCGTCTGTCTATCACAACTCT 558
Db 520 ACAGCGGAGTACCCGGTTGATGAGTCACTCACTGGCGGGCCATGCTATCCCAATCT 579
Qy 559 CAACAACCTGTTACCATACCAAGGATGCCAGTGGACAGGTGAAGACCAAGCCTCTGG 618
Db 580 CACCAATGCTGCGGAAGGCGAGGAGCTAACTGGAGCGGTGACGACGAACCTGTCTGG 639
Qy 619 CAACAAAACTGAGTGTATGCTATATCAACCCAAAGTAACACTGATGCCACCGGGCT 678
Db 640 CAGGGAATGCTGCAAGTGGTCTATACGACAAAGTACCACTAATGCCATCGGGCT 699
Qy 679 TTAAGTACCCAGACCGATGCCAAAGCAAACTCAAGGCTGGCTGATGATGATGATGATG 738
Db 700 TTAAGTACCCAGACCGATGCCAAAGCAAACTCAAGGCTGGCTGATGATGATGATGATG 759
Qy 739 CAGCTAAAGGAGTTGGTTAACTCAAGGCTCAGCGGGAACAGGTGATTAATCAATCG 798
Db 760 CAGTTAAAGGAGTTGGTTGAGCGGTGAAGGCGCAGAGTGAACAGGTGATTTAAAGTCC 819
Qy 799 CTAACCTACTCCCGCGCGGCAAAATTAACGTGAAGACACGCTAACGSGATTGTCACT 858
Db 820 CTGAGCTGGTCAAGCGGAGTCAATTAATTCGCTGAAGACACGCTAACGCGGTGGTTACG 879
Qy 859 GAATACAGCTACGAACCGGAAACCCAAAGCTTATCGGCAATACCACTCGCC----- 910
Db 880 GAGTACAGTTATGAGCGGGAACCTCAACGTCGTATAGGTATACCAACCCCGGCTGCCGA 939
Qy 911 -----GTCCATCAGACGCAAGGTGTTGCAAGACTACGCTATCAATATGACCCAGTAGGC 966
Db 940 GGGAGTCAATCAGGAGCCAGATATTGCGAGATCTACGCTATAAGTATGATCGGTGGGG 999
Qy 967 AATGTCATTAATTCGTATGATGCGGAGCCACTCGCTTTTGGCGCATCAGAAAGTA 1026
Db 1000 AATGTTATCAGTATCAATATGATGCGGAGCTACCGCTTTTGGCGTAAATCAGAAAGTG 1059
Qy 1027 GCCCGGAGAAATAGCTATACCTACGATTCCTCTATCAGCTTATCAGCGCACCGGCGC 1086
Db 1060 GAGCGGAGATCGCTATGTTATGATTTCTGTATCAGCTTATGATGCGCAGGCGGT 1119
Qy 1087 GAAATGGCAATTCGCTCAGCAAAAACAACAACTTCCCTCCCTG-----CGTACCT 1140
Db 1120 GAAATGGCTAATTCGCTCAGCAAAAGCAACAACTTCCCTCCCTGTTATACCTGTTCT 1179
Qy 1141 TCTGACACATACCTACACTACTATCTACGAGCTACAGCTATGATCAGTGTGTAAT 1200
Db 1180 ACTGACGACGACCTTATACCAATTAACCTTTCGTACCTATACCTTACCGTGGCGTAA 1239
Qy 1201 CTGACGCAATTCGGCAGCTCGCGAGCTACCGAGAACCACTACACCGTGGCTATCAC 1260
Db 1240 TTGGTTCAATTCGACACAGCTTACCGCGACTCAAAATGTTACACCAAGATATCAC 1299
Qy 1261 CTCTAAACCGCAGCAATCGGGTGTCTCAGTACGCTAACCCCGATCCAAATCAAGTG 1320
Db 1300 GTTTCAGCGCGAGTAACCGGCGGTATTGAGTACATTAACGACAGATCCAAACCGAGTG 1359
Qy 1321 GATACGTTGTTGATCGCGGTGTACCAAAACAGTTTATACCGGACAGACACTTATC 1380
Db 1360 GATGCGCTATTGTTATTCGCGCGTCTATCAGAAGATGTTAATACCGGGCAAAATCTGGAT 1419
Qy 1381 TGGACACCCAGGAGAGTTAAAGCAGGT-----TAATATGCCCGGGA 1425
Db 1420 TGAATATTCGGGTGNAATTGCAACGAGTCAACCGGTGAGCGTGAATATAGAGTGAC 1479
Qy 1426 AATGAGTGTACCGCTACGACAGCAACCGGATGAGCAAACTGAAAGTGTGATGAACGCCA 1485
Db 1480 AGTGAATGGTATCGCTATACGACGATGATGCGATCGGCTGCTAAAGTGTGATGAACGACG 1539
Qy 1486 ACCGAGATACAGGACGCAACCGGTTAATCTATTTCGCGGAGCTGTGAGCTACGAC 1545
Db 1540 ACGGGCAACAGTACTCAAGTACAAACCGGTGACTTATCTGCGCGGATTAAGAGCTACGACA 1599

Qy 1546 ACCGAGCAACGCCCAACAACCGGAAGATTACAGTTATCACACTCGGTGAAGCGGT 1605
Db 1600 ACTGGGTTTCAGATAAAACAACCGAAGATTTCAGGTGATTACGGTAGGTGAAGCGGT 1659
Qy 1606 CCGCACAGGTACGGGTGTTCACCTGGGAGAGCGGTAAAGCAAGATGTCAACAAAT 1665
Db 1660 CCGCACAGGTAAAGGATTTGCACTGGGAAGTGGTAAGCCGACATATTGACAAAT 1719
Qy 1666 CAACTACGTTACAGCTACGATAATCTGATCGGCTCCAGCCAGCTTGAACCTGGACAA 1725
Db 1720 CAGTGGCTACAGCTACGATAATCTGCTTGGCTCCAGCCAGCTTGAACCTGGATAG 1779
Qy 1726 GGAACAAATTCAGCGAGGAAGATATTATTCATTTTGGCGGACACGCTGTGGGAGCA 1785
Db 1780 GGGCAGATTCTCAGTCAGGAAGATATTATCGTATGGCGGTACGCGCATATATGGCGGCG 1839
Qy 1786 AACAGCAACAGACGACGCTATAAACGATTTCGCTATTTCCGGCAAAAGAACGAGATGCC 1845
Db 1840 AGAATCAGACAGAAAGCCAGCTACAAATTTATTCGTTACTCCGTTAAAGAGCGGATGCC 1899
Qy 1846 ACCGGTCTGTTATTTACGTTATCGTTATTAACCAACCGTGGCGGCGAGATGTTAAGC 1905
Db 1900 ACTGGATTGTTATTTACGCTACCGTTATTAACCTTGGGTGGTGTGATGTTGAGT 1959
Qy 1906 GCGGACCCGCGAGGAACCATTTGATGGCTGAAATCTTATACGAATGTAAGAAATATCCT 1965
Db 1960 GCTGATCCGCGGAACCGTGGATGGCTGAAATTTGTACCGAATGTTGAGGAATAACCCC 2019
Qy 1966 GTGAGTTTACAGATGAATAATGATTTAGCGCC 1997
Db 2020 ATCATTGACTGACCATGCGGATTTAGCACC 2051

RESULT 4

US-09-902-540-1280
; Sequence 1280, Application US/09902540
; Patent No. 6833447

GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.

; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540

; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883

; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825

; SEQ ID NO 1280
; LENGTH: 1039

; TYPE: DNA
; ORGANISM: Myxococcus xanthus

; FEATURE:
; NAME/KEY: unsure

; LOCATION: (1)..(1039)
; OTHER INFORMATION: unsure at all n locations

US-09-902-540-1280

Query Match 2.0%; Score 56.2; DB 3; Length 1039;

Best Local Similarity 42.2%; Pred. No. 8.5e-06;

Matches 307; Conservative 0; Mismatches 420; Indels 0; Gaps 0;

Qy 1974 ACAGATGAAATGGATTAGCCGACAAAGGGAATATACCAAGAGGTAATTTCTT 2033
Db 277 AAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 336
Qy 2034 TGATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2093
Db 337 ATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 396
Qy 2094 AGAGAGCAGTTATACAAAAATAAATCAATTGAAAGTGGTTGTCGTCGTTCCGATCC 2153


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; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14624
; LENGTH: 147382
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(147382)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14624

Query Match      1.7%; Score 47.4; DB 3; Length 147382;
Best Local Similarity 45.8%; Pred. No. 0.069;
Matches 243; Conservative 0; Mismatches 281; Indels 7; Gaps 2;

Qy 2161 TATTGCTAAGCCAGAGAGTTACTAAAGGTATAGAAAAGTCAAAATCATATATAGC 2220
Db 137228 TATATAAATATATATAAATATATATAAATAAATAAATAAATAAATAAATAAATAA 137169
Qy 2221 CGACTTGAAGAAAACAGCTCCCTTTTCAGAAAAATCAAAAAACGAATCTTTCTTAGGATCT 2280
Db 137168 TAAATAAATATAAATATAAATATGTAATAACATATATAAATAAATAAATAAATAA 137109
Qy 2281 GAAATATCCGGTTATATGCGCAAGAACCATACAAGATACGATATCAGAAATATGCCGAAGAG 2340
Db 137108 AATATATATAAATACATATATAAATATATAAATATATAAATATATAAATATACATAAATATG 137049
Qy 2341 CATATAATATAGN-----GTAATCACCCCTGATTTTATTCAGAACCCGATTTCTTTGGGTT 2396
Db 137048 TATAAATATATAAACAATATATTAATATAAATAAATATAAATAAATAAATAAATAAATAA 136989
Qy 2397 AATGGATAAAGTGAAAAAATGATTTATCCGGTGAAGAAAAATTTATCGGCAATGGA 2456
Db 136988 TATATATAAATATATGATATATATAAATATGTTTAAATATACATATATAAATAAATAA 136929
Qy 2457 GGTTAAGGTTTATCATGATTTAAAAATAAACAATCAGAAATACATCTCAACTATGCAAT 2516
Db 136928 TATAAAAAATATATAAATATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 136869
Qy 2517 GGCCCATCCCTATACGCAATGAGTAATGAAGAAGAGCGCTGTTCAGAACAGACAGACC 2576
Db 136868 AATATATAAATAATA---TATGAACATAATATATAAATAAATAAATAAATAAATAAATAA 136812
Qy 2577 CGCTATTGCAATAGATAGAGAAATATAATTTCAAAGGTGTTGGCAAAATTCCTGACAAATGAA 2636
Db 136811 ATATATAAATAAATATATACAAATATATATAAATAAATAAATAAATAAATAAATAAATAA 136752
Qy 2637 AGCAATTAATAAATCAATGAAAGGACATATAAATAAATTAATAGGATATCAACAGA 2687
Db 136751 ATATATAAATAAATATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 136701
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RESULT 7

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US-09-902-540-1357
; Sequence 1357, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1357
; LENGTH: 612
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
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RESULT 8

```
US-09-949-016-13539
; Sequence 13539, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13539
; LENGTH: 314798
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
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; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(612)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1357

Query Match      1.7%; Score 46.6; DB 3; Length 612;
Best Local Similarity 43.1%; Pred. No. 0.0042;
Matches 220; Conservative 0; Mismatches 291; Indels 0; Gaps 0;

Qy 2177 AAGAGTTACTAAAGGTATAGAAAAAGTCAAAATCATATATAGCCGACTTTGAAGAAAAACA 2236
Db 12 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 71
Qy 2237 GCTCCCTTTTCAGAAAAATCAAAACGAATCTTTCTTTAGGATCTGAAATATCCGGTTATA 2296
Db 72 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 131
Qy 2297 TGCAGAGAACCATACAAGATACGATATCAGAAATATGCCGAAGAGCATAAATATAGAGTA 2356
Db 132 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 191
Qy 2357 ATCACCTGATTTTATTCAGAAACCGATTTCTTTGCGTTAAATGGATAAAAGTGAAAAAAA 2416
Db 192 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 251
Qy 2417 ATGATTTATTCGGTGAAGAAAAAATTTATGCGCAATGGAGGTTAAGGTTTATCATGATT 2476
Db 252 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 311
Qy 2477 TAAAAAATAACAATCAGAAATTCATGTCACACTATGCAATGGCCCATCCCTATACGCAAT 2536
Db 312 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 371
Qy 2537 TGAGTAATGAAGAAAGAGCGCTGTTCAGAAACAGACAGCCGCTATTGCAATAGATAGAG 2596
Db 372 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 431
Qy 2597 AATATAATTTCAAAGGTGTTGGCAAAATTCCTGCAATGAAAGCAATTTAAAAAATCATTTGA 2656
Db 432 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 491
Qy 2657 AAGCAGATAAATAATTAATAGGATATCAACAGA 2687
Db 492 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 522
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; LOCATION: (1)...(314798)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13539

Query Match      1.7%; Score 45.6; DB 3; Length 314798;
Best Local Similarity 46.8%; Pred. No. 0.37;
Matches 144; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

Qy 2199 AAAAAGTCAATCATATATAGCCGACTTGAAGAAAACAGCTCCCTTTTCAGAAAATCAAA 2258
Db 18841 AAATATATATAAAATATATATATAAATATATATAAATATATATAAATATATAAATAT 18900
Qy 2259 AACGAATCTTCTTTAGGATCTGAAATATCCGGTTATATGCGCAAGAACCATACAGATAC 2318
Db 18901 ATATATAATATATAAATATATATAAATATATATAAATATATATAAATATATAAATA 18960
Qy 2319 GATATCAGATATATCCGAAGAGCATATAATATAGAAATGTAATCACCCTGATTTTATTTCAGA 2378
Db 18961 TATATAAATATATAAATATATATAAATATATATAAATATATAAATATATAAATA 19020
Qy 2379 AACCGATTTCTTCGGTTAATGGATAAAAGTGAAAAAATGATTTATCCGGTGAAGAAA 2438
Db 19021 TATATAAATATATATAAATATATAAATAAATAAATAAATAAATAAATAAATAAATA 19080
Qy 2439 AATTATGCGGCAATGAGGTTAAGGTTTATCATGATTTTAAAAAATAAACAATCAGAAAT 2498
Db 19081 TATTAAATATATTATATTATATTATAGTATATATTATAGTATATAAATAAATAAATA 19140
Qy 2499 ACATGTCA 2506
Db 19141 AATTGCCA 19148

RESULT 9
US-09-949-016-61868
; Sequence 61868, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61868
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-61868

Query Match      1.6%; Score 45.2; DB 3; Length 582;
Best Local Similarity 46.4%; Pred. No. 0.011;
Matches 143; Conservative 1; Mismatches 164; Indels 0; Gaps 0;

Qy 2199 AAAAAGTCAATCATATATAGCCGACTTGAAGAAAACAGCTCCCTTTTCAGAAAATCAAA 2258
Db 12 AAATATATATAAAATATATATAAATATATAAATATATAAATATATAAATATATAAATAT 71
Qy 2259 AACGAATCTTCTTTAGGATCTGAAATATCCGGTTATATGCGCAAGAACCATACAGATAC 2318
Db 72 ATATATAATATATAAATATATAAATATATAAATATATAAATATATAAATATATAAATA 131
Qy 2319 GATATCAGATATATCCGAAGAGCATATAATATAGAAATGTAATCACCCTGATTTTATTTCAGA 2378
Db 132 TATATAAATATATAAATATATAAATATATAAATATATAAATATATAAATATATAAATA 191

; LOCATION: (1)...(314798)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13539

Query Match      1.7%; Score 45.6; DB 3; Length 314798;
Best Local Similarity 46.8%; Pred. No. 0.37;
Matches 144; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

Qy 2199 AAAAAGTCAATCATATATAGCCGACTTGAAGAAAACAGCTCCCTTTTCAGAAAATCAAA 2258
Db 18841 AAATATATATAAAATATATATAAATATATATAAATATATATAAATATATAAATAT 18900
Qy 2259 AACGAATCTTCTTTAGGATCTGAAATATCCGGTTATATGCGCAAGAACCATACAGATAC 2318
Db 18901 ATATATAATATATAAATATATATAAATATATATAAATATATATAAATATATAAATA 18960
Qy 2319 GATATCAGATATATCCGAAGAGCATATAATATAGAAATGTAATCACCCTGATTTTATTTCAGA 2378
Db 18961 TATATAAATATATAAATATATATAAATATATATAAATATATAAATATATAAATA 19020
Qy 2379 AACCGATTTCTTCGGTTAATGGATAAAAGTGAAAAAATGATTTATCCGGTGAAGAAA 2438
Db 19021 TATATAAATATATATAAATATATAAATAAATAAATAAATAAATAAATAAATAAATA 19080
Qy 2439 AATTATGCGGCAATGAGGTTAAGGTTTATCATGATTTTAAAAAATAAACAATCAGAAAT 2498
Db 19081 TATTAAATATATTATATTATATTATAGTATATATTATAGTATATAAATAAATAAATA 19140
Qy 2499 ACATGTCA 2506
Db 19141 AATTGCCA 19148

RESULT 10
US-09-949-016-12510
; Sequence 12510, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12510
; LENGTH: 94987
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12510

Query Match      1.6%; Score 45; DB 3; Length 94987;
Best Local Similarity 45.2%; Pred. No. 0.27;
Matches 165; Conservative 0; Mismatches 200; Indels 0; Gaps 0;

Qy 2203 AGTCAATCATATATAGCCGACTTGAAGAAAACAGCTCCCTTTTCAGAAAATCAAAAACG 2262
Db 1177 AGGTAAGCCATTAGTCACCTTTTAAAAAAGCATAGCGAGTGATACAAAGTAAATAACA 1236
Qy 2263 AATCTTTTCTTTAGGATCTGAAATATCCGGTTATATGCGCAAGAACCATACAGATACGATA 2322
Db 1237 ATGAAAAATTCATCAAGCAATATAAGATACAAACAAAAGATCATTAATGAAATCTAGATC 1296
Qy 2323 TCAGATATATCCGAAGAGCATATAAATATAGAAATGTAATCACCCTGATTTTATTTCAGAAACC 2382
Db 1297 TCAGGGATTTTCCAAGAGAGATTACTTAAAGGAGAAAACAAGTTTGTTCAGTGGATAAACA 1356
Qy 2383 GATTTCTTTTCGGTTAATGGATAAAAGTGAAAAAATGATTTATCCGGTGAAGAAAATTT 2442
Db 1357 TTGTTCTATGCGTGAATAGGAGATGGAATATGCTCATTTTCTAGTTCAGGGAATGT 1416
Qy 2443 TATGCGGCAATGAGGTTAAGGTTTATCATGATTTAAAAAATAAACAATCAGAAATACAT 2502
Db 1417 CATAGATCAGGATGCGACAGAGTTAAACAATATTTCTCTGCTCTCTAATGGAAGCAT 1476
Qy 2503 GTCAACTATGATTTGGCCCATCCCTATATACCAATTTGAGTAAATGAAGAAAGAGCGCTGTTG 2562
Db 1477 AAGAAAAATTAGCTTCACTGAAGTTTAAACAAAATGGAATTAACAAGAAAAAAGAGCTATTT 1536
Qy 2563 CAAGA 2567
Db 1537 AAAAA 1541

RESULT 11
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US-09-949-016-14429
; Sequence 14429, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 14429
; LENGTH: 96987
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14429

Query Match 1.6%; Score 45; DB 3; Length 96987;
Best Local Similarity 45.2%; Pred. No. 0.27;
Matches 165; Conservative 0; Mismatches 200; Indels 0; Gaps 0;

QY 2203 AGTCAATCATATATAGCCGACTTGAAGAAACACAGCTCCCTTTTCAGAAAAATCAAAAACG 2362
DB 51177 AGGTAGCCATTAGTCACCTTTTAAAAAAGCATACGAGTGGATACAAGTAATAACA 51236

QY 2263 AATCTTTCTTAGGATCTGAATATATCGGTTATATGCGCAAGAACCATACAGATACGATA 2322
DB 51237 ATCAAAATTCATCAAGCAATATAAGATACAAACAAAGATCATTAATGAATCTAGATC 51296

QY 2323 TCAGATATGCCAAGAGCAATAATATAGAAGTAATCACCTGATTTTATTCAGAAACC 2382
DB 51297 TCAGGATTTTCAAGAGAGATTACTTAAGGAGAAAAACAAGTTTGTTCAGTGGATAAACA 51356

QY 2383 GATTCTTCTCGTTAATGGATAAAGTGAAGAAAAATGATTATTCGCGTGAAGAAAAAT 2442
DB 51357 TTGTTCTATCGTGGATAAGGAGATGGAAATGCCTCATTTTCTAGTTCAAGGGAATGT 51416

QY 2443 TATCGCGCAATGGAGGTTAAGGTTTATCATGATTTAAAAAATAAACAATCAGAAATTACAT 2502
DB 51417 CATAGATCAGGATGGCACAGAGTTAAACACATATTTCTCTGCTCTTAATGGAAGCAT 51476

QY 2503 GTCACATATGCATGGCCCATCCCTATACGCAATTGAGTAATGAAGAACGCGCTGTTG 2562
DB 51477 AAGAAAAATTAGCTTCACTGAAGTTTAAACAAAAATGGAATAACAAAGAAAAAGACTATT 51536

QY 2563 CAAGA 2567
DB 51537 AAAAA 51541

RESULT 12
US-09-806-708B-22/c
; Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; CURRENT FILING DATE: 2001-04-03
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 1141

; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1141)
; OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. PAE1 promoters
US-09-806-708B-22

Query Match 1.6%; Score 44.2; DB 3; Length 1141;
Best Local Similarity 12.3%; Pred. No. 0.032;
Matches 97; Conservative 268; Mismatches 420; Indels 5; Gaps 2;

QY 1956 AAATATCTCTGTGAGTTTACAAGATCAAAATGGATTAGCCGCAAGAAAAGGGAATATAC 2015
DB 1003 ATNNAMWYATTRWAAAYAAAKARWAGNMRMYGAAAGNKWGCMAAATWGBMWADTAGKM 944
QY 2016 CAAAGAGGTAAATTTCTTTGATGAATTAATAATTCAAATTTGGCAGCCAAAGTTCCATGT 2075
DB 943 CNNNNNNWTTDVRMAMKAKNNNNNNNAYWTACYNRAATNNKATHMKWTHGAHSHKRT 884
QY 2076 TGTCAAAATGGAACGAGAGAGAGAGAGTATACAAAAATAAATCATTTGAAAGTGGTTCG 2135
DB 883 HHTRTCRRTKYNNNNNNARTVYVYHHAARRWMAWTRTNNNNNNNNNNNACRTRTWAB 824
QY 2136 TGTCTGCTGATTCGGATCCGCTCGGTTATTGCTAAGCCAGAGAGTTACTAAAGGTAT 2195
DB 823 WKHSWNN 764
QY 2196 AGAAAAAAGTCAAAATCATATATAGCCGACTTGAAGAAAAACAGCTCCCTTTTCAGAAAAATC 2255
DB 763 HTDWCYKTMWYWDWMTTMBTTTTTRNNNTTSTNNNNNNNNNNNNNNNNNNNNNNNNNNNN 704
QY 2256 AAAAAAGCAATCTTTCTTTTAGGATCTGAAATAT---CCGGTTATATGCGCAAGAACCATACA 2312
DB 703 HATNNGCWNNNTDARRTNNTTVMRRWMTNTKTRWYSTTRRHHTGATNNNNNNNNNNNN 644
QY 2313 AGATACGATATCAGAAATATGCGAAGAGCATATAATAGAAATATCACCCTGATTTTA 2372
DB 643 NNNNSCCTCTRMNTMRMTKGDGTVRKVKWRDTCCTVYDVWADSWVMWYANMRCRD 584
QY 2373 TTCAGAAACCGATTTCTTTGCGTTAATGATGATAAGTGAAGAAAAATGATTATTCGCGTGA 2432
DB 583 VYTRNTYCKSYAHSHYVWNNAMWYRYSARNSSMARWTRNNNNNNNNNNNNNNNNNNNNNN 524
QY 2433 AAGAAAAATTTATCGCGCAATGGAGTTAAGGTTTATCATGATTTAAAAAATAAACAATC 2492
DB 523 MMRHNNNNNTDTRYVWKKWARBTTVVDSNCAKSMWGNMWRAMKMWAAANNNDAGA 464
QY 2493 AGAATTACATCAACTATGCAATGGCCCATCCCTATAGCAATTCAGTAATGAGAAG 2552
DB 463 MDHWTYMGNTTMMRRAMKMMNMAMCRRAYCCNNNNNNRACVWHKHQWRWTKYMKAA 404
QY 2553 AGCGCTGTTGCAAGAAACAGAACCCGCTATTGCAATAGATAGAGATAATAATTTCAA-- 2610
DB 403 CNNNNBKAMYMRVAMMYSRDNTTNDMMWTTSDWBWHWTVDYTMRRANNNNNNNNNRBC 344
QY 2611 GGTGTTGGCAAAATTCCTGCAATGAAAGCAATTTAAAAAATTCATTGAAAGGACATAAAAT 2670
DB 343 KTTSMWMMHDKNTHCTYGNNTWGSAYBMAASMWAAAGASBNBYVYVWCHRTYMGKMTN 284
QY 2671 AATAGATATCAACAGAGGCTATTATAATTCGCTCTCGCGGCTATCGCTGAGAAATTTAGGA 2730
DB 283 NNNNNKAYYRTKTVAWCNNRYVYDVAVWTKBNRYKYCYAYBWWYBYMYGKHWHBWRRA 224
QY 2731 ATGCGGAGAA 2740
DB 223 BHRSMNNMWV 214

RESULT 13
US-08-956-171E-631/c
; Sequence 631, Application US/08956171E
; Patent No. 6593114

APPLICANT: Peterson, David S.
 APPLICANT: Su, Xin-zhaun
 APPLICANT: Wellemis, Thomas E.
 TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
 TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Knobbe Martens Olson & Bear
 STREET: 620 Newport Center Drive 16th Floor
 CITY: Newport Beach
 STATE: California
 COUNTRY: US
 ZIP: 92660
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/487,826B
 FILING DATE: 10-SEP-1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Israelsen, Ned
 REGISTRATION NUMBER: 29,655
 REFERENCE/DOCKET NUMBER: NIH121.001CP1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 235-8550
 TELEFAX: (619) 235-0176
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19124 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-08-487-826B-13

Query Match	1.6%;	Score 44;	DB 2;	Length 19124;
Best Local Similarity	44.4%;	Pred. No. 0.2;		
Matches 220;	Conservative 0;	Mismatches 275;	Indels 1;	Gaps 1;
QY	2180	AGTTACTAAAGGTATAGAAAAAGTCAAATCATATATAGCGCGCTTCAAGAGAAACAGCT	2239	
DB	15410	ATTATATTAAAAAGAAATATAAAAAANAATTTATTAATGAAAAAGAAAAATGAA	15469	
QY	2240	CCCTTTTCAGAAAAATCAAAAAAGCAATCTTTTCTTTTAGGATCTGAAATATCCGGTTATATGG	2299	
DB	15470	ATATAAAAAAATTTATTAAAAATAAAAAANAANAANAAGGAGAAAAATTTTTT	15529	
QY	2300	CAAGAACCATACAAGATACGATATCAGAAATATGCCGAAGACATAAAATATAGAGTAAATC	2359	
DB	15530	AAAAAATAATAAAAATTAAATAAAAATATAAATTTTGTAGAAATAAAAAATGAAAAAGAT	15589	
QY	2360	ACCTCGATTTTTATTTCAGAAACCGATTTCTTTTCGCTTAATGGATAAAAAGTCAAAAAAATG	2419	
DB	15590	TATCAAAAAAANAATTTAAAAAANAATTTTATATAAAAAAANAATGATTATAAAAAAATAA	15649	
QY	2420	ATTATTCGGTGAAGAGAAAAATTTATCGGCAATGGAGGTTAAAGGTTTATCATGTTTAA	2479	
DB	15650	AAACAAAGAGAGAAAAAANAACATTTAAAAAANAANAATATATATCATTAANAACAAA	15709	
QY	2480	AAAAATAAACCAATCAGA-ATTACATGTCACTATGCAITTTGGCCCATCCCTATACGCAATTG	2538	
DB	15710	AAAAAAGAAAAAATAATATAAAAAATAAAAAATATATATCATATAAAAAAATAAATAA	15769	
QY	2539	AGTAATGAAGAAAGCGCTGTTCGAAGAACAGAACCCGCTATTTCGCAATAGATAGAGAA	2598	
DB	15770	AAATGTTAAAAAANAANAATATATACATAAAAAAANAANAATTTATTTTAAATAAAAAANAAT	15829	
QY	2599	TATAAATTTCAAAAGGTGTTCGCAAAATTCCTGACAAATGAAAGCAATTTAAAAAATTCATTGAAA	2658	

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Best Available Copy

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 19:10:31 ; Search time 9683 Seconds
(without alignments)
13263.507 Million cell updates/sec

Title: US-10-647-956A-5

Perfect score: 2745

Sequence: 1 atgagcagttacaattctgc.....taggaatcgaggagaacttca 2745

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_hic: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_est7: *
9: gb_gss1: *
10: gb_gss2: *
11: gb_gss3: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	419.6	15.3	460	9 AQ991476	AQ991476 Rfc02418
C 2	352	12.8	749	9 AQ991727	AQ991727 Rfc00357F
3	292.6	10.7	605	9 AQ990411	AQ990411 Rfc01179
C 4	239.8	8.7	494	9 AQ991400	AQ991400 Rfc02327
5	226.8	8.3	406	9 AQ990055	AQ990055 Rfc00763
C 6	192.6	7.0	594	9 AQ990688	AQ990688 Rfc01498
C 7	176.8	6.4	878	10 C2547320	CZ547320 SRAA-aad7
8	152.6	5.6	547	9 AQ990013	AQ990013 Rfc00707
9	148.8	5.4	312	9 AQ990147	AQ990147 Rfc00869
C 10	141	5.1	733	1 AQ990147	AW990147 RCO-NN101
11	74.6	2.7	1224	10 CL077121	CL077121 CH216-143
12	71.8	2.6	1299	8 DN705619	DN705619 CLJ60-F02
C 13	68	2.5	942	10 CNS0186S	AL109318 Drosophila
C 14	65.4	2.4	1811	10 CG753732	CG753732 P048-4-G0
C 15	65	2.4	1353	10 CG744812	CG744812 P037-3-B0
C 16	64.8	2.4	1683	10 AG390417	AG390417 Mus muscu
17	64.4	2.3	1364	8 DN693282	DN693282 CGX87-B03
C 18	64.2	2.3	1178	10 CL491661	CL491661 SAIL 559
C 19	63.6	2.3	1101	10 CNS0039G	AL063921 Drosophila
C 20	63.6	2.3	1137	10 CL080345	CL080345 CH216-158
21	63.4	2.3	1053	5 BU508694	BU508694 AGENCOURT
C 22	63.4	2.3	1204	8 DN432684	DN432684 LIB4217-0

23	63.2	2.3	644	1 AW901491	AW901491 RCO-NN101
C 24	63.2	2.3	1843	10 AG435185	AG435185 Mus muscu
25	63	2.3	1134	10 CL073913	CL073913 CH216-130
C 26	63	2.3	1201	10 CNS0167M	AL106396 Drosophila
27	63	2.3	1256	10 CL119201	CL119201 ISB1-76U1
C 28	62.8	2.3	2071	8 DR147304	DR147304 49027161
C 29	62.6	2.3	1433	10 CG745119	CG745119 P037-4-G0
C 30	61.4	2.2	974	10 CNS001TT	AL075432 Drosophila
31	61.4	2.2	1512	10 CL082685	CL082685 CH216-169
C 32	61.4	2.2	1528	10 CG753854	CG753854 P049-1-D0
33	61.2	2.2	1330	8 DN705530	DN705530 CLJ60-A10
34	61	2.2	1108	1 AJ926042	AJ926042 AJ926042
C 35	61	2.2	1167	1 AJ927228	AJ927228 AJ927228
C 36	61	2.2	1266	10 AJ859745	AJ859745 Braggica
37	61	2.2	1680	10 CL079033	CL079033 CH216-154
C 38	60.8	2.2	1146	10 CL649333	CL649333 CH213-227
C 39	60.8	2.2	1531	10 CG748014	CG748014 P041-4-B0
40	60.4	2.2	1055	5 BQ876453	BQ876453 AGENCOURT
C 41	60.4	2.2	1114	8 DN656077	DN656077 CSC21-A11
C 42	60.2	2.2	997	10 CNS0134P	AL102403 Drosophila
C 43	60.2	2.2	1566	10 CG757757	CG757757 P053-1-D0
44	60	2.2	1173	1 AJ926089	AJ926089 AJ926089
45	60	2.2	1558	10 CL491664	CL491664 SAIL_559

ALIGNMENTS

RESULT 1	AQ991476	460 bp	DNA	linear	GSS 14-AUG-2000
LOCUS	Rfc02418	Phototribadus luminescens strain W14 M13 library			
DEFINITION	Phototribadus luminescens genomic clone PLG02418, genomic survey sequence.				
ACCESSION	AQ991476				
VERSION	AQ991476.1	GI:9650070			
KEYWORDS	GSS.				
SOURCE	Phototribadus luminescens				
ORGANISM	Phototribadus luminescens				
REFERENCE	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Phototribadus.				
AUTHORS	1 (bases 1 to 460) Iffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T., Daborn,P.J., Bowen,D. and Blattner,F.R.				
TITLE	A genomic sample sequence of the entomopathogenic bacterium Phototribadus luminescens W14: potential implications for virulence				
JOURNAL	Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)				
PUBLISHED	10919786				
COMMENT	Contact: iffrench-Constant RH Department of Biology and Biochemistry University of Bath South Building, Bath BA2 7AY, UK Tel: (44) 1225 826621 Fax: (44) 1225 826779 Email: bsr@bath.ac.uk This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see iffrench-Constant et al. 2000, Nucleic Acids Res. Seq primer: M13 Forward Class: shotgun.				

FEATURES

source	Location/Qualifiers
1..460	/organism="Phototribadus luminescens"
	/mol_type="genomic DNA"
	/strain="W14"
	/db_xref="taxon:29488"
	/clone="PLG02418"
	/dev_stage="primary phase variant"
	/clone_lib="Phototribadus luminescens strain W14 M13 library"
	/note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

ORIGIN

Query Match 15.3%; Score 419.6; DB 9; Length 460;
Best Local Similarity 97.0%; Pred. No. 2.6e-99;
Matches 448; Conservative 0; Mismatches 11; Indels 3; Gaps 2;
QY 1266 AAACCCGAGCAATCGGGGTCTCTCAGTACGCTAACCCAGATCCAAATCAAGTGGATAC 1325
DB 1 AAACCCGAGCAATCGGGGTCTCTCAGTACGCTAACCCAGATCCAAATCAAGTGGATAC 60
QY 1326 GTTGTGTTGATCGCGGTGGTCAACAAACAGTTTATTACCCGGAGACAGACACTTATCTGGAC 1385
DB 61 GTTGTGTTGATCGCGGTGGTCAACAAACAGTTTATTACCCGGAGACAGACACTTATCTGGAC 120
QY 1386 ACCACGAGGAGGTTAAAGCAGGTTTAATATGCGCCGGGAAATGAGTGGTACCGCTACGA 1445
DB 121 ACCACGAGGAGGTTAAAGCAGGTTTAATATGCGCCGGGAAATGAGTGGTACCGCTACGA 180
QY 1446 CAGCAACGGCATGAGACAACTGAAAGTGAGTGAACGCCAACCCAGAATACTACGCAGCA 1505
DB 181 CAGCAACGGCATGAGACAACTGAAAGTGAGTGAACGCCAACCCAGAATACTACGCAGCA 240
QY 1506 ACAACGGGTAATCTATTGTCGGGACTGGAGCTACGCACAAACCCAGACAAACGCCCAAC 1565
DB 241 ACAACGGGTAATCTATTGTCGGGACTGGAGCTACGCACAAACCCAGACAAACGCCCAAC 300
QY 1566 AACGGAAGGTTACAGTTTATCATCTCGTGAAGCGGTGCGGCACAGTACGGGTGTT 1625
DB 301 AACGGAAGGTTACAGTTTATCATCTCGTGAAGCGGTGCGGCACAGTACGGGTGTT 359
QY 1626 GCACCTGGAGCGGTAAAGCCAGAGATGTCACAAATCAACTAGTTTACAGTACGA 1685
DB 360 GCACCTGGAGCGGTAAAGCCAGAGATGTCACAAATCAACTAGTTTACAGTACGA 417
QY 1686 TAATCTGATCGGTCACGACGAGCTTGAACCTGGACAAACCAAGG 1727
DB 418 TAATCTGATCGGTTCAACCCAGCTTTCAGTGGACACCCCAAGG 459

RESULT 2
AQ991727/c

LOCUS
DEFINITION
Rf00357F Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG00357F, genomic survey
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

ORGANISM

Photorhabdus luminescens
Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.

REFERENCE

1 (bases 1 to 749)
ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
10919786

JOURNAL

PUBMED

COMMENT

Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bsrfc@bath.ac.uk
This is one of a selected subset of flipped clones from the M13
library. For annotation of identified clones (BLASTX, BLASTN and
mapping to E. coli K12 genome) please see ffrench-Constant et al.
2000, Nucleic Acids Res.
Seq primer: M13 Reverse
Class: shotgun.

FEATURES

Location/Qualifiers

source

1. .749
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clone="PLG00357F"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
/note="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."

ORIGIN

Query Match 12.8%; Score 352; DB 9; Length 749;
Best Local Similarity 71.2%; Pred. No. 2.2e-81;
Matches 487; Conservative 0; Mismatches 190; Indels 7; Gaps 2;
QY 267 CGGTCCGAGTATTACCTCAATGATATTGAAAGTCGCCGGTGTGATCATCAATCAAC 326
DB 713 CGGTTCGCTGTCNCCTTNAATTATATTGAAGNCCGTCGCTACTACGGGTGNTTCAAC 654
QY 327 CGGTGTCGCCAAAACCATCGTTATGAAGATAACACCTTCCCGGTGCTGCTCGGTAT 386
DB 653 AGGENTTATAC-AAACTGCGCAATATGAAATTTTNCCTCGCCCGTNGTTTGTATCTGT 595
QY 387 CACCGAACAGTACAGCGCAGGAGAGAAACG-----ACCGAACGTTTATCTGGGCCGG 440
DB 594 TCGCGAACAAACACCCGAGGAAAAACATCCCGTATCACCGAACGTTGATTTGGGTGG 535
QY 441 CAATACCGCGCAAGAAAAAGATTACAACTCGCGCGTCAAGTGTGTCGCCCATTTACGATAC 500
DB 534 CAATACCGAGCAGAGAAAGACCATTAACCTTGCGCCAGTGGTGGTCACTATGACAC 475
QY 501 CGCGGACTTACTCAACTCAATAGCCTTCTCTGGTGGGTCGTGCTATCACAATCTCA 560
DB 474 GCGGGAGTTACCGGTTANAGAGTTTATCACTGACCGGTACTGTTTATCTCAATCCAG 415
QY 561 ACAACTGCTTACCGATAACAGGATCCGACTCGACAGAGTGAAGACAGAGCCTCTGGCA 620
DB 414 CCAACTATTGATCGACACTCAAGAGGCAAACTGGACAGGTGATAACGAAACCGTCTGGCA 355
QY 621 ACAAAACTGAGTAGTGTCTATATCACCCAAAGTAACACTGATGCCACCGGGGCTTT 680
DB 354 AAACATGCTGGTGTAGTACATCTACACAACTTGAGCACCTTCGATGCCACCGGTGCTTT 295
QY 681 ACTGACCCAGACCGATGCCAAAGGCAACATTTCAGCGGTGGCTTATGATGTGGCCGGGCA 740
DB 294 ACTGACTCAGACCGGATCGAAAGGGAACATTTCAGAGACTGGCTTATGATGTGGCCGGGCA 235
QY 741 GCTAAAGGGAGTTGGTTAACTCACTCAAGGTCAAGCGGACAGGTGATTATCAATCGCT 800
DB 234 GCTAAAGCGGAGCTGGCTAACACTCAAGAGCCAGACGGAACAAGTATTCAATCCCT 175
QY 801 AACCTACTCCGCGCGGCAAAAATTTAGCTGAAGACACGCTAAACGGGATTTGCTACTGA 860
DB 174 GACTTACTCGCGCGCGGACAAAATTTAGCTGAGGAACACGGCAATGATGTATCACCGA 115
QY 861 ATACAGCTACGAACCGGAAACCCAAACGGCTTATCGGCATTTACCACCTGCGCGTCCATCAGA 920
DB 114 ATACAGTTATGAACCGGAAACCCAAACCGGCTGATCGGTATCAAAACCCGCGTCCGTGAGA 55
QY 921 CGCCAAAGGTGTTGCAAGACCTACG 944
DB 54 CACTAAAGTGCTACAAGACCTGCG 31

RESULT 3

AQ990411

LOCUS

DEFINITION

Photorhabdus luminescens strain W14 M13 library

sequence.

ACCESSION

AQ990411

AQ990411 605 bp DNA linear GSS 14-AUG-2000
Rf001179 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01179, genomic survey
sequence.
AQ990411

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VERSION      AQ990411.1  GI:9649005
KEYWORDS     GSS.
SOURCE       Photorhabdus luminescens
ORGANISM     Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
              Enterobacteriaceae; Photorhabdus.
REFERENCE    1 (bases 1 to 605)
AUTHORS      ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
              Daborn,P.J., Bowen,D. and Blattner,F.R.
TITLE        A genomic sample sequence of the entomopathogenic bacterium
              Photorhabdus luminescens W14: potential implications for virulence
JOURNAL      Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
PUBMED       10919786
COMMENT      Contact: ffrench-Constant RH
              Department of Biology and Biochemistry
              University of Bath
              South Building, Bath BA2 7AY, UK
              Tel: (44) 1225 826621
              Fax: (44) 1225 826779
              Email: bssrfc@bath.ac.uk
              This is one of 2,122 random reads from the M13 library. For
              annotation of identified clones (BLASTX, BLASTN and mapping to E.
              coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
              Acids Res.
              Seq primer: M13 Forward
              Class: shotgun.
FEATURES     Location/Qualifiers
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              /mol_type="genomic DNA"
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              /db_xref="taxon:29488"
              /clone="PLG01179"
              /dev_stage="primary phase variant"
              /clone_lib="Photorhabdus luminescens strain W14 M13
              library"
              /notes="Genomic DNA from strain W14 was size selected (1-2
              kb) and then cloned into M13 Janus."
ORIGIN
Query Match      10.7%; Score 292.6; DB 9; Length 605;
Best Local Similarity 70.8%; Pred. No. 1e-65;
Matches 422; Conservative 0; Mismatches 160; Indels 14; Gaps 2;
QY 417 GACCGAACGCTTATCTGGCCGGCAATACGCGCAAGAAAGATTACAACCTCCCGG 476
DB 2 GACAGAGCCCTTATCTGGCGTGGGAATACACCTCGGAGAAAGATTAACCTCTCCGG 61
QY 477 TCAGTGTGTCGCGCAATACGATACCGCGGACTTACTCAACTCAATAGCCTTTCTCTGCG 536
DB 62 TCTGTGTATACGCCACTACGACACGCGGGAGTGACCCGGTTGATGAGTCAGTCACCTGGC 121
QY 537 TGGCGTGTGCTATCAATCTCAACTCTCAACTGCTTACCGATACCGAGTCCGACTGGAC 596
DB 122 GGGCGGCATGCTATCCCAATCTCACCATTGCTGGCGGAAGGCGAGGCTTAACCTGGAG 181
QY 597 AGGTGAAGACACGAGCTCTGGCAACAAAACTGAGTAGTGCTATATACCCCAAAG 656
DB 182 CGGTGACGACGAACACTGTCTGGCAGGGAATGCTGGCAAGTAGGTCTATACGACAAAG 241
QY 657 TAACTGATGCAACCGGGGCTTTACTGACCCAGACCGATGCGCAAAAGGCAACATTCAGCG 716
DB 242 TACCCTAATGCCATCGGGGCTTTACTGACCCAAACCGATGCGAAAGGCAATATTCAGCG 301
QY 717 GCTGGCTATGATGTGCGCGGAGCTTAAAGGGAGTTGTTAACTCAACTCAAGGTGAGCG 776
DB 302 TCTGGCTTATGACATTCGCGGTCAGTTAAAGGGAGTTGTTGACCGGTGAAGGCCAGAG 361
QY 777 GGAACAGGTGATTATCAATCGTCACTTCTCCGCGCGGCGCAAAAATTACGTCAAGA 836
DB 362 TGAACAGGTGATTGTTAAGTCCCTGAGCTGGTCAGCGCGGAGTCATTAATTTGGGTGAAGA 421
QY 837 GCACGGTAACGGGATTGTCACTGTAATACAGCTACGAACCGGAACCCAAACGGCTTATCGG 896

Db 422 GCACGGTAACGGCGTGGTTACCGAGTACAGTTATGAGCCCGGAAACTCAACGTCGTGATAG 481
QY 897 CATTACCCTCTCCGCTCCATCA-----GACGCCAAGGTGTTGCAAGACCTAC 943
DB 482 GTATACCACCCCGCGTGGCCCAANGGAGTCAATCANGAGCCAGAGTATTGTCAGGATCTAC 541
QY 944 GTATCAATATGACCCAGT-AGGCAATGTCAATATATATCCGTAATGATCGGGAAGC 998
DB 542 GCTATAAGTATGATCCCGTGGGGAATGATATCAGTATTTCATTAATGATGCCCNAC 597

RESULT 4
AQ991400/c
LOCUS       AQ991400.1 494 bp DNA linear GSS 14-AUG-2000
DEFINITION Photorhabdus luminescens strain W14 M13 library
              Photorhabdus luminescens genomic clone PLG02327, genomic survey
              sequence.
ACCESSION   AQ991400
VERSION     AQ991400.1  GI:9649994
KEYWORDS    GSS.
SOURCE      Photorhabdus luminescens
ORGANISM    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
              Enterobacteriaceae; Photorhabdus.
REFERENCE    1 (bases 1 to 494)
AUTHORS      ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
              Daborn,P.J., Bowen,D. and Blattner,F.R.
TITLE        A genomic sample sequence of the entomopathogenic bacterium
              Photorhabdus luminescens W14: potential implications for virulence
JOURNAL      Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
PUBMED       10919786
COMMENT      Contact: ffrench-Constant RH
              Department of Biology and Biochemistry
              University of Bath
              South Building, Bath BA2 7AY, UK
              Tel: (44) 1225 826621
              Fax: (44) 1225 826779
              Email: bssrfc@bath.ac.uk
              This is one of 2,122 random reads from the M13 library. For
              annotation of identified clones (BLASTX, BLASTN and mapping to E.
              coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
              Acids Res.
              Seq primer: M13 Forward
              Class: shotgun.
FEATURES     Location/Qualifiers
source       1..494
              /organism="Photorhabdus luminescens"
              /mol_type="genomic DNA"
              /strain="W14"
              /db_xref="taxon:29488"
              /clone="PLG02327"
              /dev_stage="primary phase variant"
              /clone_lib="Photorhabdus luminescens strain W14 M13
              library"
              /note="Genomic DNA from strain W14 was size selected (1-2
              kb) and then cloned into M13 Janus."
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Query Match      8.7%; Score 239.8; DB 9; Length 494;
Best Local Similarity 71.9%; Pred. No. 8.8e-52;
Matches 343; Conservative 0; Mismatches 127; Indels 7; Gaps 2;
QY 276 TATTACCTCAATGATTGTAAGTCGCCCGGTGTTGATCATCAATGCAACCGGTGTCG 335
DB 476 TGTGATTGAATGATTGAAGGTCGTTCCGGTAATGACAATGAATGCGCCCGGTGTCG 417
QY 336 CCAAAACCATCGTTATGAAGATAACACCCCTTCCCGTCTGCTCGCTATATCAACGAACA 395
DB 416 TCAGACCCGTCGTATGAAGGCAACA-CCTTCCCGTCTGCTTGTATTCTGTGAGCGAGCA 358
QY 396 AGT-----ACAGGCGAGGAGAGAAACGACCGCAACGCTTATCTGGGCGGCAATACGCC 449
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Db 357 AGTTTTCAACCAAGAGAGTGCTAAAGTGACAGAGCGCTTTATCTGGGCTGGGAATACAC 298
QY 450 GCAAGAAAAGATATCAACTCGCGGTCACTGTGTCGGCCATTACGATACCGGGGACT 509
Db 297 CTCGGAGAAAGATATAAACCCTCCGGTCTGTGTATACGCCACTACGACACAGCGGGAGT 238
QY 510 TACTCAACTCAATAGCCTTTCTCTGGCTGGCGTCTGTATCAATCTCAACAATGCT 569
Db 237 GACCCGGTTGATGAGTCAGTCACCTGGCGGGCGCATCTATCCCAATCTCACCAAATGCT 178
QY 570 TACCGATAACACAGGATGCCAGCTGGACAGGTGAAGACGAGAGCTCTTGGCAACAAAAC 629
Db 177 GCGGAGGCGCAGGAGCTAACTGGAGCGGTGACGACGAACTGTCTGGCAGGGAATGCT 118
QY 630 GAGTAGTGATGCTTATATCAACCAAGTAACTGATGACCGCGGCTTTACTGACCCA 689
Db 117 GGCAAGTGAGGTCTATACGACACAAAGTACCACTAATGCCATCGGGGCTTTACTGACCCA 58
QY 690 GACCGATGCCAAAGGCAACATTCAGCGCTGGCTATGATGTGGCGGCGAGCTAAA 746
Db 57 AACCGATGCCAAAGGCAATATTCAGCGCTGGCTTATGACATTCGCCGTCAGTTAAA 1

RESULT 5
AQ990055 406 bp DNA linear GSS 14-AUG-2000
LOCUS Rfc00763 Photorhabdus luminescens strain W14 M13 library
DEFINITION Photorhabdus luminescens genomic clone PLG00763, genomic survey sequence.

ACCESSION AQ990055
VERSION AQ990055.1 GI:9648649
KEYWORDS GSS.
SOURCE Photorhabdus luminescens
ORGANISM Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Photorhabdus.
1 (bases 1 to 406)
ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T., Daborn,P.J., Bowen,D. and Blattner,F.R.
A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

JOURNAL 10919786
PUBMED
REFERENCE
AUTHORS Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bsr@c Bath.ac.uk
This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res.
Seq primer: M13 Forward
Class: shotgun.
FEATURES
source Location/Qualifiers
1. .406
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clone="PLG00763"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13 library"
/note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

ORIGIN

Query Match 8.3%; Score 226.8; DB 9; Length 406;
Best Local Similarity 75.5%; Pred. No. 2.3e-48;
Matches 293; Conservative 0; Mismatches 94; Indels 1; Gaps 1;

QY 1447 AGCAACGGCATGAGACCAACTGAAAGTGAAGCAACAGCCAACTACTACGACGAA 1506
Db 1 AGCAACGGCATAGCCGCGCTAAAGTGAATGAACAACAACCTCAGATATATCCGCAACAA 60
QY 1507 CAACGGGTAACTCTATTTCGCGGACTGGAGCTACGACAAACCCAGACGCAACCAACA 1566
Db 61 CAACGGGTAACTCTATTTCGCGGCTGGAATACGTAACAACCCAGAAACGCGCAACA 120
QY 1567 AGGAAGAGTTACACGTTATCACCTCGGTGAAGCCGCTCGGCACAGGTACGGGTGTTG 1626
Db 121 ACAGAAGAGTTACACGTTATCACCTCGGTGAAGCCGCGCGCAAGTCCGAGTATTG 180
QY 1627 CACTGGGAGCGGTAAAGCAGAGATGTCAACAATAATCAACTAGTTACAGCTACGAT 1686
Db 181 CATTTGGGAGCGGTAAACCAAGATATTAATACAATCAGCTTCGTTACAGCTAGAT 240
QY 1687 AATCTCATCGGCTCCAGCCAGCTTGAATCGGCAACCAAGGCAAAATTTATCAGCG-AGGA 1745
Db 241 AATCTTATTTGGCTCCAGCCAACTTCAATTAGATAGCGAGCGCAAAATTTATCAAGTGAAGA 300
QY 1746 AGAGTATTATCCATTTTGGCGGACACCGCTGTGGGAGCAAAACAGCAACAGAGCCAG 1805
Db 301 AGAATATTATCCATTTTGGTGTACAAAGCGCTGTGGCGGNAAGGGATTAAACCGAACCCAG 360
QY 1806 CTATAAACGATTTCGCTATTCGCGCAAA 1833
Db 361 CTNTTAAACAATTCGTTATTTTGTAAAA 388

RESULT 6
AQ990688/c
LOCUS Rfc01498 Photorhabdus luminescens strain W14 M13 library
DEFINITION Photorhabdus luminescens genomic clone PLG01498, genomic survey sequence.

ACCESSION AQ990688
VERSION AQ990688.1 GI:9649282
KEYWORDS GSS.
SOURCE Photorhabdus luminescens
ORGANISM Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Photorhabdus.
1 (bases 1 to 594)
ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T., Daborn,P.J., Bowen,D. and Blattner,F.R.
A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

JOURNAL 10919786
PUBMED
REFERENCE
AUTHORS Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bsr@c Bath.ac.uk
This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res.
Seq primer: M13 Forward
Class: shotgun.
FEATURES
source Location/Qualifiers
1. .594
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clone="PLG01498"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13 library"

AO990013 547 bp DNA linear GSS 14-AUG-2000
Rfc00707 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG00707, genomic survey

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sequence.
ACCESSION AQ990013
VERSION AQ990013.1 GI:9648607
KEYWORDS
SOURCE
ORGANISM
Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE 1 (bases 1 to 547)
AUTHORS ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.
TITLE A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
PUBMED 10919786
COMMENT Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bsr@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: shotgun.
FEATURES
source
1. 547
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clone="PLG00707"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
/notes="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."
ORIGIN
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Best Local Similarity 76.18; Pred. No. 9.9e-29;
Matches 188; Conservative 0; Mismatches 59; Indels 0; Gaps 0;
QY 1753 TATCCATTTGGCGGACAGCGCTGTGGCGAGCAACAGCCAGGAGCCAGCTATAA 1812
Db 1 TATCCGTATGCGGTACCGCGATATGGCGGCGAGAAATCAGACAGAGCCAGCTACAA 60
QY 1813 ACATTCGCTATTCGCGCAAGACGAGATGCCACCGGTGTATTATTACGGTTATCGT 1872
Db 61 TTATTTCGTTACTCCGTAAGAGCGGGATGCCACTGGATTGTATTATTACGGCTACCGT 120
QY 1873 TATTACCAACCGTGGCGGCGAGATGGTTAAGCGCGACCGCGAGCAACCATTTAGTGGG 1932
Db 121 TATTATCAACCTTGGGTGGTGGATGGTTGATGGTCTGATCCGCGGGAACCGTGGATGG 180
QY 1933 CTGAATCTATACCGAATGGTAAGAAATATCTGTGAGTTTACAGATGAATAATGGATTA 1992
Db 181 CTGAATTTGATCCGAATGGTGAGGAATAACCCCATCATCTGACCTGACCATGACGGATTA 240
QY 1993 GCGCCAG 1999
Db 241 GCACCCG 247
RESULT 9
AQ990147
LOCUS 312 bp DNA linear GSS 14-AUG-2000
DEFINITION AQ990147 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG00869, genomic survey
sequence.
sequence.
ACCESSION AQ990147
VERSION AQ990147.1 GI:9648741
KEYWORDS
SOURCE
ORGANISM
Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE 1 (bases 1 to 312)
AUTHORS ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.
TITLE A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
PUBMED 10919786
COMMENT Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bsr@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: shotgun.
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1. 312
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clone="PLG00869"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
/notes="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."
ORIGIN
Query Match 5.4%; Score 148.8; DB 9; Length 312;
Best Local Similarity 71.4%; Pred. No. 8.8e-28;
Matches 222; Conservative 0; Mismatches 82; Indels 7; Gaps 2;
QY 976 AATATCGGTAATGATCGGAAGCCACTCGCTTTTGGCGCAATCAGAAAGTAGC-CCCGGA 1034
Db 2 AATATTTCGTAATGATCAGAAGCAACTCGATTCTGGCGTAATCAGAAATAGTACCCGGA 61
QY 1035 GAATAGCTATACCTACGATTCCCTGTATCAGCTTATCAGCGCCACCGGGCGGAAATGGC 1094
Db 62 AATGGGTATACCTATGATTCTCTGTACCACTTATCATAGCAACCGGCCGCGAATGGC 121
QY 1095 CAATATCGGTACGACAAACAACTTCCCTC-----CCCTGGCGTACCTTCTGACAA 1148
Db 122 TAACATTAGTCAGCAAGGAAGCCAGCTCCCTCTTTAGTTACCCCTCTTCTACCGATGA 181
QY 1149 CAATACCTACACTAATCTATCTCGAGCTACAGCTATGATCAGTGGTATCTGACGCA 1208
Db 182 CAATACCTATACCTAATCTATCTCGACTTATACCTACGAGTAGCGGCAACCTGACACA 241
QY 1209 AATTCCGACAGCTCGCCAGTACCAGAACAACTACACCGTGGCTTATCACCCCTCTCAAA 1268
Db 242 AATCCCGCATACGCTTCGCCAGGACATAACTGNCNCNAGATATTACCATTTNAAA 301
QY 1269 CCGCAGCAATC 1279
Db 302 CCGCAATAACC 312
RESULT 10
AQ901477/c
LOCUS 733 bp mRNA linear EST 24-MAY-2000

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Db 1041 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1100
Qy 2613 TGTGCAAAATTCCTGACATGAAGCAATATAAAATCATTAAGGACATAAATTA 2672
Db 1101 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1160
Qy 2673 TAGGATATCAACA 2685
Db 1161 AAAAAAAAAAAAAA 1173

RESULT 13
CNS018GS/c
LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC
DEFINITION BACN13P09 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL109318
VERSION AL109318.1 GI:5629622
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 942)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (DrosBAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.

FEATURES
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/notes="end : T7"

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Best Local Similarity 35.9%; Pred. No. 2.5e-06;
Matches 182; Conservative 61; Mismatches 264; Indels 0; Gaps 0;

Qy 2174 ACAGAGATTACTAAAGGTATAGAAAAAGTCAATATATATAGCCGACTTGAAGAA 2233
Db 593 AAGCAAAAAACGAAARGAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 534
Qy 2234 ACAGCTCCCTTCAGAAAAATCAAAACGATCTTCTTTAGATCTGAATATCCGTT 2293
Db 533 AAAAAATTNGAGACNACGAAAGAAAAAAGAAAAAGTAAAWWWWWAAACAGARAAAA 474
Qy 2294 ATATGCAAGAACCATACAGATACGATATCAGATATCGGAGAGCATATAATAGAA 2353
Db 473 ANANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 414
Qy 2354 GTAATCACCCCTGATTTTATTTCAGAAACCGATTTCTTTGCGTTAATGGATAAAGTGA 2413
Db 413 AAMACMBAARAAAAAAWAAACCGGTARAWTTTAAAWTTGTAACCRAAATATAAAAAA 354
Qy 2414 AAAATGATTTATCCGGTGAAGAAAAATTTATCGCGCAATGGAGGTTTATCATG 2473
Db 353 AAAAAAAWAAWARTAMWAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 294
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Qy 2474 ATTTAAAAATAAACAAATCAGAAATTCATGTCACTATGCTATGCTGGCCCATCCATATACG 2533
Db 293 WAAMRAAAWAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 234
Qy 2534 AATTGAGTAAATGAAGAAAGAGCGCTGTCGAAGAAACAGAACCCGCTATTGCAATAGATA 2593
Db 233 AAATTTAAATAAANAAWAAWTTGAWAAWATMGTTAAWAAATCGTTAWGAAAAWAAW 174
Qy 2594 GAGAAATATAATTTCAAAGGTGTTGGCAAAATTCCTGCAATGAAGCAATTTAAAAATCAT 2653
Db 173 AAAMWAAAAATATAAAWAAWAGCAAAATTTATGAATTWAAAAWAAWAAWAAAAWAA 114
Qy 2654 TGAAGGACATATAATTAATAGATAT 2680
Db 113 WAAAAGTAAWAAWAGCGATTTGRTTT 87

RESULT 14
CG753732/c
LOCUS P048-4-G03.ya Ppa EcoRI BAC Library Pristionchus pacificus genomic, genomic survey sequence.
DEFINITION CG753732
ACCESSION CG753732.1 GI:37978509
VERSION CG753732.1
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 1811)
AUTHORS Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K., Buntjer,J., van der Meulen,M. and Sommer,R.J.
TITLE An integrated physical and genetic map of the nematode Pristionchus pacificus
JOURNAL Mol. Genet. Genomics 269 (5), 715-722 (2003)
PUBMED 12884007
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.

FEATURES
source
1..1811
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Ppa EcoRI BAC Library"
/notes="The library was generated by a partial digest of the genomic DNA with EcoRI and cloning into the BAC vector."

ORIGIN
Query Match 2.4%; Score 65.4; DB 10; Length 1811;
Best Local Similarity 36.4%; Pred. No. 1.4e-05;
Matches 284; Conservative 0; Mismatches 461; Indels 0; Gaps 0;

Qy 1974 ACAAGATGAAATGGATTAGCGCCAGAAAAAGGAAATATACCAAGAGGTAAATTTCTT 2033
Db 1621 ANAAAAANNANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 1562
Qy 2034 TGATGAATTAATTAATTCAAATTTGCGACCCCAAAAGTTTCACATGTTGTCAATGGACGAA 2093
Db 1561 AAAAAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 1502
Qy 2094 AGAGACAGTTATACAAAAATAATTAATTCATTGAAGTGGTTGCGTGGTATCCGATCC 2153
Db 1501 AAAAAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 1442
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 17:17:29 ; Search time 1489 Seconds
(without alignments)
12286.488 Million cell updates/sec

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Perfect score: 2745
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2653.8	96.7	2748	12 ADM61381	Adm61381 Photorhab
3	2329	84.8	2748	10 ACF69438	Acf69438 Photorhab
4	2329	84.8	110000	10 ACF67367_23	Continuation (24 o
5	2329	84.8	110000	10 ACF67367_24	Continuation (25 o
6	2329	84.8	110000	10 ACF65386_4	Continuation (5 of
7	1442.2	52.5	2817	12 ADM61384	Adm61384 Photorhab
8	1440.6	52.5	2817	12 ADR18627	Adr18627 Photorhab
9	1440.6	52.5	2817	13 ADR21537	Adr21537 Photorhab
10	1321.4	48.1	2817	10 ACF69434	Acf69434 Photorhab
11	1321.4	48.1	110000	10 ACF65386_5	Continuation (6 of
12	1013.2	36.9	2811	10 ACF70848	Acf70848 Photorhab
13	1013.2	36.9	110000	10 ACF67367_39	Continuation (40 o
14	1013.2	36.9	110000	10 ACF65388_08	Continuation (9 of
15	1012.4	36.9	37948	2 AAZ06831	Aaz06831 Photorhab
16	1004.6	36.6	2883	12 ADM61382	Adm61382 Photorhab
17	1004.6	36.6	2883	12 ADR18623	Adr18623 Photorhab
18	1004.6	36.6	2883	13 ADR21526	Adr21526 Photorhab
19	989.4	36.0	2913	10 ACF69431	Acf69431 Photorhab

20	977.4	35.6	2880	10 ACF69421	Acf69421 Photorhab
21	972.4	35.4	2898	10 ACF71155	Acf71155 Photorhab
22	972.4	35.4	110000	10 ACF67367_42	Continuation (43 o
23	972.4	35.4	110000	10 ACF65388_05	Continuation (6 of
24	962	35.0	3132	2 AAT68850	Aat68850 Photorhab
25	962	35.0	3132	12 ADM61380	Adm61380 Photorhab
26	962	35.0	3132	13 ADR21505	Adr21505 Photorhab
27	960.4	35.0	3132	2 AAV29927	AAV29927 tccC gene
28	957.2	34.9	2850	12 ADM61383	Adm61383 Photorhab
29	957.2	34.9	2850	12 ADP18625	Adp18625 Photorhab
30	930	33.9	3132	10 ACF71170	Acf71170 Photorhab
31	930	33.9	110000	10 ACF67367_43	Continuation (44 o
32	930	33.9	110000	10 ACF65388_04	Continuation (5 of
33	874	31.8	110000	10 ACF65388_05	Continuation (6 of
34	730.8	26.6	2889	13 ADR21530	Adr21530 Xenorhabd
35	730.8	26.6	2889	14 AEB47813	Aeb47813 Native Xp
36	730.8	26.6	2947	13 ADR21533	Adr21533 Xenorhabd
37	730.8	26.6	2947	14 AEB47818	Aeb47818 XbaI to X
38	730.8	26.6	7508	13 ADR21534	Adr21534 Xenorhabd
39	730.8	26.6	7508	14 AEB47819	Aeb47819 XbaI to X
40	691.2	25.2	37544	3 AAA50029	Aaa50029 Cosmid CH
41	666	24.3	3048	13 ADR20366	Adr20366 Recombina
42	666	24.3	3048	13 ADR21495	Adr21495 Xenorhabd
43	666	24.3	3051	12 ADM61357	Adm61357 Xenorhabd
44	666	24.3	39005	13 ADR20357	Adr20357 Recombina
45	666	24.3	39005	13 ADR21486	Adr21486 Xenorhabd

ALIGNMENTS

RESULT 1
ABS52585
ID ABS52585 standard; DNA; 2745 BP.
XX
AC ABS52585;
XX
DT 30-DEC-2002 (first entry)
XX
DE P. luminescens (W-14) tccC2 gene.
XX
KW Gene; ds; toxin A; toxin B; TcdA; protoxin; TcdB, TccC2; transgenic;
KW monocot cell; dicot cell; oral toxin; insect; pest; TcBA.
XX
OS Photorhabdus luminescens.
XX
PH Key Location/Qualifiers
FT CDS 1..2745 /*tag= a
FT /product= "TccC2"
FT /partial
FT /note= "No stop codon shown"
XX
PN US2002078478-A1.

XX
PD 20-JUN-2002.
XX
PF 26-MAR-2001; 2001US-00817514.
XX
PR 24-MAR-2000; 2000US-0191806P.
XX
PA (FFRE/) FFRENCH-CONSTANT R H.
PA (BOWE/) BOWEN D.
PA (ROCH/) ROCHELEAU T A.
PA (WATE/) WATERFIELD N R.
XX
PI Ffrench-Constant RH, Bowen D, Rocheleau TA, Waterfield NR;
XX
DR WPI; 2002-655379/70.
XX
PT P-PSDB; ABG32653.
PT Novel nucleic acid sequences which encode genes, tcdB and tccC2 from Photorhabdus luminescens W-14, useful in heterologous expression of

orally active insect toxins.

Claim 3; Page 24-27; 40pp; English.

The invention discloses an isolated nucleic acid that encodes TcdB or TccC2 from *Photobacterium luminescens* W-14. Also disclosed is a transgenic monocot or dicot cell and a transgenic plant (including the seeds) both with genomes comprising tcdB and tccC2 nucleic acids. The nucleic acids are useful for producing Toxin A or B of *P. luminescens* W-14 in a heterologous host and for encoding TcdB or TccC2 for producing an orally active insect toxin in a host, where the host also expresses TcdA or TcdB from *P. luminescens* W-14. Heterologous expression of Toxin A does not afford the level of oral toxicity to insects as that of the native toxin, but the coexpression increases this toxicity. The transgenic plants expressing effective amounts of the toxins protect themselves from insect pests. When the insects feeds on the transgenic plant it also ingests the toxins and this deters the insect from further biting into the plant and may even harm or kill the insect. The sequence presented is the *P. luminescens* (W-14) tccC2 gene

Sequence 2745 BP; 905 A; 623 C; 606 G; 611 T; 0 U; 0 Other;

Query Match 100.0%; Score 2745; DB 6; Length 2745;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2745; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGAGCAGTTACAAATTCGCAATTCGCAAAAGACCCCTCGATTAAAGGTATTAGATAAC	60
Db	1	ATGAGCAGTTACAAATTCGCAATTCGCAAAAGACCCCTCGATTAAAGGTATTAGATAAC	60
Qy	61	AGGAAATTAATGATGACGTTTAAAGATATCTACGCACTCAAGCTGACGAAACAGTGAT	120
Db	61	AGGAAATTAATGATGACGTTTAAAGATATCTACGCACTCAAGCTGACGAAACAGTGAT	120
Qy	121	GAATTAATTAAGTTCTATGAGTTCAATATTCGCGGATTTTCAGGTAAAAGCACCAGATCCT	180
Db	121	GAATTAATTAAGTTCTATGAGTTCAATATTCGCGGATTTTCAGGTAAAAGCACCAGATCCT	180
Qy	181	CGTAAATTAATTAACAGAGCGGCGCAAAATTTCAATTCGTTCTTTTAAATCTTGC CGGTCAA	240
Db	181	CGTAAATTAATTAACAGAGCGGCGCAAAATTTCAATTCGTTCTTTTAAATCTTGC CGGTCAA	240
Qy	241	GTTTTACGTGAAGAAAGTTGATGCGCGTCCGACTATTACCCCTCAATGATATTGAAGT	300
Db	241	GTTTTACGTGAAGAAAGTTGATGCGCGTCCGACTATTACCCCTCAATGATATTGAAGT	300
Qy	301	CGCCCGGTGTTGATCATCAATGCAACCGGTGTCGCCCAAAACCAATCGTTATGAAGATAAC	360
Db	301	CGCCCGGTGTTGATCATCAATGCAACCGGTGTCGCCCAAAACCAATCGTTATGAAGATAAC	360
Qy	361	ACCTTCCCGGTGCTGCTCGCTATCACCGAAACAGTACGCGGAGGAGAGAAACGACC	420
Db	361	ACCTTCCCGGTGCTGCTCGCTATCACCGAAACAGTACGCGGAGGAGAGAAACGACC	420
Qy	421	GAACGTCTTATCTGGCGGCAATACGCGCAAGAAAGATTAACAACCTCGCCCGGTGAG	480
Db	421	GAACGTCTTATCTGGCGGCAATACGCGCAAGAAAGATTAACAACCTCGCCCGGTGAG	480
Qy	481	TGTTGCGCCATTAACGATACCGCGGACTTACTCAACTCAATAGCCCTTCTCGGCTGGC	540
Db	481	TGTTGCGCCATTAACGATACCGCGGACTTACTCAACTCAATAGCCCTTCTCGGCTGGC	540
Qy	541	GTCTGTCTATCACAATCTCAACACTGTTACCGATTAACAGGATGCGGACTGACAGGT	600
Db	541	GTCTGTCTATCACAATCTCAACACTGTTACCGATTAACAGGATGCGGACTGACAGGT	600
Qy	601	GAACACGAGCCCTCTGCAACAAAACCTGAGTAGTGATGCTATATCACCCCAAGTAAC	660
Db	601	GAACACGAGCCCTCTGCAACAAAACCTGAGTAGTGATGCTATATCACCCCAAGTAAC	660
Qy	661	ACTGATGCCACCGGGGCTTTACTGACCCAGACCCGATGCGCAAGGCAACATTCACGGCTG	720
Db	661	ACTGATGCCACCGGGGCTTTACTGACCCAGACCCGATGCGCAAGGCAACATTCACGGCTG	720

Qy	721	GCCTATGATGTGGCGGCGAGCTAAAGGGAGTTGGTTAACTCAAAAGGTACGGCGAA	780
Db	721	GCCTATGATGTGGCGGCGAGCTAAAGGGAGTTGGTTAACTCAAAAGGTACGGCGAA	780
Qy	781	CAGGTGATTATCAAAATCGCTTAACCTACTCCGCGCGCGGCAAAATTTACGTGAAGAGCAC	840
Db	781	CAGGTGATTATCAAAATCGCTTAACCTACTCCGCGCGCGGCAAAATTTACGTGAAGAGCAC	840
Qy	841	GGTAACGGGATTTGCTAATGAATACAGCTAGAAACCGGAAACCCAAAGGCTTATCGGCATT	900
Db	841	GGTAACGGGATTTGCTAATGAATACAGCTAGAAACCGGAAACCCAAAGGCTTATCGGCATT	900
Qy	901	ACCACCTCGCGCTCCATCAGACGCCAAGGTGTTGCAAGACTACGCTATCAATATGACCCA	960
Db	901	ACCACCTCGCGCTCCATCAGACGCCAAGGTGTTGCAAGACTACGCTATCAATATGACCCA	960
Qy	961	GTAGGCAATGTCAATTAATATCCGTAATGATGCGGAAGCCACTCGCTTTTGGCGCAATCAG	1020
Db	961	GTAGGCAATGTCAATTAATATCCGTAATGATGCGGAAGCCACTCGCTTTTGGCGCAATCAG	1020
Qy	1021	AAAGTAGCCCCGGAGAAATAGCTATACCTAGATTCCCTGTATCAGCTTATCAGGGCCACC	1080
Db	1021	AAAGTAGCCCCGGAGAAATAGCTATACCTAGATTCCCTGTATCAGCTTATCAGGGCCACC	1080
Qy	1081	GGCGCGAAATGCGCAATATCGGTACAGAAACCAACCTCCCTCCCTCGCTACCT	1140
Db	1081	GGCGCGAAATGCGCAATATCGGTACAGAAACCAACCTCCCTCCCTCGCTACCT	1140
Qy	1141	TCGACAAACAATACCTACACTAATCTACTCGAGCTACAGCTATGATCAAGTGGTAAAT	1200
Db	1141	TCGACAAACAATACCTACACTAATCTACTCGAGCTACAGCTATGATCAAGTGGTAAAT	1200
Qy	1201	CTGACGAAATTCGCGCAGCTCGCCAGCTACCCAGAAACCTACACCTGGGTGCTATCACC	1260
Db	1201	CTGACGAAATTCGCGCAGCTCGCCAGCTACCCAGAAACCTACACCTGGGTGCTATCACC	1260
Qy	1261	CTCTCAACCGCAGCAATCGGGGTGTTCTCAGTACCTACCAACCGATCCAAATCAAGTG	1320
Db	1261	CTCTCAACCGCAGCAATCGGGGTGTTCTCAGTACCTACCAACCGATCCAAATCAAGTG	1320
Qy	1321	GATACGTGTTGATGCGCGTGTACCAACACAGTTTATTTACCCGGACAGACACTTATC	1380
Db	1321	GATACGTGTTGATGCGCGTGTACCAACACAGTTTATTTATCCCGACAGACACTTATC	1380
Qy	1381	TGACACACGAGGAGGTTAAAGCAGTTTAAATGGCCCGGAAATGAGTGGTACCGC	1440
Db	1381	TGACACACGAGGAGGTTAAAGCAGTTTAAATGGCCCGGAAATGAGTGGTACCGC	1440
Qy	1441	TACGACAGCAACCGCATGAGCAACTGAAAGTGAGTGAAACAGCAACCCAGAAATCTACG	1500
Db	1441	TACGACAGCAACCGCATGAGCAACTGAAAGTGAGTGAAACAGCAACCCAGAAATCTACG	1500
Qy	1501	CAGCAACAAACGGGTAATCTATTTGCGGGAATGAGCTACGCAACCCAGAGCAACGCC	1560
Db	1501	CAGCAACAAACGGGTAATCTATTTGCGGGAATGAGCTACGCAACCCAGAGCAACGCC	1560
Qy	1561	ACAACAAACGGAAGGTTACGCTTTATCACTCGGTGAAGCCGCTCGCGCACAGGTACGG	1620
Db	1561	ACAACAAACGGAAGGTTACGCTTTATCACACTCGGTGAAGCCGCTCGCGCACAGGTACGG	1620
Qy	1621	GTCTTGCACTGGGAGAGCGGTAAAGCAGAGATGTCAACAATTAATCAACTACGTTACAGC	1680
Db	1621	GTCTTGCACTGGGAGAGCGGTAAAGCAGAGATGTCAACAATTAATCAACTACGTTACAGC	1680
Qy	1681	TACGATAATCTGATCGGCTCCAGCCAGCTTTGAATCTGACAAACCAAGGACAAATTTATCAGC	1740
Db	1681	TACGATAATCTGATCGGCTCCAGCCAGCTTTGAATCTGACAAACCAAGGACAAATTTATCAGC	1740
Qy	1741	GAGGAAGAGTATTATCCATTTTGGCGGAGCAGCGCTGTGGGAGCAACAGCCAAACAGAA	1800
Db	1741	GAGGAAGAGTATTATCCATTTTGGCGGAGCAGCGCTGTGGGAGCAACAGCCAAACAGAA	1800

1801 GCCAGCTATATAACGATTCCTATTCGCGCAAGAACGAGATGCCACCGGGTTGTATTAT 1860
Dbb GCCAGCTATATAACGATTCCTATTCGCGCAAGAACGAGATGCCACCGGGTTGTATTAT 1860
QyTACGGTTATCGTTATTACCAACCGTGGCGGCGGAGATGGTTAAGCGCGGACCCGCGAGGA 1920
DbbTACGGTTATCGTTATTACCAACCGTGGCGGCGGAGATGGTTAAGCGCGGACCCGCGAGGA 1920
QyACCAATTGATGGCTGGAATCTATACCGGAATGGTAAAGAAATTAATCCTGTGAGTTTACAAGAT 1980
DbbACCAATTGATGGCTGGAATCTATACCGGAATGGTAAAGAAATTAATCCTGTGAGTTTACAAGAT 1980
QyGAAAAATCGATTAGCCCGAGAAAAAGGGAATATACCAAGAGGTAAATTTCTTTGTATGAA 2040
DbbGAAAAATCGATTAGCCCGAGAAAAAGGGAATATACCAAGAGGTAAATTTCTTTGTATGAA 2040
QyTTAAAAATTTCAAAATTTGGCAGCCAAAGTTTCATGTGTTCTCAAAATGGACGAGAAAGAGAGC 2100
DbbTTAAAAATTTCAAAATTTGGCAGCCAAAGTTTCATGTGTTCTCAAAATGGACGAGAAAGAGAGC 2100
QyAGTTATACAAAAATAAATCAATTGAAAGTGGTTCGTCGCTGATTCGCGATCCGTCGGGT 2160
DbbAGTTATACAAAAATAAATCAATTGAAAGTGGTTCGTCGCTGATTCGCGATCCGTCGGGT 2160
QyTATTTGCTAAGCCACGAGAGGTACTTAAAGGTATAGAAAAAGTCAAAATCATATATAGC 2220
DbbTATTTGCTAAGCCACGAGAGGTACTTAAAGGTATAGAAAAAGTCAAAATCATATATAGC 2220
QyCGACTTGAAGAAACAGCTCCCTTTCAGAAAAATCAAAAAACGAATCTTCTTTAGGATCT 2280
DbbCGACTTGAAGAAACAGCTCCCTTTCAGAAAAATCAAAAAACGAATCTTCTTTAGGATCT 2280
QyGAAATATCCGGTTATATGGCAAGAACCATACAGATACGATATCAGAAATATGCCGAAGAG 2340
DbbGAAATATCCGGTTATATGGCAAGAACCATACAGATACGATATCAGAAATATGCCGAAGAG 2340
QyCATAAATATAGAAATATACCCCTGATTTTATTCAGAAACCGATTTCTTTGGGTTAATG 2400
DbbCATAAATATAGAAATATACCCCTGATTTTATTCAGAAACCGATTTCTTTGGGTTAATG 2400
QyGATAAAAGTCAAAAAATGATTTATTCGCGTGAAGAAAAATTTATGCGCAATGGAGGTT 2460
DbbGATAAAAGTCAAAAAATGATTTATTCGCGTGAAGAAAAATTTATGCGCAATGGAGGTT 2460
QyAAGGTTTATCATGATTTTAAAAATATAACAATCAGATTCAGATTCATGCAATGGCC 2520
DbbAAGGTTTATCATGATTTTAAAAATATAACAATCAGATTCAGATTCATGCAATGGCC 2520
QyCATCCCTATACGCAATTTAGTAATGAAGAAAGCGCTGTTGCAAGAAACAGAACCCGCT 2580
DbbCATCCCTATACGCAATTTAGTAATGAAGAAAGCGCTGTTGCAAGAAACAGAACCCGCT 2580
QyATTGCAATAGATAGAGAAATATATTTTCAAGGTGTTGGCAATTCCTGACAAATGAAGCA 2640
DbbATTGCAATAGATAGAGAAATATATTTTCAAGGTGTTGGCAATTCCTGACAAATGAAGCA 2640
QyATTAAAAAATCATTTGAAGGACATATAATTAATAGGATATCAACAGAGGCTATTAAATTT 2700
DbbATTAAAAAATCATTTGAAGGACATATAATTAATAGGATATCAACAGAGGCTATTAAATTT 2700
QyCGCTCTCGGGCTATCGCTGAGAAATTTTAGGAATGCGGAGAACTTCA 2745
DbbCGCTCTCGGGCTATCGCTGAGAAATTTTAGGAATGCGGAGAACTTCA 2745

RESULT 2
ADN61381
ID ADN61381 standard; DNA; 2748 BP.
XX
AC ADN61381;
XX
DT
XX O1-JUL-2004 (first entry)

DE Photorhabdus strain W14 tccc2 toxin complex DNA.
XX Cry; toxic; lepidopteran pest; toxin complex; insecticide; strain W14;
KW de; tccc2.
XX
OS Photorhabdus sp.
PN W02004002223-A2.
XX
PD 08-JAN-2004.
XX
PF 27-JUN-2003; 2003WO-US020082.
XX
PR 28-JUN-2002; 2002US-0392633P.
PR 21-JAN-2003; 2003US-0441647P.
XX
PA (DOWC) DOW AGROSCIENCES LLC.
XX
PI Bintrim SB, Bevan SA, Zhu B, Merlo DJ;
XX MPI; 2004-082821/08.
DR
XX Screening a culture of Paenibacillus isolate for Cry protein or toxin
PT complex protein, useful for controlling lepidopterans, comprises
PT obtaining DNA or protein from the culture and assaying the presence of
PT the gene or protein.
XX
PS Example 12; SEQ ID NO 45; 220pp; English.
XX
CC The invention relates to a novel method for screening a culture of a
CC Paenibacillus isolate for a gene encoding a protein selected from a Cry
CC protein that is toxic to a lepidopteran pest and a toxin complex protein.
CC The method comprises obtaining DNA from the culture and assaying the DNA
CC for the presence of the gene or obtaining a protein produced by the
CC culture and assaying the presence of a protein that indicates the
CC presence of the gene in the isolate. The method of the invention has
CC insecticide applications and may be useful for screening Paenibacillus
CC sp. for toxin complex (TC)-like genes and proteins which may themselves
CC be used to enhance or potentiate the activity of a stand-alone
CC xenorhabdus toxin protein. The method may also be useful for screening
CC Paenibacillus sp. and others for insecticidal thiaminase genes and
CC proteins for controlling insects, particularly lepidopterans. The current
CC sequence is that of the Photorhabdus strain W14 tccc2 toxin complex DNA
XX of the invention.
SQ
SQ Sequence 2748 BP; 907 A; 621 C; 608 G; 612 T; 0 U; 0 Other;
Query Match 96.7%; Score 2653.8; DB 12; Length 2748;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 2688; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
Qy 1 ATGAGCAGTTACAAATTCGCAATTTGACCAAAAGACCCCTCGATTAAAGTTATTAGATAAC 60
Db 1 ATGAGCAGTTACAAATTCGCAATTTGACCAAAAGACCCCTCGATTAAAGTTATTAGATAAC 60
Qy 61 AGGAAATTAATATGATGATCTACTTTAGAAATATCTACGCACTCAAGCTGACGAAAAACAGTGAT 120
Db 61 AGGAAATTAATATGATGATCTACTTTAGAAATATCTACGCACTCAAGCTGACGAAAAACAGTGAT 120
Qy 121 GAATTAATTAACGTTCTATGAGTTCAATATTCGGGATTTTCAGGTAAAAACACCGATCCT 180
Db 121 GAATTAATTAACGTTCTATGAGTTCAATATTCGGGATTTTCAGGTAAAAACACCGATCCT 180
Qy 181 CGTAAAAATTAATAACCCAGAGCGGCCCAAAATTTCAATTCGTGCTTTTAAATCTTTCGGGTCAA 240
Db 181 CGTAAAAATTAATAACCCAGAGCGGCCCAAAATTTCAATTCGTGCTTTTAAATCTTTCGGGTCAA 240
Qy 241 GTTTTACGTGAAGAAAGTGTTCGATGCGGTGCGGACTATTACCCCTCAATGATTTGAAAGT 300
Db 241 GTTTTACGTGAAGAAAGTGTTCGATGCGGTGCGGACTATTACCCCTCAATGATTTGAAAGT 300
Qy 301 CGCCCGGTGTTGATCATCAATGCAACCGGTGTCGCCCAAAACCATCGTTTATGAAGATAAC 360
Db 301 CGCCCGGTGTTGATCATCAATGCAACCGGTGTCGCCCAAAACCATCGTTTATGAAGATAAC 360

Db 301 CGCCGGTGTGATCATCAATGCAACCGGTGTCGCCCAAAACCATCGTTATGAAGATAAC 360
Qy 361 ACCCTTCCGGTGTCTGCTGCTATACCGCAACAAGTACAGGCGAGAGAAACGACC 420
Db 361 ACCCTTCCGGTGTCTGCTGCTATCACCGAAACAAGTACAGGCGAGAGAAACGACC 420
Qy 421 GAAGCTCTTACTCTGGGCGGCAATACGCCGCAAGAAAGATTACAACTTCGCGGTAC 480
Db 421 GAAGCTCTTACTCTGGGCGGCAATACGCCGCAAGAAAGATTACAACTTCGCGGTAC 480
Qy 481 TGTGTCGCCATTACGATACCGCGGACTTACTCAACTCAATAGCCTTTCTGCTGGC 540
Db 481 TGTGTCGCCATTACGATACCGCGGACTTACTCAACTCAATAGCCTTTCTGCTGGC 540
Qy 541 GTGCTGTATCACAATCTCAACAACTGTTACCGATTAACGAGGATGCCGACTGACAGGT 600
Db 541 GTGCTGTATCACAATCTCAACAACTGTTACCGATTAACGAGGATGCCGACTGACAGGT 600
Qy 601 GAAGACGAGCCTCTCGCAACAAAACCTGAGTAGTGTATATCAACCAAGTAAC 660
Db 601 GAAGACAAAAGCCTCTCGCAGCAAAAACCTGAGCAGTGTATATCAACCAAAAATAA 660
Qy 661 ACTGATGCCACCGGGCTTTACTGACCCAGACCGATGCCAAAGGCAACATTCAGCGCTG 720
Db 661 GCCGATGCCACCGGGCTTTATTGACCCAGACCGATGCCAAAGGCAACATCCAGCGTCTG 720
Qy 721 GCCTATGATGTGGCCGGCAGCTAAAAGGAGTTGGTTAACTCACTCAAAGTTCAGGCGAA 780
Db 721 GCCTACGACGCTAGCCGGCAGCTAAAAGGCTTTGGTTGACACTCAAAAGTTCAGGCGAG 780
Qy 781 CAGTGATTAATCAATCGCTAACCTACTCCGCCCGGGCAAAAATTCAGTGAAGACAC 840
Db 781 CAAGTGATTAATCAATCGCTAACCTACTCCGCCCGGGCAAAAATTCAGGGAAGACAC 840
Qy 841 GGTAACGGGATTGCTACCTGAATACAGCTACGAACCGGAAACCCAAACCGCTTATCGGCATT 900
Db 841 GGTAACGGGTTATCACTGAATACAGCTATGAACCAAGAACCCAAACCGCTTATCGGTATT 900
Qy 901 ACCACTCGCGTCCATCAGACGCAAGGTGTGCAAGACCTACGCTATCAATATGACCCA 960
Db 901 GCCACCGCGCTCGCTCAGACGCAAAAGTTGCAAGACTTACGCTATCAATATGACCCG 960
Qy 961 GTAGGCAATGCAATTAATCCGTAATGATCGGAGGCCACTCGCTTTTGGCGCAATCAG 1020
Db 961 GTAGGCAATGATCAATATCCGTAATGATCGGAGGCCACCCGCTTTTGGCGCAATCAG 1020
Qy 1021 AAAGTAGCCCCGAGAAATAGCTATACCTTACGATTCCTGTATCAGCTTATCAGCGCCACC 1080
Db 1021 AAAGTGTCCCGGAGAAATAGCTATACCTTACGATTCCTGTATCAGCTTATCAGTCCACC 1080
Qy 1081 GGGCGGAAATGGCCAAATCGGTACGAAACCAACCAACTTCCCTCCCTGCGCTACCT 1140
Db 1081 GGGCGGAAATGGCTAATATAGGTACGAAATAACCAACTGCGCTCCCTGCGCTACCT 1140
Qy 1141 TCTGACAACTACTCACTAACTATCTACGAGCTACAGCTATGATCAAGTGTAAAT 1200
Db 1141 TCTGACAACTAACTCACTAACTATCTACGAGCTACAGCTATGATCAAGTGTAAAT 1200
Qy 1201 CTGACGCAAAATTCGGCAGCTCGCCAGTACCCAGAACCAACTACCGTGGCTATCAC 1260
Db 1201 CTGACGCAAAATTCGGCAGCTCGCCAGTACCCAGAACCAACTACCGTGGCTATCAC 1260
Qy 1261 CTCTCAAAACCCGAGCAATTCGGGGTGTCTCAGTAGTACGCTAACCAACGATCAAGTG 1320
Db 1261 CTCTCAAAACCCGAGCAATTCGGGGTGTCTCAGTAGTACGCTAACCAACGATCAAGTG 1320
Qy 1321 GATACGTTGTTGATCCGGTGTGTCACCAACCAAGTTTATTCACCGGACGACTTATC 1380
Db 1321 GATACGTTGTTGATCCGGTGTGTCACCAACCAAGTTTATTCACCGGACGACTTATC 1380
Qy 1381 TGGACACACGAGGAGGTTAAAGCAGGTTAAATATGCCCCGGAAATGAGTGTACCGC 1440
Db 1381 TGGACACACGAGGAGGTTAAAGCAGGTTAAATATGCCCCGGAAATGAGTGTACCGC 1440

Qy 1441 TACGACAGCAACGGCATGAGCAAACTGAAAGTGAGTGAACAGCCAAACCCAGAATACTACG 1500
Db 1441 TACGACAGCAACGGCATGAGCAAACTGAAAGTGAGTGAACAGCCAAACCCAGAATACTACG 1500
Qy 1501 CAGCAACAAACGGGTAAATCTATTTCGCGGACTGGAGCTACGCAACAACCCAGAGCAACGCC 1560
Db 1501 CAGCAACAAACGGGTAAATCTATTTCGCGGACTGGAGCTACGCAACAACCCAGAGCAACGCC 1560
Qy 1561 ACAACAAACGGAAGAGTTACACGTTATCACTCGGTGAAAGCCGTCGCGCACAGGTACGG 1620
Db 1561 ACAACAAACGGAAGAGTTACACGTTATCACTCGGTGAAAGCCGTCGCGCACAGGTACGG 1620
Qy 1621 GTGTTGCACTGGGAGAGCGGTAAAGCAGAGATGTCAACAATAATCAACTACGTTACAG 1680
Db 1621 GTGTTGCACTGGGAGAGCGGTAAAGCAGAGATGTCAACAATAATCAACTACGTTACAG 1680
Qy 1681 TAGATAAATCTGATCGGCTCCAGCCAGCTTGAACCTGGACAACCAAGGACAAAATTTATCAG 1740
Db 1681 TAGATAAATCTGATCGGCTCCAGCCAGCTTGAACCTGGACAACCAAGGACAAAATTTATCAG 1740
Qy 1741 GAGGAAGAGTATTTATCCATTTGGCGGACAGCGCTGTGGGCGACAAACAGCCAAACAGAA 1800
Db 1741 GAGGAAGAGTATTTATCCATTTGGCGGACAGCGCTGTGGGCGACAAACAGCCAAACAGAA 1800
Qy 1801 GCCAGCTATAAAGCAGTTCCGTTATCCGCAAGAGACGAGATGCCACCGGGTTGTATTAT 1860
Db 1801 GCCAGCTATAAAGCAGTTCCGTTATCCGCAAGAGACGAGATGCCACCGGGTTGTATTAT 1860
Qy 1861 TAGCGTTATCGTTATTAACAAACCGTGGCGGCGAGATGTTAAGCGCGACCCGCGCAGGA 1920
Db 1861 TAGCGTTATCGTTATTAACAAACCGTGGCGGCGAGATGTTAAGCGCGGACCCGCGCAGGA 1920
Qy 1921 ACCATTGATGGCTGAATCTATACCGAATGGTAAAGAAATACTCTGTAGTTTACAAGAT 1980
Db 1921 ACCATTGATGGCTGAATCTATACCGAATGGTAAAGAAATACTCTGTAGTTTACAAGAT 1980
Qy 1981 GAAAAATGGATTAGCCGACAGAAAAGGAATATACCAAGAGGTAAATTTCTTTTGTATGAA 2040
Db 1981 GAAAAATGGATTAGCCGACAGAAAAGGAATATACCAAGAGGTAAATTTCTTTTGTATGAA 2040
Qy 2041 TTAATAATTCAAAATTTGGCAGCCAAAAGTTTCACTGTTGTCAAATGGAAACGAGAAAGAGC 2100
Db 2041 TTAATAATTCAAAATTTGGCAGCCAAAAGTTTCACTGTTGTCAAATGGAAACGAGAAAGAGC 2100
Qy 2101 AGTTATACAAAAATAAATCAATTTGAAAGTGGTTGTTGTCGGTGATTTCCGATCCGTCGGT 2160
Db 2101 AGTTATACAAAAATAAATCAATTTGAAAGTGGTTGTTGTCGGTGATTTCCGATCCGTCGGT 2160
Qy 2161 TATTTGCTAAGCCACAGNAGTTACTAAGAGGTATAGAAAAGTCAAAATCATATATAGC 2220
Db 2161 TATTTGCTAAGCCACAGNAGTTACTAAGAGGTATAGAAAAGTCAAAATCATATATAGC 2220
Qy 2221 CGACTTTGAAGAAAACAGCTCCCTTTTCAGAAAAATCAAAAAACGAATCTTTCTTTAGGATCT 2280
Db 2221 CGACTTTGAAGAAAACAGCTCCCTTTTCAGAAAAATCAAAAAACGAATCTTTCTTTAGGATCT 2280
Qy 2281 GAAATATCCGGTTATATGGCAAGAACCATACAAGATACGATATCAGATATGCCGAAGAG 2340
Db 2281 GAAATATCCGGTTATATGGCAAGAACCATACAAGATACGATATCAGATATGCCGAAGAG 2340
Qy 2341 CATAAATATAGAAGTAATCACCTGATTTTATTCAGAAAACCGATTTCTTTGGGTTAATG 2400
Db 2341 CATAAATATAGAAGTAATCACCTGATTTTATTCAGAAAACCGATTTCTTTGGGTTAATG 2400
Qy 2401 GATAAAGTGAAGAAAATGATTTATTCGGTGAAGAAAAATTTATTCGGCAATGGAGGTT 2460
Db 2401 GATAAAGTGAAGAAAATGATTTATTCGGTGAAGAAAAATTTATTCGGCAATGGAGGTT 2460
Qy 2461 AAGGTTTATCATGTTTAAAAATAAACAATCAAGATTAACATGTCAACTATGCAATTGGCC 2520
Db 2461 AAGGTTTATCATGTTTAAAAATAAACAATCAAGATTAACATGTCAACTATGCAATTGGCC 2520

Qy	961	GTAGGCAATGTCAATTAATATCCGTAATGATCGGGAAGCCACTCGCTTTTGGCGCAATCAG	1020
Db	961		
Qy	1021	AAAGTAGCCCGGAGAAATAGCTATACCTACGATTCCCTGTATACAGTTATCAGCGCCACC	1080
Db	1021		
Qy	1081	GGGCGGAAATGGCCAAATATCGGTTCAGCAAAACCAACTTCCCTCCCTGGCTACCT	1140
Db	1081		
Qy	1141	TCTGACAAACATACCTACACTAACTATACCTCGCAGCTACAGCTATGATACAGTGGTAAT	1200
Db	1141		
Qy	1201	CTGACGCAAAATTCGGGCACAGCTCCGCAGCTACCCAGAACAACTACACCGTGGCTATCAC	1260
Db	1201		
Qy	1261	CTCTCAAACCCGACCAATCGGGGTCTCAGTACGCTAACCCAGGATCCAAATCAAGTG	1320
Db	1261		
Qy	1321	GATACGTTGTTGATGCCGTGGTCCACCAACCAAGTTTATTACCCTGGACAGACACTTTATC	1380
Db	1321		
Qy	1381	TGGACACCAAGGAGAGTTAAAGCAGGTTAATATGGCCCGGAAATGAGTGGTACCGC	1440
Db	1381		
Qy	1441	TACGACAGCAACGGCATGAGACAACCTGAAAGTGTGAAACGCAACCCAGATACCTACG	1500
Db	1441		
Qy	1501	CAGCAACAAAGGGTAATCTATTTCGGGAGCTGAGCTACGCAACCCAGCAACGCC	1560
Db	1501		
Qy	1561	ACAAACACGGAAGAGTTACAGTTTATCACACTCGGTGAAGCGGTTCGCGCACAGGTACGG	1620
Db	1561		
Qy	1621	GTGTTGCACTGGGAGAGGGTAAGCCAGAAATGTCAACAATATCACTACGTTACAGC	1680
Db	1621		
Qy	1681	TACGATATCTGATCGGCTCCAGCCAGCTTGAACTGGACACCAAGGACAAATTTATCAGC	1740
Db	1681		
Qy	1741	GAGGAAGAGTATTATCCATTCGGCGGCACACGATGTGGGCAGCCATAGCCNAACAGAA	1800
Db	1741		
Qy	1801	GCCAGCTATAAAGCATTCGCTATTTCGGGCAAGAAACGAGATGCCACGGGTTGTATAT	1860
Db	1801		
Qy	1861	TACGTTATCGTTATTACCAACCGTGGCGGCAGATGGTTAAGCGGACCCCGCAGGA	1920
Db	1861		
Qy	1921	ACCAATTGATGGCTGAATCTATACCGAATGTGTAAGAAATAATCTCTGTGAGTTTACAAGAT	1980
Db	1921		
Qy	1981	GAAATGGAATTAGCCCGCAAAAAGGGGAAATATATACCAAGAGGTAATTTCTTTTGATGAA	2040
Db	1981		

Qy	2041	TTAAATTTCAAATTCGAGCCAAAAGTTTCAATGTTGTCAAATGGAACGAGAAAGAGAGC	2100
Db	2041		
Qy	2101	AGTTATACAAAATAAATCAATTTGAAAGTGGTTCGTTGTCGGTGAATCCCGATCCGTCCGGT	2160
Db	2101		
Qy	2161	TATTTCTAGCCACCAAGAGTTTACTTAAAGGTATAGAAAAAGTCAAATCATATATAGC	2220
Db	2161		
Qy	2221	CGACTTGAAGAAAACAGCTCCCTTTTCAGAAAAATCAAAAAACGAATCTTTCTTTAGGATCT	2280
Db	2221		
Qy	2281	GAAATATCAGAGTAAATCAACAGATACGATATCAGATATCAGAAATATGCGGAAGAG	2340
Db	2281		
Qy	2341	CATATAATATAGAGTAAATCAACCTGATTTTATTCAGAAAACCGATTTCTTTGCGTTAATG	2400
Db	2341		
Qy	2401	GATAAAGTGAAAAAATGATTTCCGGTGAAAGAAAAATTTATGCGCAATGGAGGTT	2460
Db	2401		
Qy	2461	AAGTTTATCATGTTTAAAAATAAACAATCAAGATTTACATGTCACATATGCACTGGCT	2520
Db	2461		
Qy	2521	CATCCCTATACGCAATTTGAGTAATGAAGAACGCGCTGTCGAAGAAACAGAACCCGCT	2580
Db	2521		
Qy	2581	ATTGCAATAGATAGAGATATAATTTCAAAGGTGTTGGCAAAATTCCTGCACAATGAAAGCA	2640
Db	2581		
Qy	2641	ATTAAAAATCATTTGAAAGGCGCAGAGATCAATAAAAAATTAACAGAGGCTATTATAATT	2700
Db	2641		
Qy	2701	CGCTCTCGGCTATCCGTCAGATTTTAGGAATCGGAGAGCTTCA	2745
Db	2701		

RESULT 4

ACF67367_23

Continuation (24 of 57) of ACF67367 from base 2300001 (Photorhabdus luminescens nucleoti

WP Sequence split into 57 fragments LOCUS ACF67367 Accession ACF67367

WP	Fragment Name	Begin	End
WP	ACF67367_00	1	110000
WP	ACF67367_01	100001	210000
WP	ACF67367_02	200001	310000
WP	ACF67367_03	300001	410000
WP	ACF67367_04	400001	510000
WP	ACF67367_05	500001	610000
WP	ACF67367_06	600001	710000
WP	ACF67367_07	700001	810000
WP	ACF67367_08	800001	910000
WP	ACF67367_09	900001	1010000
WP	ACF67367_10	1000001	1110000
WP	ACF67367_11	1100001	1210000
WP	ACF67367_12	1200001	1310000
WP	ACF67367_13	1300001	1410000
WP	ACF67367_14	1400001	1510000
WP	ACF67367_15	1500001	1610000
WP	ACF67367_16	1600001	1710000
WP	ACF67367_17	1700001	1810000
WP	ACF67367_18	1800001	1910000

WP	ACF67367_19	1900001	2010000	
WP	ACF67367_20	2000001	2110000	
WP	ACF67367_21	2100001	2210000	
WP	ACF67367_22	2200001	2310000	
WP	ACF67367_23	2300001	2410000	
WP	ACF67367_24	2400001	2510000	
WP	ACF67367_25	2500001	2610000	
WP	ACF67367_26	2600001	2710000	
WP	ACF67367_27	2700001	2810000	
WP	ACF67367_28	2800001	2910000	
WP	ACF67367_29	2900001	3010000	
WP	ACF67367_30	3000001	3110000	
WP	ACF67367_31	3100001	3210000	
WP	ACF67367_32	3200001	3310000	
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WP	ACF67367_38	3800001	3910000	
WP	ACF67367_39	3900001	4010000	
WP	ACF67367_40	4000001	4110000	
WP	ACF67367_41	4100001	4210000	
WP	ACF67367_42	4200001	4310000	
WP	ACF67367_43	4300001	4410000	
WP	ACF67367_44	4400001	4510000	
WP	ACF67367_45	4500001	4610000	
WP	ACF67367_46	4600001	4710000	
WP	ACF67367_47	4700001	4810000	
WP	ACF67367_48	4800001	4910000	
WP	ACF67367_49	4900001	5010000	
WP	ACF67367_50	5000001	5110000	
WP	ACF67367_51	5100001	5210000	
WP	ACF67367_52	5200001	5310000	
WP	ACF67367_53	5300001	5410000	
WP	ACF67367_54	5400001	5510000	
WP	ACF67367_55	5500001	5610000	
WP	ACF67367_56	5600001	5648894	
Query Match				84.8%; Score 2329; DB 10; Length 110000;
Best Local Similarity				90.5%; Pred. No. 0;
Matches 2485; Conservative				0; Mismatches 260; Indels 0; Gaps 0;
Qy	1	ATGAGCAGTTACAAATCTCGAATTGACCAAAAGACCCCTCGATTAAAGTATTAGATAAC	60	
Db	100781	ATGAGCAGTTATCGTTCTGAAATTGACAAAAAAACCAATTATTCAGTGTATTGGATAAC	100840	
Qy	61	AGGAATTAATGATGCTACTTTAGAAATATCTAGGCTCAAGTGAACGAAAACAGTGAT	120	
Db	100841	AGGAGGTTAAATGTACGTACTTTAGAAATATCTAGTACTCAAGCTGATGAAAACAGTGAT	100900	
Qy	121	GAATTAATTACGTTCTATGAGTTCAATATTCGGGATTTTCAGGTAAAGAACCGATCCT	180	
Db	100901	GAATTTGATCACACTCTATGAGTTCAATATTTCAAGGATTTGAGGTAAAGATCTGATCCT	100960	
Qy	181	CGTAAATAATAAACACAGACGGCCCAAAATTTTCATTCGTCTTTTAAATCTTTGCGGTCAA	240	
Db	100961	CGTAAAGATTAATAATCAGAGGGCCCGAAATTTTCATTCGCGTCTTTTAAATCTCGGGTCAG	101020	
Qy	241	TTTTTACGTGAAGAAAGTTTGATGCGGTGCGGCTCGGACTATTAACCTCAATGATATTGAAGT	300	
Db	101021	GTTCACGTGAAGAAAGGGTTGATGCGGTGCGGCTCGAATATCTATCCTCAACGATGTTGAAGT	101080	
Qy	301	CGCCCGGTGTGATCATCAATGCAACCGGTGCGCCAAACCATCGTTATGAAGATAAC	360	
Db	101081	CGCCCGGTATTAAACCATCAATGCAACCGGTGCGCCAAAGCTATCATCTACGAAGATAAC	101140	
Qy	361	ACCTTCCCGGTGCTGCTGCTCGTATCACCGAAACAAAGTACAGGCAGGAGAGAAAACGACC	420	
Db	101141	ATCCTACCGGTGCTTACTTGTCTATCACCGAACAGGTGAGGCAGGAGAGAAAATGACC	101200	
Qy	421	GAACGTCTTATCTGGGCGGCAATACGCCGCAAGAAAAGATTACAACTTCGCGGTTCAG	480	

Db	101201	GAGCGCCTTATCTGGGCGGCAATACGCCCAAGAAAAGAGTACAACTTGTGCTGTCAG	101260	
Qy	481	TGTGTCGCCATTACGATACCGGGGACTTACTCAACTCAATAGACTTTCTCTGGGTGGC	540	
Db	101261	TGTGTCGCCACTACGATACCGCTGGACTCACTCAACTCAACAGCTTTCTCTGGGTGGC	101320	
Qy	541	GTGCTGCTATCAGATCTCAACACTGCTTACCGATAACAGGATGCGGATCGGACAGGT	600	
Db	101321	GTGCTGCTATCAATCTCAACACTGCTCGTCGATGATCAAAATGCCAGTGGACAGGT	101380	
Qy	601	GAAGACGAGCCTCTGGCAACAAAACTGAGTAGTGATGTCTATATCAACCAAGGTAAAC	660	
Db	101381	GAAGATCAAGGCTCTGGCAGCAAAAACCTGAGCAGTGATGTCTATACCAACCAATAGC	101440	
Qy	661	ACTGATGCCACCGGGCTTTTACTGACCCAGACCGATGCCAAAGGCAACATTCAGCGGTG	720	
Db	101441	ACTGATGCCACCGGGCTTTTACTTATCCAGACCGATGCCAAAGGCAACATCCAGCGCTG	101500	
Qy	721	GCTATGATGTGGCGGGCAGCTTAAAGGGAGTTGGTTAACACTCAAGGTGAGGCGGAA	780	
Db	101501	GCTATGATGTAGCGGGCAGCTTAAAGGCTGTGGTTAACACTCAAGGTCAAGCGGAA	101560	
Qy	781	CAGGTGATTTACAAATCGCTAACTACTCCGCGCGGGGCAAAAATTTACGTGAAGAGCAC	840	
Db	101561	CAAGTATTTACAAATCGCTGACCTACTCTGCGCGCGGCAAAAATTTACGTGAAGAGCAC	101620	
Qy	841	GSTAACGGGATTTGTCACTGAATACAGTACGAAACCGGAAACCAACGGCTTTATCGGCATT	900	
Db	101621	GSTAACGGGTTTATCACCCGAATACAGCTATGAACAGAAACCCCAACGGCTTTATGGTATC	101680	
Qy	901	ACCACCTGGCGTCCATCAGACGCAAGGTGTTGCAAGACCTAGGCTATCAATATGACCCA	960	
Db	101681	ACTACCGCGCTCGTCAGATACCAAGGTGTTGCAAGACTTACGCTATCAATATGATCCG	101740	
Qy	961	GTAGGCAATGTCTAATTAATTCGTAAATGATGGGAAGCCACTCGCTTTTGGCGCAATCAG	1020	
Db	101741	GTAGGCAATGTGATCAATATCCGTAACGATGGGAAGCCACCGCTTTTGGCGCAATCAG	101800	
Qy	1021	AAAGTAGCCCCGGAGAAATAGCTATACCTACGATTCCTCTGTATCAGCTTATCAGCGCAC	1080	
Db	101801	AAAGTGTCTCCGGAGAAATAGCTATACCTAGGACTCCTGTACAGCTTATCAGTGTACT	101860	
Qy	1081	GGCGCGAAATGGCCAAATTCGCTCAGCAAAACCAACCACTTCCCTCCCTCGCTACCT	1140	
Db	101861	GGCGGTGAATGGCCAAATTAGTCTCAGCAAAAATTAATCAACTGCTCCCTCGCTACCT	101920	
Qy	1141	TCTGCAACAATACCTACACTAATCTACTCGCAGCTACAGCTATCATCAGTGTGTAAT	1200	
Db	101921	TCGCAACAATACCTACACTAATCTACTCGCCGCTACAGTTATGATCAGCGGTAAT	101980	
Qy	1201	CTGACGCAAAATTCGGCACAGCTCGCCAGCTACCCAGAAACAACTACACCGTGGCTATCACC	1260	
Db	101981	CTGACGCAAAATTCGGCACAGTTTCATCGGCTACCCAAATAAATACACCGCTATCACC	102040	
Qy	1261	CTCTAAACCGCAGCAATCGGGGTGTTCTCAGTACGCTAACCAACCGATCCAAATCAAGTG	1320	
Db	102041	ATCTGAAATCGCAGTAAACCGCGGTTCCTCAGTACGCTCAGCAACAGATCCAAATCAAGTG	102100	
Qy	1321	GATACGTTGTTGATCGCGTGGTCCAAACCAAGTTTATACCGGACAGACACTTATC	1380	
Db	102101	GATACGTTTATGATCGCGTGGTCCAAACCAAGTTTATACCGGTCAGACACTGGTC	102160	
Qy	1381	TGGACACACGAGGAGGTAAAGCAGGTTAATAATGGCGCGGAAATGAGTGGTACCGC	1440	
Db	102161	TGGACATACGAGGAGGTAAAGCAGGTCAATACGGTTTCAGGAATGAATGTTACCGA	102220	
Qy	1441	TACGACAGCAACGGCATGAGACAACTGAAAGTGAGTGAAACAGCCAAACCCAGAAATCTACG	1500	
Db	102221	TACGGCAGCAACGGAATGAGACAACTGAAAGTGAGTGAAACAGCCAAACCCAGAAATCTACG	102280	
Qy	1501	CAGCAACAGCGGTATCTATTTGCGGGNCTGGAGCTACGCAACCCAGAGCAACGCC	1560	
Db	102281	CAGCAGCAGCGGTATCTATCTGCGCGGGCTGGAACTACGCAACCCAGAGCAACGCC	102340	

Qy 1561 ACAACAACGAGAGTTACACGTTTATCACACTCGGTGAAGCGGTTCGCGCACAGGTACGG 1620
Db 102341 ACAACAACAGAGAGTTACACGTTTATCACACTAGTGAAGCGGTTCGCGCACAGGTACGG 102400
Qy 1621 GTGTTGCACTGGGAGAGCGGTAAAGCAGAGATGTCAACATATCAACTACGTTACAGC 1680
Db 102401 GTGCTGCACCTGGGAGAGCGGTAAACCAAGAGGTATCAACAAATCAGTACGTTACAGC 102460
Qy 1681 TACGATTAATCTGATCGGCTCAGCGAGCTTGAACCTGGACAAACCAAGACAAATTTATCAGC 1740
Db 102461 TACGATAATCTGATCGGCTCAGCGAGCTTGAACCTGGACAAACCAAGAGCGATTTATAGT 102520
Qy 1741 GAGGAAGAGTATTATCCATTTGGCGGACACGCGTGTGGCGAGCAAAACAGCCAAACAGAA 1800
Db 102521 GAGGAAGAGTATTATCCATTTGGCGGACACGCGATGTGGCGAGCAATAGCCAAACAGAA 102580
Qy 1801 GCCAGCTATAAAGCGATTCGCTATTTCGGCGAAAGACGAGATGCCCGGGTTCGTTATAT 1860
Db 102581 GCCAACTATAAAGCTATTTCGCTATTTCAGGCAAAAGACGCGATACACCGGCTGTATTAT 102640
Qy 1861 TACGGTTATCGTTATTACCAACCGTGGCGGGCGAGATGGTTAAGCGGAGCCCGGACAGGA 1920
Db 102641 TACGGTTACCGCTATTATCAACCGTGGCGGGCGAGATGGTTAAGCGGAGTCCCGGACAGGA 102700
Qy 1921 ACCATTGATGGCTGGAATCTATACCGAATGCTAAGAAATATCTGTGAGTTTACAAGAT 1980
Db 102701 ACCATTGATGGCTGGAATCTATACCGAATGCTAAGAAATATCTGAGTAAGTTTCAGCAT 102760
Qy 1981 GAAATGGAATTAGCGCCAGAAAGGAAATATATACCAAGAGGTAAATTTCTTTGATGAA 2040
Db 102761 GAAATGGAATTAGCACCAAGAGGAAATATATCAAGAGGTGAATTTCTTTGATGAA 102820
Qy 2041 TTAAATTTCAAATTTGGCGCAACAAAGTTCAATGTTGTCAAATGGAACGAGAAAGAGAGC 2100
Db 102821 TTAAATTTCAAATTTGGCGCAACAAATTTCAATGTTGTCAAATGGAACGAGAAAGAGT 102880
Qy 2101 AGTTATACAAAATAAATCAATCGAAGTGGTTCGTGCGGTGATTCGATCCGTCGGGT 2160
Db 102881 AGTTATACAAAATAAATCAATCGAAGTGGTTCGTGCGGTGATTCGATCCGTCGGGT 102940
Qy 2161 TATTTGCTAAGCCAGAGAGTTACTAAAGGTATAGAAAAAGTCAAATCATATATAGC 2220
Db 102941 TATTTGCTAAGCCAGAGAGTTACTAAAGGTATAGAAAAAGTCAAATCATATATAGC 103000
Qy 2221 CGACTTGAAGAAAACAGCTCCCTTTTCAGAAAAATCAAAAAAGATCTTTCTTTAGGATCT 2280
Db 103001 CGGCTCGAAGAAAAACAGATCCCTTTTCAGAAAAATCAAAAAAGATCTTTCTTTGGATCT 103060
Qy 2281 GAAATATCCGGTTATATGCGCAAGAACCATACAAGATACGATATCAGATATGCGCAAGAG 2340
Db 103061 GAAATATCCGGTTATATGCGCAAGAACCATACAAGATACGATATCAGATATGCGCAAGAG 103120
Qy 2341 CATAAATAGAAAGTAATCACCCGTATTTTATTTCAGAAACCGATTTCTTTGCGTTAATG 2400
Db 103121 CATAGGTATAGAAAGTAATCACCCGTATTTTATTTCAGCAACAGATTTCTTTGCTTTAATG 103180
Qy 2401 GATAAAGTGAAGAAAAATGATTTTCGGTGAAGAAAAATTTATGCGGCAATGGAGGTT 2460
Db 103181 GATAAAGTGAAGAAAAATGATTTTCGGTGAAGAAAAATTTATGCGGCAATGGAGGTT 103240
Qy 2461 AAGGTTTATCATGATTTTAAAAATAAACAATCAGATTTACATGTCAACTATGCAATGCGC 2520
Db 103241 AAGGTTTATCATGATTTTAAAAATAAACAATCAGATTTACATGTCAACTATGCACTGGCT 103300
Qy 2521 CATCCCTATAGCAATTCAGTAATGAAGAAAGAGCGCTGTTCGAAGAAACAGAACCCGCT 2580
Db 103301 CATCCCTATAGCAATTCAGTAATGAAGAGAGCGCTGTTCGAAGAAACAGAACCCGCT 103360
Qy 2581 ATTGCAATAGATAGAAATATAATTTCAAAGTGTTCGCAAAATTCCTGACATGAAGCA 2640
Db 103361 ATTGCAATTAATAGAAATATAATTTCAAAGCGTTCGTTAAATTCCTGCAATGAAGCA 103420

Qy 2641 ATTTAAAAATCATTTGAAAGGACATAAAAATTAATAGGATATCAACAGAGGCTATTATATT 2700
Db 103421 ATTTAAAAATCATTTGAAAGGCGAGAGATCAATAAAAAATATCAACAGAGGCTATTATATT 103480
Qy 2701 CGCTCTCGCGCTATTCCTCGAGATTTTAGGAATCGCGAGAACTTCA 2745
Db 103481 CGCTCTCGCGCTATTCCTCGTAAGAATTTAGGAATCGCGAGAGCTTCA 103525

RESULT 5
ACF67367_24
Continuation (25 of 57) of ACF67367 from base 2400001 (Photorhabdus luminescens nucleotide
WP Sequence split into 57 fragments LOCUS ACF67367 Accession ACF67367
WP Fragment Name Begin End
WP ACF67367_00 1 110000
WP ACF67367_01 100001 210000
WP ACF67367_02 200001 310000
WP ACF67367_03 300001 410000
WP ACF67367_04 400001 510000
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WP ACF67367_55 5500001 5610000
WP ACF67367_56 5600001 564894

Query Match 84.8%; Score 2329; DB 10; Length 110000;

Best Local Similarity 90.58; Pred. No. 0; Mismatches 260; Indels 0; Gaps 0; Matches 2485; Conservative 0;

QY	1	ATGAGCAGTTACAAATCTGCAATTGACCAAAAGACCCCTCGATTAAGGTATTAGATAAC	60
DB	781	ATGAGCAGTTATCGTCTGAAATGACAAAAACCACTTATCAGTGTATTGGATAAC	840
QY	61	AGGAATTAATGATGACGTTACTTAGAATATCTACGCACTCAAGCTGACGAAACAGTGAT	120
DB	841	AGGAGGTAAATGTACGTACTTTAGAAATATCTACGTACTCAAGCTGATGAAAAACAGTGAT	900
QY	121	GAATTAATTAAGTTCTATGAGTTCAATATTCCGGGATTTTCAGGTAAAGACACCGATCCT	180
DB	901	GAATTTGATCACTCTATGAGTTCAATATTCAAGGATTTTGAAGTAAAGATCTGATCCT	960
QY	181	CGTAAAAATAAAAACAGAGCGGCCCAAAATTTCAATTCGTCTTTTAATCTTTGCCGCTCA	240
DB	961	CGTAAAGATAAANAATCAGAGCGGCCCAAAATTTCAATTCGCGCTTTTAATCTCGCGGTG	1020
QY	241	GTTTTACGTGAAGAAAGTTGATGCGGTGCGGCTGGAATTAACCTCAATGATATTGAAGT	300
DB	1021	GTTCCTACGTGAAGAAAGGGTTGATGCGGTGCGGCTGGAATTTCAATTCGCGCTTTTAATCTCGCGGTG	1080
QY	301	CGCCCGGTGTTGATCAATCAATGCAACCGGTGCGGCAACCAATCGTTATGAAGATAAC	360
DB	1081	CGCCCGGTATTAAACCATCAATGCAACCGGTGCGGCAACCAATCGTTATGAAGATAAC	1140
QY	361	ACCCTTTCCCGGTGCTGCTGCTATCACCAGAAACAGTACAGGAGAGAGAAAAACGACC	420
DB	1141	ATCCTACCGGTGCTGCTGCTATCACCAGAAACAGTACAGGAGAGAGAAAAACGACC	1200
QY	421	GAACGTCTTATCTGGGCGGCAATACGCCGCAAGAAAAAGATTACAACCTGCGCGGTGAG	480
DB	1201	GAGCGCCTTATCTGGGCGGCAATACGCCGCAAGAAAAAGATTACAACCTGCGCGGTGAG	1260
QY	481	TGTGTGCGCCATTACGNTACCGCGGACCTTACTCAACTCAATGACCTTCTCTGGCTGGC	540
DB	1261	TGTGTGCGCCATTACGNTACCGCGGACCTTACTCAACTCAATGACCTTCTCTGGCTGGC	1320
QY	541	GTGCTGCTATCAAACTCTCAAACTGCTTACCGATAACCAAGATGCCGACTGGACAGGT	600
DB	1321	GTGCTGCTATCAAACTCTCAAACTGCTTACCGATAACCAAGATGCCGACTGGACAGGT	1380
QY	601	GAAGACAGAGCCTCTGGCAACAAAACTGAGTAGTGATGCTATATACCCAAAGTAAC	660
DB	1381	GAAGATCAAAAGCCTCTGGCAGCAAAACTGAGCAGTGATGCTATACCAACCAAAATAGC	1440
QY	661	ACTGATGCCACCGGGCTTTACTGACCCAGACCGATGCCAAAGGCAACATTCAGCGCTG	720
DB	1441	ACTGATGCCACCGGGCTTTACTGATCCAGACCGATGCCAAAGGCAACATTCAGCGCTG	1500
QY	721	GCCTATGATGTGGCGGCGAGCTAAAGGGAGTTGGTTAACTCAAGAGTCAAGCGGAA	780
DB	1501	GCCTATGATGTAGCGGCGAGCTAAAGGGAGTTGGTTAACTCAAGAGTCAAGCGGAA	1560
QY	781	CAGGTGATTCAAACTCGCTAACTTCTCGCGCGCGGCAAAATTTACGTGAAGAGCAC	840
DB	1561	CAAGTGATTCAAACTCGCTAACTTCTCGCGCGCGGCAAAATTTACGTGAAGAGCAC	1620
QY	841	GGTAAACGGGATTTGCTACTGAAATACAGTACGAACCGGAAACCCAAACGGCTTTATCGGCATT	900
DB	1621	GGTAAACGGGATTTGCTACTGAAATACAGTACGAACCGGAAACCCAAACGGCTTTATCGGCATT	1680
QY	901	ACCACTCGCGCTCATCAGACCGCAGGTGCTGCAAGACCTACGCTATCAATATGACCCA	960
DB	1681	ACTACCGCGCTCGCTCAGATACCAAGGTGTCGAAGCTTACGCTATCAATATGATCCG	1740
QY	961	GTAGGCAATGTCAATTAATCCGTAATGATGCGGAGGCCACTCGCTTTTGGCGCAATCAG	1020
DB	1741	GTAGGCAATGTGATCAATATCCGTAATGATGCGGAGGCCACTCGCTTTTGGCGCAATCAG	1800
QY	1021	AAAGTAGCCCGGAGAAATAGCTATACCTACGATTCCTGTTATCAGCTTATCAGCGCAC	1080
DB			

DB	1801	AAAGTGGTCCCGAGAAATAGCTATATCTTAGACTCCCTGTACAGCTTATCAGTGTCTACT	1860
QY	1081	GGGCGGAAATGGCCAAATATCGGTACGAAAAACAACTTCCCTCCCTCGCTACCT	1140
DB	1861	GGGCGTGAATGGCCAAATATAGGTACGAAAAATTAATCAACTGCGCTCCCTCGCTACCT	1920
QY	1141	TCGACAAACAATACCTTACATACTATCTCGCAGTACAGCTATGATCAGTGTGTAAT	1200
DB	1921	TCGACAAACAATACCTTACATACTATCTCGCAGTACAGCTATGATCAGCAGGTAAAT	1980
QY	1201	CTGACCAAAATTCGGCAGCTCGCCAGCTACCCAGAAACAATACACCGGTGGCTATCAC	1260
DB	1981	CTGACCAAAATTCGGCAGCTCGCCAGCTACCCAGAAACAATACACCGGTGGCTATCAC	2040
QY	1261	CTCTCAAAACCGCAGCAATCGGGTGTCTCAGTACGCTAACCAACCAATCAAGTG	1320
DB	2041	ATCTCGAATCGCAGTAACCGCGCGTCTCAGTACGCTGACAACAGATCCAAATCAAGTG	2100
QY	1321	GATACGTTGTTGATGCGGTGCTACCAAAACAGTTTATTTACCCCGGACAGACTTATC	1380
DB	2101	GATACGTTTATTTGATGCGGTGCTACCAAAACAGTTTATTTACCCCGTACAGACTGGTC	2160
QY	1381	TGGACACACGAGGAGAGTTAAAGCAGGTTAATTAATGGCCCGGAAATGAGTGGTACCGC	1440
DB	2161	TGGACATACGAGGAGAGTTAAAGCAGGTCAATTAACGGTTCAGGAAATGATGGTACCGA	2220
QY	1441	TACGACAGCAACCGGCAATGAGACAACTGAAAGTGAGTGAAACAGCCCAAGTACTACG	1500
DB	2221	TACGACAGCAACCGGCAATGAGACAACTGAAAGTGAGTGAAACAGCCCAAGTACTACG	2280
QY	1501	CAGCAACACGGGTAACTTATTTCCCGGACTGAGCTACGCAACCCAGCAGCAACGCC	1560
DB	2281	CAGCAGCAGCGGTAACTTATCTGCGCGGTGGAATCTACGCAACCCAGCAGCAACGCC	2340
QY	1561	ACAAACACGAGAGTTACAGTTTACACTCGGTGAAAGCGGTGCGCAGAGGTACGG	1620
DB	2341	ACAAACACGAGAGTTACAGTTTACACTCGGTGAAAGCGGTGCGCAGAGGTACGG	2400
QY	1621	GTGTTGCATCTGGGAGAGCGTTAAGCCAGAGAGTGTCAACAATAATCAACTTACCTTACAGC	1680
DB	2401	GTGTTGCATCTGGGAGAGCGTTAAGCCAGAGAGTGTCAACAATAATCAACTTACCTTACAGC	2460
QY	1681	TACGATAATCTGATCGGCTCCAGCAGCTTGAATCTGGACAAACCAAGGATTAATTCAGC	1740
DB	2461	TACGATAATCTGATCGGCTCCAGCAGCTTGAATCTGGACAAACCAAGGAGATTAATTCAGC	2520
QY	1741	GAGGAGAGTATTATCCATTTGCGGAGCAGCGCTGTTGGGAGCAACAGCCCAACAGAA	1800
DB	2521	GAGGAGAGTATTATCCATTTGCGGAGCAGCGCTGTTGGGAGCAACAGCCCAACAGAA	2580
QY	1801	GCCAGCTATAAAACGATTCGCTATTTCCGGCAAGAAACGAGATGCCACCGGCTTGTATTAT	1860
DB	2581	GCCACTATATAAATCTATTCGCTATTTCCAGCAAGAAACGGGATACCAACCGGCTTGTATTAT	2640
QY	1861	TACGTTATTCGTTATTAACAAACCGTGGGCGGAGATGGTTAAGCGGAGCCCGGAGGA	1920
DB	2641	TACGTTATTCGCTTATTAACAAACCGTGGGCGGAGATGGTTAAGCGGAGCCCGGAGGA	2700
QY	1921	ACCATTTGATGGGTGATCTATACCGAATGTTAAGAAATAATCTCTGTGAGTTTACAGAT	1980
DB	2701	ACCATTTGATGGGTGATCTATACCGAATGTTAAGAAATAATCTCTGTGAGTTTACAGAT	2760
QY	1981	GAAATGGGATTTAGCGCCAGAAAAAGGAAATATATCAAAAGAGGTAATTTCTTTGATGAA	2040
DB	2761	GAAATGGGATTTAGCACCAGAAAGAGGAAATATATCTAAGAGGTGATTTCTTTGATGAA	2820
QY	2041	TTAAATTAATTAATTTGACGCCAAAGTTTCAATGTTGTCAATGTAAGCAAGAGAGC	2100
DB	2821	TTAAATTAATTTGACGCCAAAGTTTCAATGTTGTCAATGTAAGCAAGAGAGC	2880
QY	2101	AGTTATCAAAAAATAAATCAATTTGAAGTGGTTCGTTGCGGTGATTCCTGCTCGGT	2160
DB	2881	AGTTATCAAAAAATAAATCAATTTGAAGTGGTTCGTTGCGGTGATTCCTGCTCGGT	2940

Qy	2161	TATTTGCTAAGCCACGAAGTCTTACTAAAGGTATAGAAAAAGTCAAAATCATATATAGC	2220
Db	2941	TATTTGCTAAGCCACGAAGTCTTACTAAAGGTATAGAAAAAGTCAAAATCATATATAGC	3000
Qy	2221	CGACTTGAAGAAAAACAGTCCCTTTTCAGAAAAATCAAAAAACGAATCTTTCTTTAGGATCT	2280
Db	3001	CGGCTCGAAGAAAAACAGATCCCTTTTCAGAAAAATCAAAAAACGAATCTTTCTTTGGGATCT	3060
Qy	2281	GAATATATCCGGTTATATGGCAGAACCATACAGATACGATATCAGATATATGCCGAAGAG	2340
Db	3061	GAATATATCCGGTTATATGGCAGAACCATACAGATACGATATCAGATATATACGAAGGG	3120
Qy	2341	CATAAATATAGAAGTAATCACCCGTATTTTATTCAGAAACCGGATTTCTTTGGCGTTAATG	2400
Db	3121	CATAGGTATAGAAGTAATCATCCGATTTTATTCGCAACAGATTTCTTTGCTTTAATG	3180
Qy	2401	GATAAAAGTGAAGAAAAATGATTATTCGGGTGAAAAAGAAAAATTTATGGCGCAATGGAGGTT	2460
Db	3181	GATAAAAGTGAAGAAAAATGATTATTCGGGTGAAAAAGAAAAATTTATGGCGCAATAGAGGTT	3240
Qy	2461	AAGTTTATCATGATTTTAAAAAATAAACAATCAGAAATTAATGTCAACTATGCAATTTGGCC	2520
Db	3241	AAGTTTATCATGATTTTAAAAAATAAACAATCAGAAATTAATGTCAACTATGCACTGGCT	3300
Qy	2521	CATCCCTATACGCAATTCAGTAATGAAGAGAGCGCTGTTGCAAGAAAAACAGAACCCGCT	2580
Db	3301	CATCCCTATACGCAATTCAGTAATGAAGAGAGCGCTGTTGCAAGAAAAACAGAACCCGCT	3360
Qy	2581	ATTGCAATAGATAGAGAAATATAATTTCAAAGGTGTGGCAAAATTCCTGACAAATGAAAGCA	2640
Db	3361	ATTGCAATAGATAGAGAAATATAATTTCAAAGGTGTGGCAAAATTCCTGCGCAATGAAAGCA	3420
Qy	2641	ATTAAAAAATCATTTGAAAGGACATATAATTAATAGGATATCAACAGAGGCTATTAAATTT	2700
Db	3421	ATTAAAAAATCATTTGAAAGGACAGATCAATAAAATATCAACAGAGGCTATTAAATTT	3480
Qy	2701	CGCTCTCGGCTATCGCTGAGAAATTTAGGAATGCGGAGAACTTCA 2745	
Db	3481	CGCTCTCGGCTATCGCTAAGAAATTTAGGAATGCGGAGAGCTTCA 3525	
RESULT 6			
ACF65386_4/c			
Continuation (5 of 7) of ACF65386 from base 400001 (Photorhabdus luminescens nucleotide			
WP Sequence split into 7 fragments LOCUS ACF65386 Accession Acf65386			
WP	Fragment Name	Begin	End
WP	ACF65386_0	1	110000
WP	ACF65386_1	100001	210000
WP	ACF65386_2	200001	310000
WP	ACF65386_3	300001	410000
WP	ACF65386_4	400001	510000
WP	ACF65386_5	500001	610000
WP	ACF65386_6	600001	700779
Query Match 84.8%; Score 2329; DB 10; Length 110000;			
Best Local Similarity 90.5%; Pred. No. 0;			
Matches 2485; Conservative 0; Mismatches 260; Indels 0; Gaps 0;			
Qy	1	ATGAGCAGTTACAATTTCTGCAATTGACCAAAAGACCCCTCGATTAAAGGTATTAGATAAC	60
Db	97845	ATGAGCAGTTATCGTTCTGAAATTTGACAAAAAACAACCATTAATACAGTGTATTGATAAC	97786
Qy	61	AGGAAATTAATAGTACGTACTTTTGAATATCTAGCACTCAAGCTGACGAAAAACAGTGAT	120
Db	97785	AGGAGTTTAAATGTACGTACTTTTGAATATCTAGCACTCAAGCTGATGAAAAACAGTGAT	97726
Qy	121	GAATTAATTCGTCTATGAGTTCAATATTCGGGATTTTCAGGTAAAAAGCACCGATCCT	180
Db	97725	GAATTGATCACACTATGAGTTCAATATTTCAAGGATTTGAGGTAAAAAAGTACTGATCCT	97666
Qy	181	CGTAAAAATAAAAAACAGAGGGGCCAAATTTCAATTCGTGTCTTTTAATCTTTGCCGGTCAA	240

Db	97665	CGTAAGATAAAAAATCAGAGCGCGCGAAATTTTATTCGGGTCTTTTAAATCTCGCGGTCTAG	97606
Qy	241	GTTTTACGTGAAGAAAGTGTGTATGCCGTTCGAGCTATTACCTCTCAATGATATTGAAAGT	300
Db	97605	GTCTACGTGAAGAGGGTGTATGCCGTTCGAACTATCATCTCAACGATTTGAAGGT	97546
Qy	301	CGCCCGGTGTGTATCAATCAACCCGGTGTCCGCAAAACCATCGTTTATGAAGATAAC	360
Db	97545	CGCCCGGTATTAAACCATCAATCAACCCGGTGTCCGCAAAAGATCATCACTACGAAGATAAC	97486
Qy	361	ACCCTTCCCGGTCTGTCTCGCTATACCGAAACAAGTACAGCAGAGAGAAAAACGACC	420
Db	97485	ATCTTACCCGGTCTGTCTTACTGTCTATCAGCAACAGGTGAGCGAAGAAAAATGACC	97426
Qy	421	GAAGCTTTTATCTGGCGCGCAATACGCGCAAGAAAAAGATTACAACTCTCGCGGTCTAG	480
Db	97425	GAGCGCTTATCTGGCGCGCAATACGCGCAAGAAAAAGATTACAACTCTGTGTCTAG	97366
Qy	481	TGTGTCCGCCATTACGATACCGCGGACTTACTCAACTCAATAGCCCTTTCTTGGCTGGC	540
Db	97365	TGTGTCCGCCACTACGATACCGCTGGACTCACTCAACTCAACAGCCCTTTCTTGGCTGGC	97306
Qy	541	GTCTGTCTATCAATCTCAAACTGTCTTACCGATAACAGAGTACCGACTCGACAGGT	600
Db	97305	GTCTGTCTATCAATCTCAAACTGTCTGTCTGATGATCAAAATGCCGACTCGACAGGT	97246
Qy	601	GAAGACAGAGCCCTCTGGCAACAAAACTGAGTGTGTGTCTATATCACTCAACAAAGTAAC	660
Db	97245	GAAGATCAAGCCCTCTGGCAGCAAAAACCTGACGAGTGTGTCTATACCAACCAATATAGC	97186
Qy	661	ACTGATGCCACCGGGCTTTTACTGACCCAGACCGATGCCAAAGGCAACATTTACAGCGCTG	720
Db	97185	ACTGATGCCACCGGGCTTTTACTTATCCAGACCGATGCCAAAGGCAACATTTACAGCGCTG	97126
Qy	721	GCCTATGATGTGCCCGGAGCTTAAAGGGAGTTGGTTAACTCAACACTCAAGGTACAGCGGAA	780
Db	97125	GCCTATGATGTAGCCGGGAGCTTAAAGGGTGTGTGGTTAACTCAACAGGTCAAGCGGAA	97066
Qy	781	CAGTGTATTAATAATCGCTTAACCTACTCGCCGCGCGGCAAAAATTTACGTGAAGAGCAC	840
Db	97065	CAAAGTATTAATAATCGCTGACCTACTCTGCCGCGCGCAAAAATTTACGTGAAGAGCAC	97006
Qy	841	GGTAACGGGATTTCTACTGAATACAGTACGAACCGGAAACCCCAACGGCTTTATCGGCATT	900
Db	97005	GGTAACGGGTTATCACCGGAATACAGTATGAACCAAGAAACCCCAACGGCTTTATGGTATC	96946
Qy	901	ACCATCGCGCTCCATCAGACGCGGAGGTGTTCGAAAGACTACGCTATCAATATGACCCA	960
Db	96945	ACTACCGCGCTCCGTGAGATACCAAGGTGTTCGAAAGACTTACGCTATCAATATGATCCG	96886
Qy	961	GTAGGCAATGTCTAATTAATCCGTAATGATGCGGAAGCCACTCGCTTTTGGCGCAATCAG	1020
Db	96885	GTAGGCAATGTGATCAATATCCGTAATGATGCGGAAGCCACCCGCTTTTGGCGCAATCAG	96826
Qy	1021	AAAGTAGCCCCCGGAGATAGCTATACCTAGATTTCCCTGTATCAGCTTATCAGCGCCACC	1080
Db	96825	AAAGTGTCCCGGAGATAGCTATACTTACGACTCCCTGTACAGCTTATCAGTGTACT	96766
Qy	1081	GGGCGGAAATGGCCAAATTCGCTCAGCAAAAACCAACACTTCCCTCCCTCGGCTACCT	1140
Db	96765	GGGCGTGAATGGCCAAATATAGTCTCAGCAAAAATTAATCAACTGCCCTCCCTCGGCTACCT	96706
Qy	1141	TCCTGACAACTACCTACACTACTACTCTCGAGCTTACAGCTATGATCAAGTGTGTAAT	1200
Db	96705	TCGACAACTAACTACCTACTACTACTCTCGGCTTACAGTATGATCAAGCGGTAAAT	96646
Qy	1201	CTGACGCAAAATTCGGCACAGCTCGCCAGCTTACCGCAACAACTACACCGTGGCTATCACC	1260
Db	96645	CTGACGCAAAATTCGGCACAGTTTCACTCGGCTTACCCAAAATAACTACACCGCTATCACC	96586
Qy	1261	CTCTCAAAACCGAGCAATTCGGGTGTTCTCAGTACGCTACCAACCGATTCCAATCAAGTG	1320
Db	96585	ATCTCGAATCGCAGTAACCGCGGCTTCTCAGTACGCTGACCAAGATCCAAATCAAGTG	96526

QY 1321 GATACGTTGTTGATGCCGGTGGTCAACAAACAGTTTATTACCGGACAGACACTTATC 1380
DB 96525 GATACGTTATTTGATGCCGGTGGTCAACAAACAGTTTATTACCGGTCAGACACTGGTC 96466
QY 1381 TGGACACACGAGGAGAGTTAAAGCAGTTTAAATATGCGCCCGGAAATAGTGGTACCGC 1440
DB 96465 TGGACATCACGAGGAGAGTTAAAGCAGTTTAAATATGCGGTTCAAGGAATGAATGGTACCGA 96406
QY 1441 TACGACAGCAACGGCATGAGACAACTGAAAGTGAGTGAACAGCAACACCCAGAACTACTACG 1500
DB 96405 TACGGCAGCAACGGAATGAGACAACTGAAAGTGAGTGAACAGCAACACCCAGAACTACTACG 96346
QY 1501 CAGCAACAAACGGGTAACTTATTTGCGGGACTGGAGCTACGCAACACCCAGAGCAACGCC 1560
DB 96345 CAGCAGCAGCGGTAACTTATTTGCGGCGGTGGAACCTACGCAACACCCAGAGCAACGCC 96286
QY 1561 ACAACACCGAAGAGTTACAGTTTATCACCTCGGTGAACCGCGGTCCGCCACAGGTACGG 1620
DB 96285 ACAACACAGAGAGTTTACAGCTGATCACCTAGGTGAACCGCGGTCCGCCACAGGTACGG 96226
QY 1621 GTGTTGCACCTGGAGAGCGGTAAAGCCAGAGAGTGTCAACAATACTCAACTACGTTACAGC 1680
DB 96225 GTGCTGCACTGGAGAGCGGTAAACCCAGAGAGGTATCAACAACATCAGCTACGTTACAGC 96166
QY 1681 TACGATAATCTGATCGGCTCCAGCCAGCTTGAACTGGACAAACCAAGGACAAATTTATCAGC 1740
DB 96165 TACGATAATCTGATCGGCTCCAGCCAGCTTGAACTGGACAAACCAAGGAGAGTTATTAAT 96106
QY 1741 GAGGAAGAGTATATTCATTTGCGGGAAGAGCGCTGTGGGAGCAACAGCCAAACAGAA 1800
DB 96105 GAGGAAGAGTATATTCATTTGCGGGAAGAGCGATGTGGGAGCAACAGCCAAACAGAA 96046
QY 1801 GCCAGCTATAAACAGTTCGCTATTCCGCAAGAACAGAGATGCCACCGGTTGTATTAT 1860
DB 96045 GCCAATATAAACCTATTTCGCTATTCCGCAAGAACAGAGATGCCACCGGTTGTATTAT 95986
QY 1861 TACGGTTATCGTTATPACCAACCGTGGCGGCGAGATGGTTAAGCGCGACCCGCGCAGGA 1920
DB 95985 TACGGTTACCGCTATTATCAACCGTGGCGGCGAGATGGTTAAGCGCGATCCGCGCAGGA 95926
QY 1921 ACATTGTAGGCTGATCTATACCGAATGGTAAAGAAATAATCTGTGAGTTTACAGAT 1980
DB 95925 ACCATTGTAGGCTGATCTATACCGAATGGTAAAGAAATAATCTGTGAGTTTACAGAT 95866
QY 1981 GAAATGGATTAGCGCCAGAAAGGAAATATACCAAGAGGTAATTTCTTTGATGAA 2040
DB 95865 GAAATGGATTAGCACCAAGAAAGGAAATATATAAGAGGTAATTTCTTTGATGAA 95806
QY 2041 TTAATAATTCAAATTTGGCAGCCAAAGTTTCAACATGTTGTCAAATGGAAACGAGAAAGAGC 2100
DB 95805 TTAATAATTCAAATTTGGCAGCCAAAGTTTCAACATGTTGTCAAATGGAAACGAGAAAGC 95746
QY 2101 AGTTATACAAATAAATCATTTAAAGTGGTTTCGTTGCGGTGATTTCCGATCCGTCGGGT 2160
DB 95745 AGTTATACAAATAAATCATTTAAAGTGGTTTCGTTGCGGTGATTTCCGATCCGTCGGGT 95686
QY 2161 TATTTGCTAAGCCAGCAGGTTACTTAAAGGTATAGAAAGTCAAAATCATATATACG 2220
DB 95685 TATTTGCTAAGCCAGCAGGTTACTTAAAGGTATAGAAAGTCAAAATCATATATACG 95626
QY 2221 CGACTTGAAGAAACAGCTCCCTTTTCAGAAAAATCAAAACGAATCTTTCTTTAGGATCT 2280
DB 95625 CGCTCGAAGAAACAGATCCCTTTTCAGAAAAATCAAAACGAATCTTTCTTTAGGATCT 95566
QY 2281 GAAATATCCGTTTATATGCAAGAACCATACAGATACGATATCAGAAATATGCCGAAGAG 2340
DB 95565 GAAATATCCGTTTATATGCAAGAACCATACAGATACGATATCAGAAATATACAGAAAGG 95506
QY 2341 CATAAATATAGATTAATCACCTGATTTTATTCAGAAACCGATTTCTTTGGTTAATG 2400
DB 95505 CATAGTATAGAGCAATCATCCCGATTTTATTCAGCAACAGATTTCTTTGCTTTAATG 95446

QY 2401 GATAAAGTGAATAAATGATTTATTCGGTGAAGAAATAATTTATTCGGCAATGAGAGTT 2460
DB 95445 GATAAAGTGAATAAATGATTTATTCGGTGAAGAAATAATTTATTCGGCAATGAGAGTT 95386
QY 2461 AAGGTTTATCATGATTTAAATAATAAACAATCAGAAATACATGTCAACTATGCACTGGCC 2520
DB 95385 AAGGTTTATCATGATTTAAATAATAAACAATCAGAAATACATGTCAACTATGCACTGGCT 95326
QY 2521 CATCCTATACCAATTTGAGTAATGAAGAAAGAGCGCTGTTTCAAGAAACAGAACCCGCT 2580
DB 95325 CATCCTATACCAATTTGAGTAATGAAGAGAGAGCGCTGTTTCAAGAAACAGAACCCGCT 95266
QY 2581 ATTGCAATAGATAGAGAAATATATTTCAAGGTGTTGCAAAATTCCTGCAATGAAGCA 2640
DB 95265 ATTGCAATAAATAGAGAAATATATTTTCAAGCGTGTGTAATTCCTGCAATGAAGCA 95206
QY 2641 ATTAATAAATCAATTCGAAGGACATAAATAATTAATAGATATCAACAGAGCTTATTAATT 2700
DB 95205 ATTAATAAATCAATTCGAAGGAGAGATCAATAAATAATCAACAGAGCTTATTAATT 95146
QY 2701 CGCTCTGCGGCTATCGCTGAGAAATTTAGGAATGCGGAGAACTTCA 2745
DB 95145 CGCTCTGCGGCTATCGCTAAGAAATTTAGGAATGCGGAGAGCTTCA 95101

RESULT 7
ADN61384
ID ADN61384 standard; DNA; 2817 BP.
XX ADN61384;
XX
DT 01-JUL-2004 (first entry)
DE Photorhabdus strain W14 tccC5 toxin complex DNA.
XX
KW Cry; toxic; lepidopteran pest; toxin complex; insecticide; strain W14;
XX ds; tccC5.
XX Photorhabdus sp.
XX
PN WO2004002223-A2.
XX
PD 08-JAN-2004.
XX
PF 27-JUN-2003; 2003WO-US020082.
XX
PR 28-JUN-2002; 2002US-0392633P.
XX
PR 21-JAN-2003; 2003US-0441647P.
XX
(DOWC) DOW AGROSCIENCES LLC.
XX
PI Bintrim SB, Bevan SA, Zhu B, Merlo DJ;
XX
DR WPI; 2004-082821/08.
XX
PT Screening a culture of Paenibacillus isolate for Cry protein or toxin
PT complex protein, useful for controlling lepidopterans, comprises
PT obtaining DNA or protein from the culture and assaying the presence of
PT the gene or protein.
XX
PS Example 12; SEQ ID NO 48; 220pp; English.
XX
CC The invention relates to a novel method for screening a culture of a
CC Paenibacillus isolate for a gene encoding a protein selected from a Cry
CC protein that is toxic to a lepidopteran pest and a toxin complex protein.
CC The method comprises obtaining DNA from the culture and assaying the DNA
CC for the presence of the gene or obtaining a protein produced by the
CC culture and assaying the presence of a protein that indicates the
CC presence of the gene in the isolate. The method of the invention has
CC insecticide applications and may be useful for screening Paenibacillus
CC sp. for toxin complex (TC)-like genes and proteins which may themselves
CC be used to enhance or potentiate the activity of a stand-alone
CC Xenorhabdus toxin protein. The method may also be useful for screening

CC	Paenibacillus sp. and others for insecticidal thiaminase genes and	
CC	proteins for controlling insects, particularly lepidopterans. The current	
CC	sequence is that of the Photorhabdus strain W14 tcc05 toxin complex DNA	
CC	of the invention.	
XX		
SQ	Sequence 2817 BP; 902 A; 700 C; 614 G; 601 T; 0 U; 0 Other;	
	Query Match 52.5%; Score 1442.2; DB 12; Length 2817;	
	Best Local Similarity 82.9%; Pred. No. 0;	
	Matches 1664; Conservative 0; Mismatches 328; Indels 15; Gaps 1;	
QY	21 AATGTACCAAAAGACCCCTCGATTAGGTATTAGATAACAGGAAATTAATATGCTATAC 80	921 TCGCCGTCCATCAGACGCCCAAGGTGTTCAGACCTACGCTATCAATATGACCCAGTAGG 980
DB	21 ACTTTATCACCATACGCTACCGTACGTGTTACAGATAACCGTGGACTAGCTATCCGTAA 80	966 CAAATGCTAATAATCCGTAATGATGCGGAAGCCCACTCGCTTTTGGCGCAATCAGAAAGT 1025
QY	81 TTTAGAAATATCTACGACTCAAGCTGACGAAACAGTGATGAATTAATACGTTCTATGA 140	981 CAAATGCTAATGATCCGTAATGATGCGGAAGCCCACTCGCTTTTGGCGCAATCAGAAAGT 1040
DB	81 TATTAGTTTTTACCGCACTACCGCAGAAAGCAATACCGATACCGGTATTATACCGCCATCA 140	1026 AGCCCGGAGAAATAGCTATACCTACGATTCCCTGTATCAGCTTTATCAGCGCCACCGGGCG 1085
QY	141 GTTCAATATTCGGGATTTTCAGGTAAAGCAACCGATCCTCGTA-----A 185	1041 AGCCCGGAGAAATAGCTATACCTACGATTCCCTGTATCAGCTTTATCAGCGCCACCGGGCG 1100
DB	141 ATATAATGCGGGGATTTTGAACCAAGCATTTGATCCTCGCCTGTATGACGCCAAACA 200	1086 CGAAATGGCAATATCGGTACGAAACAAACAACTTCCCTCCCTCCCTGCGCTACCTTCTGA 1145
QY	186 AATAAAAAACAGAGCGGCCCAAAATTTTCAATTCGTGTCTTTAAATCTTGGCGGTCAAGTTT 245	1101 CGAGATGGCAATATCGGTACGAAAGCAACAACTTCCCTCTCCGCGCTACCTTCTGA 1160
DB	201 GACTAACACGCTGTACACCGAATTTTATCTGGCGACATAATTTGACCGGCAATATCCT 260	1146 CAACTAATCCTACACTTAATCTACTGCGAGCTACAGCTATGATCAAGTGGTAACTCTGAC 1205
QY	246 ACGTGAAGAAAGTTGATGCGCGTGGACTATTACCTCAATGATATTGAAAGTGCCTCC 305	1161 TAACTAATCCTACCACTATCTCGCACTTATCTTATGACCGTGGCGGCANNTTGAC 1220
DB	261 GCGAAACAGAGAGCGTGCATGCGGTGCGAGCATTTACCTCAACGATATTGAGGCGGCC 320	1206 GCAAAATTCGGCACAGCTCGCCAGCTACCCAGAACAACTACACCGTGGCTATCAACCTCTC 1265
QY	306 GGTGTTGATCATCAATGCAACCGGTGTCGCGCAAAACCATCGTTTGAAGATACACCT 365	1221 GAAATTCAGCATAGTTTACAGCGCGCAAAATTAATAACAGCGATATAACGGTTTC 1280
DB	321 GGTGTTGACCATCAATGACCGCGGTGTCGCGCAAAACCATCGTTTGAAGATACACCT 380	1266 AAACCGCAGAAATCGGGGTGTTCTCAGTAGCTTAACCAAGATCCAAATCAAGTGTATAC 1325
QY	366 TCCCGGTGCTGCTGCTCTATCCGAAACAAAGTACAGGAGAGAGAAACGACCGAAGC 425	1281 AAATCGCAGCAACCGCGGTACTCAGCAATTTGACCGCAGATCCAACCTCAAGTCGATGC 1340
DB	381 GCCCGTGCCTGCTGCTATCAGGAAACAAAGGACAGGAGAGAAACGACCGAGCG 440	1326 GTTGTGTTGATGCGGTGTCACCAACACAGTTTATTTACCGGACAGACACTTATCTGGAC 1385
QY	426 TCTTATCTGGCGCGCAATACGCGCAAGAAAGATTACAACTCGCCGCTCAGTGTGT 485	1341 CTTATTGATGCGGGAGGCCATCAACACAGCTTGTATTCCGGCCAAGTTCTAACTTGGAC 1400
DB	441 CTTTATCTGGCGCGCAATACGCGCAAGAAAGATTACAACTCGCCGCTCAGTGTGT 500	1386 ACCACGAGGAGAGTTTAAAGCAGGTTAATAATGGCCCGGAAATGAGTGGTACCGCTACGA 1445
QY	486 CCGCATATAGCATACGCGGACTTACTCAACTCAATAGCTTTCTCTGGCTCGGCTCGT 545	1401 ACCGCGAGCGAATTTGAACCAAGCCAACTAGCGCAGGAAATGAGTGGTATCGTACGA 1460
DB	501 CCGCATATAGCATACGCGGACTTACTCAACTCAATAGCTTTCTCTGGCTCGGCTCGT 560	1446 CAGCAACCGCATGAGACAACTGAAAGTGTGAAAGCCAAACCCAGAAATCTAGCGCAGCA 1505
QY	546 GCTATCAAAATCTCAACAACTGTTTACCGATAACAGGATGCCGACTGGACAGGTGAAGA 605	1461 TAGCAACGCGCATACCGCAGCTAAAGTGAATGAACAACTCAGAAATATCCCGCAACA 1520
DB	561 TCTATCAAAATCTCAACAACTGTTTACCGATAACAGGATGCCGACTGGACAGGTGAAGA 620	1506 ACAACGGGTAACTATTTCGCGGACTGGAGCTACGCACAACCCAGAGCAACCCCAAC 1565
QY	606 CAGAGCCTCTGGCAACAAACCTGAGTAGTGTCTATATCAACCAAGTAACTGA 665	1521 ACAAGGGTAACTTATCTACCGGGCTGGAAATACGTACAACCCAGCAACCCCAAC 1580
DB	621 CCAGAGCCTCTGGCAACAAACCTGAGTAGTGTCTATATCAACCAAGTAACTGA 680	1566 AACGGAAGAGTTTACAGCTTATCACACTCGGTGAAGCCGGTTCGCGCAACAGGTACGGTGT 1625
QY	666 TGCACCGGGCTTTACTGACCCAGACCGATGCCAAGGCAACATTCAGCGCTGGCCTA 725	1581 AACAGAGAGTTTACAGCTTATCACACTCGGTAAAGCCGCGCGCAAGTCCGAGTATT 1640
DB	681 TGCACCGGGCTTTACTGACCCAGACCGATGCCAAGGCAACATTCAGCGCTGGCCTA 740	1626 GCACTGGGAGAGCGGTAAAGCAGAAAGTGTCAACAAATATCAACTACGTTCAGCTACGA 1685
QY	726 TGATGTGGCGGGCAGCTAAAGGGAGTTGGTTAACTCAACTCAAAAGGTGAGCGGAACAGGT 785	1641 GCATTGGGAGAGCGGTAAACCCAGAGATATTATTAACAATCAGCTTCGTTACAGCTACGA 1700
DB	741 TGATGTGGCGGGCAGCTAAAGGGAGTTGGTTAACTCAACTCAAAAGGTGAGCGGAACAGGT 800	1686 TAATCTGATCGGCTCCAGCCAGCTTGAACCTGGACAACCAAGGACAATATTCAGCGAGGA 1745
QY	786 GATTATCAAAATCGGTAACTTACTCCGCGCGCGGCAAAAATTTACGTGAAGAGCAGGTAA 845	1701 TAATCTTATTGGCTCCAGCCCACTTCAATAGATAGCGGAGCAAAATTTATCAGTGNAGA 1760
DB	801 GATTATCAAAATCGGTAACTTACTCCGCGCGCGGCAAAAATTTACGTGAAGAGCAGGTAA 860	1746 AGAGTATTATCCATTTTGGCGGAGCAGCGCTGTGGGAGCAACACAGCCAAACAGAAAGCCAG 1805
QY	846 CGGATTTGCTCACTGAATACAGTACGAAACCGGAACCCACCGCTTATCGCATTAACAC 905	1761 AGAATATTATCCATTTTGGTGTACAGCGCTGTGGCGGCAAGGAATCAAAACCGAAGCCAG 1820
DB	861 CGGATTTGCTCACTGAATACAGTACGAAACCGGAACCCACCGCTTATCGCATTAACAC 920	1806 CTATAAAACGATTCGCTATTTCGCGCAAAAGAACAGATGCCACCGGGTGTATTATTACGG 1865
QY	906 TCGCGCTCCATCAGACGCCAAGGTGTTCAGAGACCTACGCTATCAATATGACCCAGTAGG 965	1821 CTATAAAACCATTCGTTATTTCGTTAAAGAGCGGGATGTTTACCGGGCTGTATTATTATGG 1880

DB	921 TCGCCGTCCATCAGACGCCCAAGGTGTTCAGACCTACGCTATCAATATGACCCAGTAGG 980	
QY	966 CAAATGCTAATAATCCGTAATGATGCGGAAGCCCACTCGCTTTTGGCGCAATCAGAAAGT 1025	
DB	981 CAAATGCTAATGATCCGTAATGATGCGGAAGCCCACTCGCTTTTGGCGCAATCAGAAAGT 1040	
QY	1026 AGCCCGGAGAAATAGCTATACCTACGATTCCCTGTATCAGCTTTATCAGCGCCACCGGGCG 1085	
DB	1041 AGCCCGGAGAAATAGCTATACCTACGATTCCCTGTATCAGCTTTATCAGCGCCACCGGGCG 1100	
QY	1086 CGAAATGGCAATATCGGTACGAAACAAACAACTTCCCTCCCTCCCTGCGCTACCTTCTGA 1145	
DB	1101 CGAGATGGCAATATCGGTACGAAAGCAACAACTTCCCTCTCCGCGCTACCTTCTGA 1160	
QY	1146 CAACTAATCCTACACTTAATCTACTGCGAGCTACAGCTATGATCAAGTGGTAACTCTGAC 1205	
DB	1161 TAACTAATCCTACCACTATCTCGCACTTATCTTATGACCGTGGCGGCANNTTGAC 1220	
QY	1206 GCAAAATTCGGCACAGCTCGCCAGCTACCCAGAACAACTACACCGTGGCTATCAACCTCTC 1265	
DB	1221 GAAATTCAGCATAGTTTACAGCGCGCAAAATTAATAACAGCGATATAACGGTTTC 1280	
QY	1266 AAACCGCAGAAATCGGGGTGTTCTCAGTAGCTTAACCAAGATCCAAATCAAGTGTATAC 1325	
DB	1281 AAATCGCAGCAACCGCGGTACTCAGCAATTTGACCGCAGATCCAACCTCAAGTCGATGC 1340	
QY	1326 GTTGTGTTGATGCGGTGTCACCAACACAGTTTATTTACCGGACAGACACTTATCTGGAC 1385	
DB	1341 CTTATTGATGCGGGAGGCCATCAACACAGCTTGTATTCCGGCCAAGTTCTAACTTGGAC 1400	
QY	1386 ACCACGAGGAGAGTTTAAAGCAGGTTAATAATGGCCCGGAAATGAGTGGTACCGCTACGA 1445	
DB	1401 ACCGCGAGCGAATTTGAACCAAGCCAACTAGCGCAGGAAATGAGTGGTATCGTACGA 1460	
QY	1446 CAGCAACCGCATGAGACAACTGAAAGTGTGAAAGCCAAACCCAGAAATCTAGCGCAGCA 1505	
DB	1461 TAGCAACGCGCATACCGCAGCTAAAGTGAATGAACAACTCAGAAATATCCCGCAACA 1520	
QY	1506 ACAACGGGTAACTATTTCGCGGACTGGAGCTACGCACAACCCAGAGCAACCCCAAC 1565	
DB	1521 ACAAGGGTAACTTATCTACCGGGCTGGAAATACGTACAACCCAGCAACCCCAAC 1580	
QY	1566 AACGGAAGAGTTTACAGCTTATCACACTCGGTGAAGCCGGTTCGCGCAACAGGTACGGTGT 1625	
DB	1581 AACAGAGAGTTTACAGCTTATCACACTCGGTAAAGCCGCGCGCAAGTCCGAGTATT 1640	
QY	1626 GCACTGGGAGAGCGGTAAAGCAGAAAGTGTCAACAAATATCAACTACGTTCAGCTACGA 1685	
DB	1641 GCATTGGGAGAGCGGTAAACCCAGAGATATTATTAACAATCAGCTTCGTTACAGCTACGA 1700	
QY	1686 TAATCTGATCGGCTCCAGCCAGCTTGAACCTGGACAACCAAGGACAATATTCAGCGAGGA 1745	
DB	1701 TAATCTTATTGGCTCCAGCCCACTTCAATAGATAGCGGAGCAAAATTTATCAGTGNAGA 1760	
QY	1746 AGAGTATTATCCATTTTGGCGGAGCAGCGCTGTGGGAGCAACACAGCCAAACAGAAAGCCAG 1805	
DB	1761 AGAATATTATCCATTTTGGTGTACAGCGCTGTGGCGGCAAGGAATCAAAACCGAAGCCAG 1820	
QY	1806 CTATAAAACGATTCGCTATTTCGCGCAAAAGAACAGATGCCACCGGGTGTATTATTACGG 1865	
DB	1821 CTATAAAACCATTCGTTATTTCGTTAAAGAGCGGGATGTTTACCGGGCTGTATTATTATGG 1880	
QY	1866 TTATCGTTATTACCAACCGTGGCGGCGAGATGTTTAAAGCGCGGACCCCGCAGCAACCAT 1925	
DB	1881 CTACCGTTATTATCAACCGTGGCGGCGCAGATGTTTAAAGTGCAGACCCCGCAGCAACCAT 1940	
QY	1926 TGATGGCTGAATCTATACCGAAATGGTAAGAAATAATCTCTGTGAGTTTACAAGATGAAA 1985	
DB	1941 TGATGGACTGAATTTATATCGCATGGTGAGAAATAATCCCGGTGACGCAATTTGATGTTCA 2000	
QY	1986 TGATTTAGCGCCAGAAAGGGGAAATA 2012	
DB	2001 GGGATTATCATCCGCGCAACAGAAACAGA 2027	

186	AAATAAAACACAGAGCGGCCAAATTTTCATTCGTGTCTTTAATCTTTCGGGTCAAGTTTT	QY
201	GACTAACACGCTGTACAAACGGAATTTTATCTGGCGACATAAATTTGACCGCAATATCCT	DB
246	ACGTGAAGAAAGTGTGTGATGCGGTGCGGACTATTACCCCTCAATGATATTGAAAGTCGCCC	QY
261	GCNAACAGAGAGCGTCGATGCGGTGCGACGATTACCCCTCAACGATATTGAAGCGCGCC	DB
306	GGTGTGATCATCAATGCAACCGGTGTCCGCAAAACCATCGTTATTGAAAGTATACACCT	QY
321	GGTGTGACCATCAATGACGCGGTGTCCGCAAAACCATCGTACGAAAGTATACACCT	DB
366	TCCCGTGTCTGCTGCTTATCACCGAAACAAGTACAGGCAGAGAGAAACGACGAAACG	QY
381	GCCCGTGCCTGCTGCTTATCAGCGAACAGAGACAGGCAAGAGAAACGACGAGCG	DB
426	TCTTATCTGGGCGGCAATACGCGCAAGAAAGATATTAACTCTGCGCGTCAAGTGT	QY
441	CCTTATCTGGGCGGCAATACGCGCAAGAAAGATATTAACTCTGCGCGTCAAGTGT	DB
486	CGCCCATTTACGATACGCGGAGCTTACTCAACTCAATAGCCCTTCTCTGGCTGGCGTGT	QY
501	CGCCCATTTACGATACGCGGAGCTTACTCAACTCAATAGCCCTTCTCTGGCTGGCGTGT	DB
546	GCTATCACAACTCTCAACAACTGCTTACCGATAACACAGGATGCCAGCTGCGACAGGTGAAGA	QY
561	TCTATCACAACTCTCAACAACTGCTTACCGATAACACAGGATGCCAGCTGCGACAGGTGAAGA	DB
606	CCAGAGCTCTCGGCAACAAAACCTGAGTAGTGATGTCTATATACCCCAAGTAACTACCTGA	QY
621	CCAGAGCTCTCGGCAACAAAACCTGAGTAGTGATGTCTATATACCCCAAGTAACTACCTGA	DB
666	TGCCACCGGGGCTTTACTTGACCCAGACCGATGCCAAAGGCAACATTTACAGCGCTGGCCCTA	QY
681	TGCCACCGGGGCTTTACTTGACCCAGACCGATGCCAAAGGCAACATTTACAGCGCTGGCCCTA	DB
726	TGATGTGCGCGGCGAGCTAAAGAGGAGTTGGTTAACTCAAGCTCAAGCGGCAACAGGT	QY
741	TGATGTGCGCGGCGAGCTAAAGAGGAGTTGGTTAACTCAAGCTCAAGCGGCAACAGGT	DB
786	GATTATCAATCGCTAACTACTCCGCGCGCGGCAAAATTTAGTGAAGACGACGGTAA	QY
801	GATTATCAATCGCTAACTACTCCGCGCGCGGCAAAATTTAGTGAAGACGACGGTAA	DB
846	CGGGATTGTCACTGAATACAGCTACGAACCGGAAACCCAAAGGCTTTATCGGCATTACAC	QY
861	CGGGATTGTCACTGAATACAGCTACGAACCGGAAACCCAAAGGCTTTATCGGCATTACAC	DB
906	TGCGCGTCCATCAGACGCGCAAGGTGTTGCAAGACCTACGCTATCAATATGACCCAGTAGG	QY
921	TGCGCGTCCATCAGACGCGCAAGGTGTTGCAAGACCTACGCTATCAATATGACCCAGTAGG	DB
966	CAATGTCAATTAATATCCGTAATGATGCGAAGCCACTCGCTTTTGGCGCAATCAGAAAGT	QY
981	CAATGTCAATTAATATCCGTAATGATGCGAAGCCACTCGCTTTTGGCGCAATCAGAAAGT	DB
1026	AGCCCCGAGAAATAGCTATACCTACGATTTCCCTGTGATCAGCTTTATCAGCGCCACCGGCG	QY
1041	AGCCCCGAGAAATAGCTATACCTACGATTTCCCTGTGATCAGCTTTATCAGCGCCACCGGCG	DB
1086	CGAAATGGCCCAATATCGGTGAGCAAAACCAACCACTTCCCTCCCTCGGCTACCTTCTGA	QY
1101	CGAGATGGCCCAATATCGGTGAGCAAAACCAACCACTTCCCTCCCTCGGCTACCTTCTGA	DB
1146	CAACATACCTACACTAATATCTACTCGAGGTACAGCTATGATCAGCTGGTGAATCTGAC	QY
1161	TAACATACCTACACCACTATCTACTCGCACTTATCTACTTATGACCGTGGCGCAATTTGAC	DB
1206	GCAATTCGGCAAGCTGCGCAGCTACCCAGAAACCACTACACCGTGGCTATCACCTCTC	QY
1221	GAATTCAGCATAGTTTACCGCGCGCAAAATTAACCTACACGACGGATATAACGGTTTC	DB

PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.
 XX Claim 2; SEQ ID NO 7901; 1205pp; French.
 XX The invention relates to the isolation of genes and their encoded
 CC proteins from *Photobacterium luminescens*. The isolated sequences are
 CC sources of probes and primers for detecting the genome of *P. luminescens*
 CC and related species; to study polymorphisms; for gene analysis and for
 CC detection/amplification of the genes. Antibodies (Ab) raised against the
 CC polypeptides encoded by the genes are used for detection/identification
 CC of *P. luminescens*, e.g. in foods. The genes, proteins, Ab and cells that
 CC carry a gene-containing vector are used to select compounds that
 CC modulate, regulate, induce or inhibit expression of the genes in plants,
 CC animals or microorganisms other than *P. luminescens* and are able to alter
 CC response or sensitivity to toxins and antibiotics produced by *P.*
 CC *luminescens*. Cells transformed to express the genes are useful for
 CC recombinant production of the proteins, particularly toxins and
 CC antibacterials useful as insecticides, bactericides and fungicides. The
 CC genes, proteins, vectors containing the genes and Ab are also useful
 CC therapeutically (to treat microbial infection by bacteria or fungi that
 CC are sensitive to *P. luminescens*-encoded toxins or antibiotics) and as
 CC biopesticides. Other uses of the genes and the proteins are as virulence
 CC factors and for identifying targets of human diseases for which *P.*
 CC *luminescens* is a model (particularly plague and whooping cough). This
 CC sequence represents one of the isolated *P. luminescens* genes
 XX
 SQ Sequence 2817 BP; 922 A; 682 C; 588 G; 625 T; 0 U; 0 Other;
 Query Match 48.1%; Score 1321.4; DB 10; Length 2817;
 Best Local Similarity 78.7%; Pred. No. 0;
 Matches 1596; Conservative 0; Mismatches 416; Indels 15; Gaps 1;
 1 ATGAGCAGTACAAATCTGCAATTGACCAAAAGACCCCTCGATTAAAGGTATTAGATAAC 60
 1 ATGAAAAACATTGACCCCTAAACCTTATCACCATAACGCCGACCCGTCAGTGTTCACGATAAC 60
 61 AGGAAATTAATGATGACCTACTTTAGATAATCTACGCACTCAAGTCAGCAAAACAGATGAT 120
 61 CGTGGATCGGTATCCCGTAAATATTAGTATTTTACC CGCGCTACCGCAAGCAAAATACCGAT 120
 121 GAATTAATATGTTCTATGATGTTCAATATTTCGGGATTTTCAGGTAAAAAGCACCAGATCCT 180
 121 CCGGTATTACTCGCCATCAATATAATGCGCGGGATATTGTAACCAACGATTTGATCCT 180
 181 CGTA-----AAATAAAAAACAGAGCGGCCCAATTTTCATTCGTGCTTT 225
 181 CGCTGTATGATGCTAAGCAGACTTAACAACGCCGTACACCGAATTTTATCTGCGCAT 240
 226 AATCTTCGGGTCAAGTTTACGTGAAGAAGTGTGATGCGCGTCCGCTATTACCCCTC 285
 241 AATTGACCGCAATATCTCGCAACAGAGAGCGTGTGATGCTGGCCGCAATTTACCCCTC 300
 286 AATGATATTGAAGTCCCGGTGTTGATCATCAATGCAACCGGTGTCGCGCAAAACCAT 345
 301 AACGATATTGAGTCCCGGTATTGACCATCAGCGCAACCGGTGTCGCGCAAAATCAC 360
 346 CGTTATGAAGATACACCTTTCCCGTCTGCTGCTATCACCGAACAGTACAGGCA 405
 361 CTTTATGAAGATACACCTTACCGGTGCTGCTATCTCGCAATCACCGAACAGCAGACA 420
 406 GGAGAGAAAACGACCGAAGCTTTATCTGGCGCGCAATACGCGCAAGAAAAGATTAC 465
 421 GAAGAGAAAACACCGAGCGTCTTATCTGGCGCGCAATACGCGCAAGAAAAGATTAC 480
 466 AACCTTCGCGTCAAGTGTGTCGCAATTACGATACCGCGGACTTACTCAACTCAATAGC 525
 481 AACCTTGTGTGATGATACCGGTCAATACGATACCGCGGACTCGCTCAACTCAACAGC 540
 526 CTTTCTCTGGTGGCGGTGCTATCAATCTCAACAACTGCTTACCGATAACAGGAT 585
 541 CTTGCGCTGACCGCGCGCTTTTATCAATCTCAACAAACCGCTCGTCGATAACCAAGAT 600
 586 GCGGACTGGACAGGTGAACGACGAGCTCTGCGCAACAAAACACTGATGATGATCTAT 645

601 GCCGACTGACAGGTGAAGACACAGAGCTCTGCGACAAAACCTGATGATGCTAT 660
 646 ATCACCACCAAGTAACTGATGCCACCGGGCTTTACTGACACAGACCGATGCAAGGC 705
 661 ACCACCAAAATAAACCCGATGCCACCGGGTTTACTTTACCCAGACCGATGCTAAAGGC 720
 706 AACATTACCGGCTGCGCTATGATGGCGGGAGCTAAAGGGAGTGGTTAAACACTC 765
 721 AACATTACCGGCAAGCCCTATGATGGCGGGTACGCTAAAGGGAGCTGGCTTAACATTA 780
 766 AAAGGTGACGCGGAAACAGAGTGAATTAACAATCGCTAACTCTCCCGCGCGGCAAAA 825
 781 AAAGGTGACGCGCAACAGAGTGAATTAACAATCGCTAACTCTCCCGCGCGGCAAAA 840
 826 TTACGTGAAGAGACCGGTAAACCGGATGTCCTAGTAATACAGTACAGAACCGGAAACCCAA 885
 841 TTACGCGAAGAGACCGGTAAACCGGATGTCCTAGTAATACAGTATGAACCGGAAACCTCAG 900
 886 CGGCTTATCGGCAATACCACTCGCGTCCATCAGACGCGCAAGGTGTTGCAAGACCTACGC 945
 901 CGGCTTATCGGCAATACCACTCGCGTCCATCAGACGCGCAAGGTGTTGCAAGACCTACGC 960
 946 TATCAATATGACCCAGTAGGCAATGTCATTAATATATCCGTAATGATCGGAAGCACTCGC 1005
 961 TATCAATATGACCCGCTAGGCAATGTCATTAATATATCCGTAATGATCGGAAGCACTCGC 1020
 1006 TTTTGGCGCAATCAGAAAGTAGCCCGGAGATAGCTATACCTACGATTCCTGTATCAG 1065
 1021 TTTTGGCGCAATCAAAAGTATCCCGGAGATAGCTATACCTACGATTCCTGTATCAG 1080
 1066 CTTTATCAGTCCACCGGCGGCAATGCGCAATATAGGTCAGCAATTAACCCACTCCCTCCC 1125
 1081 CTTTATCAGTCCACCGGCGGCAATGCGCAATATAGGTCAGCAATTAACCCACTCCCTCCC 1140
 1126 TCCCTTCGCTACCTTCTGACCAACATCTACACTAACTATATCTCGCAGCTACAGCTAT 1185
 1141 TCCCTTCGCTACCTTCTGACCAACATCTACACTAACTATATCTCGCAGCTACAGCTAT 1200
 1186 GATCAGAGTGTAACTGACGCAAAATTCGCGACAGCTCGCGCAGTACCCAGAACACTAC 1245
 1201 GACCGTGGCGGCAATTTGATGAAATTCAGCATAGTTTCACTGCCAGCAAAATACTAC 1260
 1246 ACCGTGCTATCACCTCTCAACCCGCAATCGGSGTGTCTCAGTACGCTAACCAAC 1305
 1261 ACAGCAATATAACCGTTCCTAATTAAGCAACCGTGGCTATTAAGTACACTGACCGCA 1320
 1306 GATCCCAATCAAGTGGATAGTGTGTTGATGCGCGTGGTCCACCAACCACTTTATTACCC 1365
 1321 GATCCCAACCAAGTTCGATGCTTTGATTCGGGAGGCCATCAACCACTTTATTATCC 1380
 1366 GGAAGACACTTATCTGGACACCAAGAGAGAGTTAAAGCAGGTTAAATATGCGCCGGGA 1425
 1381 GGTCAAGTCTAATATATGACACCGCGGCGAATTTGAAACAAGTCAACAGTACGACGCA 1440
 1426 AATGAGTGTGTCGCTACGACAGCAACCGCATCAGCAACTGAAGTGAAGTGAACAGCA 1485
 1441 AATGAGTGTGTTACCTACGATAGCAACCGCATCAGCAACTGAAGTGAAGTGAACAGCA 1500
 1486 ACCCAAGTAATCACTACGACGCAACCAACCGGTAACTTATTTGCGGGGACTTGGAGTACGCA 1545
 1501 ACTCAGATATCGGCAACAGCAAGAGTCACTTATCTCGCGGGCTAGAACTACGCA 1560
 1546 ACCGAGACCAACCGCAACCAACCGAGAGGTTAAGCCAGAGTGAAGTGAAGTGAAGTGA 1605
 1561 ACCCAACATGGCAGTACTACCAAGGATTTTCAAGATTTATCACTCGTAAAGTGGT 1620
 1606 CGCGCAAGTACGGGTGTTGCTACGAGAGCGGTTAAGCCAGAGTGAAGTGAAGTGAAGTGA 1665
 1621 CGTGGCAAGTCCGGGTATTTACATTTGGGAGCGGAAACCCGAGATATCAACACAT 1680
 1666 CAATACGTTTACAGTACGATATATCTGATCGGCTCCAGCGCTTGAACCTGGACCAACCA 1725

Db	1681	CAACTTCGTTACAGCTACGATAATCTTATCGGTTCCAGCCAACTTGAATTAGATACGGAA	1740
Qy	1726	GGACAAATATTACGAGGAGAGATATTATCCATTTTGGCGGAGACGCGTGTGGCGAGCA	1785
Db	1741	GGACAAATATTACGAGGAGAGATATTATCCATTTTGGCGGTACAGCTCTGTGGCGAGCA	1800
Qy	1786	AACAGCCAAACAGACGACCTATAAAACGATTTCGCTATTCCGGCAAGAACAGAGATGCC	1845
Db	1801	AGGAATCAAAACCAAGCCAGCTATAAAACCATTCGTTATTTCAGGTAAAGAGCGGGATGCT	1860
Qy	1846	ACCGGGTGTATTATTACGGTATTCTGTTATTACAAACCGTGGCGGCGAGATGGTTAAGC	1905
Db	1861	ACCGGGTGTATTATTACGGTACCCTATTACAAACCGTGGCGGCGAGATGGTTAAGT	1920
Qy	1906	GGGACCCCGGACGAAACCAATTGATGGCTGAATCTATACCGAATGGTAAAGAAATATCCT	1965
Db	1921	GGGACCCCGGACGAAACCAATTGATGGCTGAATTTATATCGCATGGTGAAGAAATATCCG	1980
Qy	1966	GTGAGTTTACAAGATGAAATGGATTAGCGCCAGAAAAAGGGAAATA	2012
Db	1981	GTGACACAATTTGATGTTTCAGGGATTATCTCCGGCTAACAGAACAGA	2027
RESULT 11			
ACF65386_5/c			
Continuation (6 of 7) of ACF65386 from base 500001 (Photorhabdus luminescens nucleotide			
WP Sequence split into 7 fragments LOCUS ACF65386 Accession ACF65386			
WP	Fragment Name	Begin	End
WP	ACF65386_0	1	110000
WP	ACF65386_1	100001	210000
WP	ACF65386_2	200001	310000
WP	ACF65386_3	300001	410000
WP	ACF65386_4	400001	510000
WP	ACF65386_5	500001	610000
WP	ACF65386_6	600001	700779
Query Match 48.1%; Score 1321.4; DB 10; Length 110000;			
Best Local Similarity 78.7%; Pred. No. 0;			
Matches 1596; Conservative 0; Mismatches 416; Indels 15; Gaps 1;			
Qy	1	ATGAGCATTTACATTTCTGCAATTTGACCAAAAGACCCCTCGATTAAGTTATTAGATAAC	60
Db	15073	ATGAAAAACATTTACCCCTAACTTTATCACCATACGCCGACCGTCTAGTTTCAGATAAC	15014
Qy	61	AGCAAAATTAATGTACGTACTTTAGAAATATCTACGCACTCAAGCTGACAGAAACAGATGAT	120
Db	15013	CTGGACTCGCTATCCGTATATTAGTTTTCACCGGCTACCGAGAGCAATACCGAT	14954
Qy	121	GAATTAATACGTTCTATAGTTTCAATATTCCGGGATTTTCAGGTAAAAAGCACCGATCCT	180
Db	14953	CCGCGTATTACTCGCCATCAATATATATGCGCGGGATATTGTAACCAAGCATTTGATCCT	14894
Qy	181	CGTA-----AAATAAACACAGCGCGGCCAAATTTTCATTCGTGTCCTT	225
Db	14893	CGCCTGTATGATGCTAAGCAGACTTAACACCGCGTACACCGAAATTTTATCTGGCAGCAT	14834
Qy	226	AATCTTCGCGTCAAGTTTACGTGAAGAAAGTTTGTATCCCGTTCGGACTATTACCCCTC	285
Db	14833	AATTTGACCGGCAATATCTTCGGACAGAGAGCGTGTATGCTGGCCGAACTATTACCCCTC	14774
Qy	286	AATGATATTGAAGTCCCGCGGTGTTGATCATCAATGCAACCGGTGTCGCCCAAAACCAT	345
Db	14773	AACGATATTGAAGTCCCGCGGTATTGACCATCAGCGCAACCGGTGTCGCCCAAAATCAC	14714
Qy	346	CGTTATGAAGATACACCCCTTCGCGTGTCTGCTATCACCGAAGATACAGGCA	405
Db	14713	CTTTATGAAGATAACACCCCTACCGGTTCGCTACTTCGCAATCACCGAACAAGCACAGACA	14654
Qy	406	GGAGAGAAAACGACCGAATCTTATCTGGCGGCAATACGCGCAAGAAAAAGATTAC	465
Db	14653	GAAGAGAAAAACACCGAGCGTCTTATCTGGCGGCAATACGCGCAAGAAAAAGATTAC	14594
Qy	466	AACCTCGCGGTGATGTGTGTCGCGCAATTACGATACCGCGGACTTACTCAACTCAATAGC	525

Db	14593	AACCTTTGTTGGTCAGTGTACCCGTCAATTACGATACCGCGGACTCGTCAACTCAACAGC	14534
Qy	526	CTTTCTCTGGCTGGCGTCTGTCTATCACAATCTCAACAACACTGTCTACCGATAACCAAGAT	585
Db	14533	CTTTGCGCTGACCGGCGCGTTTATCACAATCTCAACAACCGCTCGTCGATAACCAAGAT	14474
Qy	586	GCGGACTGACAGGTGAAGACCAAGACCTCTGGCAACAAAAACTGAGTAGTGTCTAT	645
Db	14473	GCGGACTGACAGGTGAAGACCAAGACCTCTGGCAACAAAAACTGAGTAGTGTCTAT	14414
Qy	646	ATCACCCAAAGTAACACTGATGCCACCGGGCTTTTACTGACCCAGACCGATGCAAAAGGC	705
Db	14413	ACCACCCAAATATAAACCGATGCCCGGGTTTTTACTTACCAGACCGATGCTTAAAGGC	14354
Qy	706	AACATTCAGCGGTGGCCCTATGATGTGGCGGCGCAGCTAAAAGGGAGTTGGTTTAAACATC	765
Db	14353	AACATTCAGCGGCAAGCCCTATGATGTGGCGGTCAGCTAAAAGGGAGCTGGCTTAAACATTA	14294
Qy	766	AAAGTTCAGCGGACAGGTGATTATCAAAATCGCTAACTTCTCCGCGCGCGGCAAAAA	825
Db	14293	AAAGTTCAGACCGCAACAAGTGATTATCAAAATCGCTGACCTTCTCCGCGCGGCAAAAA	14234
Qy	826	TTACGTGAAGACACCGTAAACGGATTGTCACTGAATACAGCTACGAACCGGAAACCCAA	885
Db	14233	TTACGCGAAGACACCGTAAACGGATTATTAACGAATACAGCTATGAACCGGAAACTCAG	14174
Qy	886	CGGCTTATCGGCATTACCACTCGCCGTCCTCAGAGCGCAAGGTGTTGCAAGACCTACGC	945
Db	14173	CGGCTTATCGGCATTACCACTCGCCGTCCTCAGAGCGCAAGGTGTTGCAAGACCTACGC	14114
Qy	946	TATCAATATGACCCAGTAGCGCAATGTATTAATATCCGTAATATATGCGGAAGCACTCGC	1005
Db	14113	TATCAATATGACCCAGTAGCGCAATGTATTAATATCCGTAATATATGCGGAAGCACTCGC	14054
Qy	1006	TTTTGGGCAATCAGAAAGTAGCCCGGAGATAGCTATACCTACCATTCCTCTGTATCAG	1065
Db	14053	TTTTGGGCAATCAGAAAGTAGCTCCCGGAGATAGCTATACCTACCATTCCTGTATCAG	13994
Qy	1066	CTTATCAGCGCCACCGGGCGGAAATGGGCAATATCGGTGAGCAAAACCAACTTTCCC	1125
Db	13993	CTTATCAGTGGCCACCGGAGTGAATGGCCNATATAGGTGAGCCAAATATACCCACTCCC	13934
Qy	1126	TCCCTCGCTACCTTTCTGACAACTATACCTACCTATATCTCGAGCTACAGTAT	1185
Db	13933	TCCCTCGCTACCTGCTGATAACACCTTACCTATACCTACCTACCTACCTATAGTTAT	13874
Qy	1186	GATCAGTGGTATCTGACGCAATTCGCGCAGCTCGCCAGCTACCGAGACNACTAC	1245
Db	13873	GACCGTGGCGGCAATTTGATGAAATTCAGCATAGTTTCACTCCACGCAAAATAACTAC	13814
Qy	1246	ACCGTGGCTATCACCTCTCAAAACCGCAGCAATCGGGGTGTTCTCAGTAGCTTAACCAAC	1305
Db	13813	ACGACGAATATAACGGTTTCTAATACGCAACCGTGGCGGTATTAAGTACACTGACCGAA	13754
Qy	1306	GATCCAAATCAAGTGGATAGTTGTTGATGCGCGGTGTCACCAACCACTTTATTATACC	1365
Db	13753	GATCCAAACCAAGTTGATGCTTTATTTGATTGCGGAGGCCATCAAAACCACTTTATTATCC	13694
Qy	1366	GGACAGACTTATCTGGACCAACCGAGAGGTAAAGCAGGTTAATATATGSCCGCGGA	1425
Db	13693	GGTCAAGTTCTAATATATGGACCGCGGAGCGCAATTGAAAACAGTCAACAGTAGCGCAGGA	13634
Qy	1426	AATGAGTGGTACCGCTACGACCAACCGCATGAGCAACTGAAAGTGTAGTGAACGCCA	1485
Db	13633	AATGAGTGGTATCACTACGATACAGGCAACGCAACGAGTAAAGTGAATGAACAACAA	13574
Qy	1486	ACCAGAAATACTACGACGCAACACCGGTAACTTATTTGCGGGACTTGGAGCTACGCACA	1545
Db	13573	ACTCAGATATCGGCAACAGCAAGAGTCACTTATCTGCGGGGCTAGAACTACGCACA	13514
Qy	1546	ACCAGAGCAACCGCAACAAACGGAAGAGTTACGTTTATCATCACTCGTGAAGCGGT	1605

Db 13513 ACCCAACATGCGAGTACTACACGGAATATTGTCAGGTATTACACTCGGTAAAGCTGGT 13454
Qy 1606 CGGCAAGTACGGGTGTTGCACTGGAGAGCGGTAAAGCCAGAGATGTCACAAATAAT 1665
Db 13453 CGTGGCAAGTCCGGGTATTACATTGGGAGAGCGGAAACCCGGAAGATATCAACAAAT 13394
Qy 1666 CAACTAGCTTACAGCTACGATAATCTGATCGGCTCCAGCGAGCTTGAACCTGGACAAACAA 1725
Db 13393 CAACTTCGTTACAGCTACGATAATCTTATCGGTTCCAGCCAACTTGAATTAGATAGCGAA 13334
Qy 1726 GGACAAATTTACGAGGAGAGATATTATTCATTTGGCGGACAGCGCTGTGGCGAGCA 1785
Db 13333 GGACAAATTTACGAGGAGAGATATTATTCATTTGGCGGTACAGCTCTGTGGCGAGCA 13274
Qy 1786 AACGACCAACAGAGCCAGCTATAAAACGNTTCGCTATTCCGCGCAAGAACAGAGATGCC 1845
Db 13273 AGGAATCAAAACCGAAGCAGCTATATAAACCAATTCGTTATTTCAGGTAAAGAGCGGGATGCT 13214
Qy 1846 ACCGGGTTGTATTATTACGGTTATCGTTATTACCAACCGTGGGCGGCAGATGTTAAGC 1905
Db 13213 ACCGGGCTGTATTATTACGGCTACCGTTATTACCAACCGTGGGCGGCAGATGTTAAGT 13154
Qy 1906 GCGACCCGCGCAGGAACCAATTGATGGCTGAATCTATACCGAATGGTAAGAAATAATCCT 1965
Db 13153 GCGACCCGCGCAGGAACCAATTGATGGCTGAATTTATATCGCATGTTGAGAAATAATCCG 13094
Qy 1966 GTGAGTTTACAGATGAAATGGATTAGCGCCAGCAAAAGGGAATA 2012
Db 13093 GTGACAAATTTGATGTTTCAGGGATTATCTCCGCTAACAGAACAGA 13047

RESULT 12

ACF70848
ID ACF70848 standard; DNA; 2811 BP.
XX
AC ACF70848;
XX
XX
DT 20-NOV-2003 (first entry)
XX
XX Photorhabdus luminescens nucleotide sequence #9315.
XX
XX Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;
KW detection; food; gene expression; plant; animal; microorganism; toxin;
KW antibiotic; biopesticide; virulence factor; disease model; plague;
KW whooping cough; gene; ds.
XX
XX Photorhabdus luminescens.
XX
XX WO200294867-A2.
XX
XX PD 28-NOV-2002.
XX
XX 07-FEB-2002; 2002WO-IB003040.
XX
XX 07-FEB-2001; 2001FR-00001659.
XX
XX (INSP) INST PASTEUR.
XX (CNRS) CNRS CENT NAT RECH SCI.
XX
XX Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;
PI Buchrieser C;
XX
XX WPI; 2003-148459/14.
XX
XX Genomic sequence of Photorhabdus luminescens and encoded polypeptides,
PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.
XX
XX Claim 2; SEQ ID NO 9315; 1205pp; French.
PS
XX The invention relates to the isolation of genes and their encoded
CC proteins from Photorhabdus luminescens. The isolated sequences are
CC sources of probes and primers for detecting the genome of P. luminescens
CC and related species; to study polymorphisms; for gene analysis and for

CC detection/amplification of the genes. Antibodies (Ab) raised against the
CC polypeptides encoded by the genes are used for detection/identification
CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that
CC carry a gene-containing vector are used to select compounds that
CC modulate, regulate, induce or inhibit expression of the genes in plants,
CC animals or microorganisms other than P. luminescens and are able to alter
CC response or sensitivity to toxins and antibiotics produced by P.
CC luminescens. Cells transformed to express the genes are useful for
CC recombinant production of the proteins, particularly toxins and
CC antibacterials useful as insecticides, bactericides and fungicides. The
CC genes, proteins, vectors containing the genes and Ab are also useful
CC therapeutically (to treat microbial infection by bacteria or fungi that
CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as
CC biopesticides. Other uses of the genes and the proteins are as virulence
CC factors and for identifying targets of human diseases for which P.
CC luminescens is a model (particularly plague and whooping cough). This
CC sequence represents one of the isolated P. luminescens genes
XX
SQ Sequence 2811 BP; 929 A; 660 C; 631 G; 591 T; 0 U; 0 Other;
Query Match 36.9%; Score 1013.2; DB 10; Length 2811;
Best Local Similarity 70.5%; Pred. No. 3.2e-272;
Matches 1415; Conservative 0; Mismatches 573; Indels 18; Gaps 4;
Qy 1 ATGAGCAGATTACAAATTCGCAATTTGACCAAAAGACCCCTCGATTAAAGGTATTAGATAAC 60
Db 1 ATGATTCGTTACAAATTCGCAATTTACCGAATTAACCCCATCTCTCAGCGTACGAGATAAT 60
Qy 61 AGAAATTAATGTACGTACTTTAGAAATATCTACGCACCTCAAGCTACAGCAA---ACAGT 117
Db 61 CGAGGGTTAAATATACATACGCTGGAATATCTCGGACTCAAGCTGATGAAGCAATAGC 120
Qy 118 GATGAATTAATTAAGTCTTATGATGTTCAATATTCGCGGATTTCCAGGTAAAGAACCCCGAT 177
Db 121 AACGNAATTGATCACTCGCTATCAATTTAATACTACGGAATTCAGAGTAAAGAAAGCACAGAC 180
Qy 178 CCTCGTAAATAAATAAACACAGAGCGGCCAAATTTCAATTCGTCTTTTAATCTTTCGCGGT 237
Db 181 CCAGGTAGATATAAAACCCAGAGTGGTTCNAATCTCACTCGTATCTTTAGTCTCGCTGGG 240
Qy 238 CAAGTTTTACGTGAAGAAAGTGTGTATGCGCGTGGACTATTAACCTCAATGATATTGAA 297
Db 241 AATACACTGCGTGAAGAAAGTATCGATGCTGGCGAAGCATTAACCTTTGAACGATATCGAA 300
Qy 298 AGTCGCCCGGTGTGATCATCAATGCAACCGGTGTCGCCAACCACCATCTGTATGAAGAT 357
Db 301 GSAAGCCCGAGTACTGACTATCAATGCAATCGCGCTCGTCAGACCCCATCATATGAAGGT 360
Qy 358 AACACCCCTTCCCGTCTGCTCGCTATCACCGAAACAAGTACAGGAGGAGAGAAACG 417
Db 361 AATACCTTGGCCGCGCTGCTGGCTGTACCGAGTTAATACAAAGAACGAGAAACCC 420
Qy 418 ACCGAACGCTTTATCTGGCGCGCAATACGCCGCAAGAAAGATTACAACCTTCGCGGT 477
Db 421 ACGGAGCGCTTTATTTGGGCAACAATACAGATGCGAGAGAAACACAGAAATCTCGCGGG 480
Qy 478 CAGTGTCTCGCCATTAAGATACGCGGGACTTACTCAACTCAATAGCCCTTCTCTGGCT 537
Db 481 CAATGTATACGCCATTTATGATCTCGCGGGCTGGTCAACTGGGAAAGTTTGTCTCTTAACA 540
Qy 538 GCGTCTGTCTATCACAAATCTCAACAACTGCTTACCAGTAAACCCAGGATGCGGACTGGACA 597
Db 541 GGATCGGTTTTATCACAGTCTCGTCAATTAATAGCCGACCGATCAGGAAGCTGATTGGCGC 600
Qy 598 GGTGAAGACCAAGCCCTCTCGCAACAAAACTGAGTAGTGTATATATACCCCAAGT 657
Db 601 GGTGATGATGAAATAGCTGGCGTACAAAACCTGAATGGCAACATATTCAGGACTCAACAT 660
Qy 658 AACACTGATGCCCGGGGCTTTACTACCCAGACCGATGCCAAGGCAACATTCACGGG 717
Db 661 AAAATGATGCCATTTGTTGCTGCTAACTCAAAATCGACCGCAAGGGAATATGCAACGG 720
Qy 718 CTGSCCTATGATGTGGCGCGGAGCTAAAGGGAGTTGGTTAACTCACTCAAGGTCAGGCG 777

Db 721 |||||CTGCGCTATGATGTCGGGCGCCAACTGAAAGGTAGTGGTTAACACTAAAGGCCAAGCC 780
Qy 778 GAACAGGTGATTAATCAAAATCGCTAAACTACTCCGCGCGCGGCAAAATTAATCGTGAAGAG 837
Db 781 GAAAAAGTTATTGTACAGTCTATTACCTGCTCAGCAGCGGACAAAAATTAACGAGAAGAG 840
Qy 838 CACGTTAACGGGATTTGCTACCTGAATACAGTACGACGGAACCCGGAACCCAGCGCTTATCGGC 897
Db 841 CACGGTAATGGCGTTATTACGGAATATACCTATGAAACACGAGACCCCAACGATTAAATTAAC 900
Qy 898 ATTACCACTCGCGCTCATCAGA---CGCCAAGGTGTTCAAGACCTTACGCTATCAATAT 954
Db 901 ATTACACCCGCGAAGTACAGATAGTACAAAACCACTACAAGTTTACGTTAATGAATAT 960
Qy 955 GACCCAGTAGGCAATGTCATTAAATATCCGTAATGATCGGGAAGCCACTCGCTTTTGGCGC 1014
Db 961 GATCCCGTTGGCAATGTGATCAATATTCGTAAATGATGACAGAACAACCGGATTCTGGCGT 1020
Qy 1015 AATCAGAAAGTAGCCCGGAGAATAGCTATACCTACGATTCCTCTGTATCAGCTTATCAGC 1074
Db 1021 AATCAGAAATAGTACCGGAAATGCAATATTCCTATGATTTCTGTACCAACTCATCCAA 1080
Qy 1075 GCCACGGGCGGAAATGGCCAATATCGGTACGAAACCAACCACTTCCCTC-----C 1128
Db 1081 GCAACGGCGCGAATGGCTTAACATTTGTCAGCAAGGAAGCAGCTCCCTCCTTTAATT 1140
Qy 1129 CTTGCGCTACTCTTGACAAATACCTACACTAATCTATCTCGCAGCTACAGCTATGAT 1188
Db 1141 ACCCTCTTCTACCGATGACATACTTTACTAATATTTCTGTTACTTATACCTACGAC 1200
Qy 1189 CACAGTGGTAACTCGACGCAAAATTCGGCAGCAGCTCGCAGCTACCCAGAACAACTACCC 1248
Db 1201 GATAGCGGCAACCTGACACAAATCCAGCAGCAGTCTCCGCAAGTAACAACTACAC 1260
Qy 1249 GTGGCTATCACCTCTCAAAACCGCAATCGGGTGTCTCAGTACGCTAAACACCGAT 1308
Db 1261 ACAAATATCAACATTTCAAAACCGTAATAACCGGGTGTCTCAGTACCTCACCAACGAC 1320
Qy 1309 CCAATCAAGTGATAGTTGTTGATCGCGGTGGTCAACCAACCAAGTTTATTACC CGGA 1368
Db 1321 CCBAATCTGTTGATACATTTCTTTGATCAGGTGGTTCATCAACACGCTGTTCTCAGGG 1380
Qy 1369 CAGACACTTATCTGGACACCAACGAGGAGGTTAAAGCAGTTAA-----TAATGCCCCG 1422
Db 1381 CAATCTTAAACTGGACACCAACGCGGAGAACTACAACAGTGAACCAAGTGGTAATACC 1440
Qy 1423 GGAATGAGTGGTACCGCTACGACAGCAACGGCATGAGCAACTGAAAGTGAACAG 1482
Db 1441 GC CGGTGAGTGGTACCCTATGACGTGACGGCATCGGGTACTGAAAAATAAACGAACAG 1500
Qy 1483 CCAACCCAGAAATACTAGCGAGCAACACGGGTAACTCTATTTCGGGACTGGAGCTACGC 1542
Db 1501 CAAACATCCAAATACCGCAGCAGCAACGAGTCACTATCTGCAGGGTTGGAATTACAC 1560
Qy 1543 ACAACCCAGAGCAACGCCAACCAACGGAAGTTACAGCTTATCACTCCGTGAAGCC 1602
Db 1561 ACCACACAAAGCGGCAACCAATATCACCGAAGACTTACAAGTTTACTGTACGCAAGCA 1620
Qy 1603 GGTGCGGCACAGGTACGGGTGTTGCACTGGGAGAGCGGTAAGCCAGAAGATGTCAACAAT 1662
Db 1621 GGAAGAAGCACAAGTACGCGTACTACACTGGGAAAAAGGCCAACCCCGGCATAAAATAAC 1680
Qy 1663 AATCAACTAGTTACAGTACGATAATCTCATCGGCTCCAGCCAGCTTGAACCTGGACAAC 1722
Db 1681 GATCAAGTCAGATATAGCTACGATAATCTTACACAGCAGCAAGTAATAGAACTGGATATG 1740
Qy 1723 CAAGGACAAATTAATCAGCAGGAGAGTATTATTCATTTTCGGCGGACAGCGCTGTGGCA 1782
Db 1741 CACGGAGAAATGATCAGTTGGGHAAGATATTACCCCTATGTTGGTCCGACCGCAGTATGGCA 1800
Qy 1783 GCAACAGCCAAACAGAACCGCACTATAAACGATTCGCTATTTCGGCAAGAACGAGAT 1842
|||||

Db 1801 GCAAGAAATCAGATTGAAGCTGGTTACAAAACCAATTCGTTATTTCAGTAAAGAACGTGAT 1860
Qy 1843 GCCACCGGTTGTATTATTACGTTATCGTTATTACCAACCGTGGGCGGCAGATGTTA 1902
Db 1861 GCAACGGGACTGTACTATTACGCTACCGCTATTATCAACCGTGGCCGCTAGATGTTA 1920
Qy 1903 AGCGCGACCCCGCAGAACCACTTATGATGGCTGAATCTATACCGAATGTTAAGAAATAAT 1962
Db 1921 AGCGCTGACCCGCTGGAACCGTAGATGGTCTGAATTTTGCTATGTTAGAAATAAT 1980
Qy 1963 CTTGTGAGTTTACAAGATGAAAAATGG 1988
Db 1981 CCAATGACCGGCATAGATGAAGATGG 2006
|||

RESULT 13
ACF67367_39/c
Continuation (40 of 57) of ACF67367 from base 3900001 (Photorhabdus luminescens nucleotide
WP Sequence split into 57 fragments LOCUS ACF67367 Accession ACF67367
WP Fragment Name Begin End
WP ACF67367_00 1 110000
WP ACF67367_01 100001 210000
WP ACF67367_02 200001 310000
WP ACF67367_03 300001 410000
WP ACF67367_04 400001 510000
WP ACF67367_05 500001 610000
WP ACF67367_06 600001 710000
WP ACF67367_07 700001 810000
WP ACF67367_08 800001 910000
WP ACF67367_09 900001 1010000
WP ACF67367_10 1000001 1110000
WP ACF67367_11 1100001 1210000
WP ACF67367_12 1200001 1310000
WP ACF67367_13 1300001 1410000
WP ACF67367_14 1400001 1510000
WP ACF67367_15 1500001 1610000
WP ACF67367_16 1600001 1710000
WP ACF67367_17 1700001 1810000
WP ACF67367_18 1800001 1910000
WP ACF67367_19 1900001 2010000
WP ACF67367_20 2000001 2110000
WP ACF67367_21 2100001 2210000
WP ACF67367_22 2200001 2310000
WP ACF67367_23 2300001 2410000
WP ACF67367_24 2400001 2510000
WP ACF67367_25 2500001 2610000
WP ACF67367_26 2600001 2710000
WP ACF67367_27 2700001 2810000
WP ACF67367_28 2800001 2910000
WP ACF67367_29 2900001 3010000
WP ACF67367_30 3000001 3110000
WP ACF67367_31 3100001 3210000
WP ACF67367_32 3200001 3310000
WP ACF67367_33 3300001 3410000
WP ACF67367_34 3400001 3510000
WP ACF67367_35 3500001 3610000
WP ACF67367_36 3600001 3710000
WP ACF67367_37 3700001 3810000
WP ACF67367_38 3800001 3910000
WP ACF67367_39 3900001 4010000
WP ACF67367_40 4000001 4110000
WP ACF67367_41 4100001 4210000
WP ACF67367_42 4200001 4310000
WP ACF67367_43 4300001 4410000
WP ACF67367_44 4400001 4510000
WP ACF67367_45 4500001 4610000
WP ACF67367_46 4600001 4710000
WP ACF67367_47 4700001 4810000
WP ACF67367_48 4800001 4910000
WP ACF67367_49 4900001 5010000
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WP	ACF67367_53	5300001	5410000																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
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RESULT 14		Continuation (9 of 13) of ACF65388 from base 80001 (Photorhabdus luminescens nucleotide		76055		CTGGCTATGATGTCGGGGCCAACTGAAAGGTAGCTGGTTAACTAAAGGCCAAGCC	76114	
ACF65388_08		WP Sequence split into 13 fragments LOCUS ACF65388 Accession ACF65388		QY		778	GAACAGGTGATTATCAAAATCGCTAACTACTCCGCGCGCGGCAAAAATTAACGTGAAGAG	837
WP		Fragment Name		DB		76115	GAAGAAAGTTATTGTACAGTCTATTACTGTGTCAGCAGCGGACAAATAATTAACGAGAAGAG	76174
WP		Begin		QY		838	CACGGTAACGGGATTTGTCACTGAATACAGTACGAACCGGAAACCCACCGCTTATCGGC	897
WP		End		DB		76175	CACGGTAATGGCGTTATTACGGGAATATACCTATGAACCCAGAGACCCCAACGATTAAATTAAC	76233
WP		ACF65388_00		QY		898	ATTACCACTCGCGCTCCATCAGA---CGCCAAGGTGTTGCAAGACCTACGCTTATCAATAT	954
WP		ACF65388_01		DB		76235	ATTACAAACCGCGCAACTAGAGATAGTACAAAACCACTACAAGATTTAGCTTATGNAATAT	76293
WP		ACF65388_02		QY		955	GACCAGTAGGCAATGTCTAATTAATCCGTAATATGATGCGGAAGCCACTCGCTTTTGGCGC	1014
WP		ACF65388_03		DB		76295	GATCCCGTTGGCAATGTGATCAATATTCGTAATGATGCAAGCAACCCGATTCTGGCGT	76355
WP		ACF65388_04		QY		1015	AATCAGAAAGTAGCCCGGAGAAATAGCTATACCTACGATTCCTGTATCAGCTTATCAGC	1074
WP		ACF65388_05		DB		76355	AATCAGAAATATAGTACCGGAAATGCATATTCCTATGATTTCTGTACCAACTCATCCAA	76414
WP		ACF65388_06		QY		1075	GCACCGGGCGGAAATGGCCAAATATCGGTACGCAAAAACAACCACTTCCCTC-----C	1128
WP		ACF65388_07		DB		76415	GCACCGGGCGGAAATGGCTAACTTTGGTCAGCAAGGAAGCAGCTCCCTCTTTAAAT	76474
WP		ACF65388_08		QY		1129	CTGCGCTACTCTTCGACAACTACTACACTAACTATCTCGCAGCTACAGCTATGAT	1188
WP		ACF65388_09		DB		76475	ACCCCTCTTCTACCGATGACATATCTTACTTACTATATTTCTGTACTTATACCTACGAC	76534
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RESULT 15
AAZ06831
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XX
AC AAZ06831;
XX
XX 09-NOV-1999 (first entry)
XX
XX Photorhabdus luminescens 38kb DNA fragment.
XX
XX Symbiotic bacterium; nematode; insect; larva; toxin; insecticide; ds.
XX
XX Photorhabdus luminescens.
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FH Key Location/Qualifiers
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PR 20-JAN-1999; 99US-0116439P.
XX
XX (NOVS ) NOVARTIS AG.
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
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PI Chen JS;
XX
XX WPI; 1999-527479/44.
DR P-PSDB; AAY33728, AAY33729, AAY33730.
XX
XX New nucleic acid from Photorhabdus luminescens encoding insecticidal
PT toxins, used for making resistant transgenic plants.
XX
XX Claim 1; Page 99-130; 148pp; English.
XX
XX This sequence represents an approximately 38kb fragment of Photorhabdus
CC luminescens DNA comprised in the plasmid pNOV2400 (NRRL B-30077). This
CC sequence contains 16 open reading frames (orfs) which encode three
CC insecticidal toxins. This sequence was isolated from a P. luminescens
CC cosmid library which had been screened for insecticidal activity. P.
CC luminescens is a member of the Enterobacteriaceae family and is a
CC symbiotic bacterium of nematodes of the genus Heterorhabditis. The
CC nematodes colonise insect larvae, kill them, and their offspring feed on
CC the dead larvae. However, the insecticidal agents are produced by P.
CC luminescens rather than the nematodes. The toxins have activity against
CC Lepidopteran insects such as Cabbage Looper (Trichoplusia ni), European
CC Corn Borer (Ostrinia nubilalis) and Fall Armyworm (Spodoptera frugiperda)
CC and also against Coleopteran insects (e.g., Colorado Potato Beetle,
CC Leptinotarsa decimlineata). In addition the toxins are active against
CC strains resistant to known insecticides. This sequence can be used to
CC generate transgenic plants of various species that are resistant to
CC economically important insect pests and also for recombinant production
CC of toxins for use as insecticides
XX
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Query Match 36.9%; Score 1012.4; DB 2; Length 37948;
Best Local Similarity 69.5%; Pred. No. 2.le-271;
Matches 1414; Conservative 0; Mismatches 596; Indels 24; Gaps 2;
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Job time : 1499 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 19:08:12 ; Search time 13299 Seconds
(without alignments)
11732.858 Million cell updates/sec

Title: US-10-647-956A-5

Perfect score: 2745

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Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2329	84.8	349519	1	BX571862 Phototrab
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7	1012.4	36.9	37948	6	AR166758 Sequence
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ALIGNMENTS

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DEFINITION Sequence 5 from patent US 6639129.
ACCESSION AR427909
VERSION AR427909.1 GI:40186940
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2745)
AUTHORS ffrench-Constant,R.H., Bowen,D.J., Rocheleau,T.A. and Waterfield,N.R.
TITLE DNA sequences from photorhabdus luminescens
JOURNAL Patent: US 6639129-A 5 28-OCT-2003;
Wisconsin Alumni Research Foundation and University of Bath;
Madison, WI
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DEFINITION
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island 1, partial sequence.
ACCESSION
AF346500 AY144119
VERSION
AF346500.2 GI:27479637
KEYWORDS
SOURCE
Photorhabdus luminescens
ORGANISM
Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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REFERENCE
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AUTHORS
Waterfield,N.R., Bowen,D.J., Fetherston,J.D., Perry,R.D. and
ffrench-Constant,R.H.
TITLE
The tc genes of Photorhabdus: a growing family
JOURNAL
Trends Microbiol. 9 (4), 185-191 (2001)
PUBMED
11286884
2 (bases 1 to 127816)
REFERENCE
3 (bases 1 to 127816)
AUTHORS
ffrench-Constant, R.H., Bowen, D.J. and Waterfield, N.R.
TITLE
Direct Submission
JOURNAL
Submitted (19-JAN-2001) Biology and Biochemistry, University of
Bath, Claverton Down, Bath BA2 7AY, UK
4 (bases 1 to 127816)
REFERENCE
5 (bases 1 to 127816)
AUTHORS
Waterfield,N.R. and ffrench-Constant, R.H.
TITLE
Direct Submission
JOURNAL
Submitted (22-AUG-2002) Biology and Biochemistry, University of
Bath, Claverton Down, Bath BA2 7AY, UK
REMARK
Sequence update by submitter
COMMENT
On Jan 3, 2003 this sequence version replaced gi:16416925.
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LOCUS CQ824622 2817 bp DNA linear PAT 21-JUN-2004

DEFINITION Sequence 15 from Patent WO2004044217.

ACCESSION CQ824622

VERSION 1

KEYWORDS CQ824622.1 GI:49021703

SOURCE .

ORGANISM Photorhabdus luminescens

Photorhabdus luminescens

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

Enterobacteriaceae; Photorhabdus.

REFERENCE 1

AUTHORS Ffrench-Constant,R.H. and Waterfield,N.R.

TITLE Dna sequences from tcd genomic region of photorhabdus luminescens

JOURNAL Patent: WO 2004044217-A 15 27-MAY-2004;

UNIVERSITY OF BATH (GB)

FEATURES

Location/Qualifiers

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Db 2001 GGGATTATCACCGGCCAACAGAACAGA 2027

RESULT 5
CQ854091
LOCUS 2817 bp DNA linear PAT 23-AUG-2004
DEFINITION Sequence 57 from Patent WO2004067727.
ACCESSION CQ854091
VERSION CQ854091.1 GI:51510128
KEYWORDS
SOURCE
ORGANISM Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE 1
AUTHORS Hey, T.D., Schlieper, A.D., Bevan, S.A., Bintrim, S.B., Mitchell, J.C.,
Li, Z.S., Ni, W., Zhu, B., Merlo, D.J. and Apel-Birkhold, P.C.
TITLE Mixing and matching tc proteins for pest control
JOURNAL Patent: WO 2004067727-A 57 12-AUG-2004;
Dow Agrosciences LLC (US)
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exon
ORIGIN

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RESULT 6

BX571874

LOCUS

DEFINITION

349907 bp

DNA

linear

BCT 17-APR-2005

Photorhabdus luminescens subsp. laumondii

TT01 complete genome;

segment 16/17.

ACCESSION	BX571874 BX470251		
VERSION	BX571874.1 GI:36787718		
KEYWORDS	complete genome.		
SOURCE	Photorhabdus luminescens subsp. laumondii TT01		
ORGANISM	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Photorhabdus.		
REFERENCE	1		
AUTHORS	Duchaud,E., Rusniok,C., Frangeul,L., Buchrieser,C., Taourit,S., Bocs,S., Boursaux-Eude,C., Chandler,M., Passa,E., Derose,R., Derzelle,S., Freysinet,G., Gaudriault,S., Givaudan,A., Glaser,P., Medigue,C., Lanois,A., Powell,K., Siguier,P., Wingate,V., Zouine,M., Boenare,N., Danchin,A. and Kunst,F.		
TITLE	Complete genome sequence of the entomopathogenic bacterium Photorhabdus luminescens		
JOURNAL	Nat. Biotechnol. 11 (1) (2003) In press		
REFERENCE	2		
AUTHORS	Duchaud,E., Frangeul,L., Rusniok,C. and Kunst,F.		
TITLE	Direct Submission		
JOURNAL	Submitted (23-APR-2003) L. Frangeul, Institut Pasteur, Genopole, 25 rue du Docteur Roux, 75724 Paris Cedex 15, FRANCE. E-mail: lfrangeu@pasteur.fr, fkunst@pasteur.fr		
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Dn	29521	CCAAATGACCGGCATAGATGAAGTGG	29546
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VERSION			
KEYWORDS			
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AUTHORS			
TITLE			
JOURNAL			
FEATURES			
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ORIGIN			
Query Match			
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Matches 1414; Conservative			
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Qy	181	CGTAAAAATAAAAAACAGAGCGGCCCAATTTCAATTCGTGCTTTTAACTCTTGGCGGTCAA	240
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RESULT 9
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DEFINITION Sequence 11 from Patent WO2004044217.
ACCESSION CQ824618
VERSION CQ824618.1 GI:49021695
KEYWORDS Photorhabdus luminescens
SOURCE Photorhabdus luminescens
ORGANISM Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE 1
AUTHORS French-Constant R.H. and Waterfield N.R.
TITLE Dna sequences from tcd genomic region of photorhabdus luminescens
JOURNAL Patent: WO 2004044217-A 11 27-MAY-2004;
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Query Match		36.68;	Score 1004.6;	DB 6;	Length 2883;
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Qy	226	AATCTCCGGTCAAGTTTACGTGAAGAAAGTGTGATGCGGTGCGGACTATTACCCCTC	285		
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KEYWORDS
Photorhabdus luminescens
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Photorhabdus luminescens
ORGANISM
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE
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AUTHORS
Hey, T.D., Schleper, A.D., Bevan, S.A., Bintrim, S.B., Mitchell, J.C.,
Li, Z.S., Ni, W., Zhu, B., Merlo, D.J. and Apel-Birkhold, P.C.
TITLE
Mixing and matching to proteins for pest control
JOURNAL
Patent: WO 2004067727-A 46 12-AUG-2004;
Dow Agrosciences LLC (US)
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DEFINITION		segment 15/17.	
ACCESSION		BX571873 BX470251	
VERSION		BX571873.1 GI:36787441	
KEYWORDS		complete genome.	
SOURCE		Photorhabdus luminescens subsp. laumondii TTO1	
ORGANISM		Photorhabdus luminescens subsp. laumondii TTO1	
REFERENCE		Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	
AUTHORS		Enterobacteriaceae; Photorhabdus.	
TITLE		1	
JOURNAL		Duchaud,E., Rusniok,C., Frangeul,L., Buchrieser,C., Taourit,S.,	
REFERENCE		Bocs,S., Bourseaux-Eude,C., Chandelier,M., Daesa,E., Derose,R.,	
AUTHORS		Derzelle,S., Freysinet,G., Gaudriault,S., Givaudan,A., Glaser,P.,	
TITLE		Medigue,C., Lanois,A., Powell,K., Siguler,P., Wingate,V.,	
JOURNAL		Zouine,M., Boemare,N., Danchin,A. and Kunst,F.	
REFERENCE		Complete genome sequence of the entomopathogenic bacterium	
AUTHORS		Photorhabdus luminescens	
TITLE		Nat. Biotechnol. 11 (1) (2003) In press	
JOURNAL		2	
REFERENCE		Duchaud,E., Frangeul,L., Rusniok,C. and Kunst,F.	
AUTHORS		Direct Submission	
TITLE		Submitted (23-APR-2003) L. Frangeul, Institut Pasteur, Genopole, 25	
JOURNAL		rue du Docteur Roux, 75724 Paris Cedex 15, FRANCE. E-mail:	
REFERENCE		lfrangeul@pasteur.fr, fkunst@pasteur.fr	
AUTHORS			
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ORIGIN								
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Photorhabdus luminescens
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REFERENCE 1 (bases 1 to 25655)
AUTHORS Waterfield,N.R., Bowen,D.J., Fetherston,J.D., Perry,R.D. and
ffrench-Constant,R.H.
TITLE The tc genes of Photorhabdus: a growing family
JOURNAL Trends Microbiol. 9 (4), 185-191 (2001)
PUBMED 11286884
REFERENCE 2 (bases 1 to 25655)
AUTHORS ffrench-Constant,R.H., Bowen,D.J. and Waterfield,N.R.
TITLE Direct Submission
JOURNAL Submitted (19-JAN-2001) Biology and Biochemistry, University of
Bath, Claverton Down, Bath BA2 7AY, UK
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Job time : 13315 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 14, 2005, 10:14:39 ; Search time 7364 Seconds
(without alignments)
5813.441 Million cell updates/sec

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Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	721.5	15.2	460	9 AQ991476	AQ991476 Rfc02418
C 3	716	15.1	605	9 AQ990411	AQ990411 Rfc01179
C 4	580	12.2	878	10 CZ547320	CZ547320 SRAA-aad7
C 5	559	11.8	733	11 AW901477	AW901477 RCO-NN101
C 6	529	11.2	494	9 AQ991400	AQ991400 Rfc02327
C 7	503	10.6	406	9 AQ990055	AQ990055 Rfc00763

C 8	487	10.3	594	9 AQ990688	AQ990688 Rfc01498
C 9	409.5	8.6	547	9 AQ990013	AQ990013 Rfc00707
C 10	371	7.8	312	9 AQ990147	AQ990147 Rfc00869
C 11	309.5	6.5	644	1 AW901491	AW901491 RCO-NN101
C 12	180	3.8	795	10 CZ532972	CZ532972 SRAA-aac8
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C 24	144.5	3.0	6246	10 AY413475	AY413475 Homo sapi
C 25	143.5	3.0	808	9 CC111285	CC111285 NDL.38D12
C 26	143.5	3.0	6315	4 AY321333	AY321333 Rattus no
C 27	142	3.0	19677	11 DQ051895	DQ051895 Homo sapi
C 28	141	3.0	8025	10 CL961005	CL961005 OaIFCC005
C 29	138	2.9	881	10 CZ545184	CZ545184 SRAA-aad6
C 30	138	2.9	4741	4 AK029802	AK029802 Mus muscu
C 31	137	2.9	7787	11 DQ048663	DQ048663 Homo sapi
C 32	136.5	2.9	1383	9 BZ565560	BZ565560 p8c92-164
C 33	135	2.8	3064	4 AK004607	AK004607 Mus muscu
C 34	135	2.8	3836	4 AK088238	AK088238 Mus muscu
C 35	134.5	2.8	614	9 AQ991166	AQ991166 Rfc02049
C 36	134	2.8	1016	9 BZ571923	BZ571923 mah2_2138
C 37	133.5	2.8	874	9 BZ567033	BZ567033 p8c92-164
C 38	133	2.8	340	2 BE092381	BE092381 IL2-BT073
C 39	133	2.8	2173	10 AY409388	AY409388 Mus muscu
C 40	133	2.8	2415	4 CR858297	CR858297 Pongo pyg
C 41	133	2.8	3750	4 AK019545	AK019545 Mus muscu
C 42	132.5	2.8	843	9 BZ570678	BZ570678 mah2_1482
C 43	132.5	2.8	4609	11 DQ050672	DQ050672 Homo sapi
C 44	132	2.8	2439	10 CL982610	CL982610 OaIFSC048
C 45	131.5	2.8	814	9 CC851172	CC851172 NDL.121N1

ALIGNMENTS

RESULT 1

AQ991727/c

LOCUS

DEFINITION

Photorhabdus luminescens genomic clone PLG00357F, genomic survey

sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

AQ991727 749 bp DNA linear GSS 14-AUG-2000

Rfc00357F Photorhabdus luminescens strain W14 M13 library

Photorhabdus luminescens genomic clone PLG00357F, genomic survey

sequence.

AQ991727

AQ991727.1 GI:9650223

GSS.

Photorhabdus luminescens

Photorhabdus luminescens

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

Enterobacteriaceae; Photorhabdus.

1 (bases 1 to 749)

french-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,

Daborn,P.J., Bowen,D. and Blattner,F.R.

A genomic sample sequence of the entomopathogenic bacterium

Photorhabdus luminescens W14: potential implications for virulence

Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

10919786

Contact: french-Constant RH

Department of Biology and Biochemistry

University of Bath

South Building, Bath BA2 7AY, UK

Tel: (44) 1225 826621

Fax: (44) 1225 826779

Email: bss@bath.ac.uk

This is one of a selected subset of flipped clones from the M13

library. For annotation of identified clones (BLASTX, BLASTN and

mapping to E. coli K12 genome) please see french-Constant et al.

2000, Nucleic Acids Res.

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Seq primer: M13 Reverse
Class: shotgun.
Location/Qualifiers
FEATURES
  source
    1. .749
    /organism="Photorhabdus luminescens"
    /mol_type="genomic DNA"
    /strain="W14"
    /db_xref="taxon:29488"
    /clone="PLG00357P"
    /dev_stage="primary phase variant"
    /clone_lib="Photorhabdus luminescens strain W14 M13
    library"
    /notes="Genomic DNA from strain W14 was size selected (1-2
    kb) and then cloned into M13 Janus."

ORIGIN
Alignment Scores:
Pred. No.: 1.56e-76 Length: 749
Score: 806.00 Matches: 164
Percent Similarity: 80.35% Conservatve: 20
Best Local Similarity: 71.62% Mismatches: 41
Query Match: 17.00% Indels: 5
DB: 9 Gaps: 2

US-10-647-956A-6 (1-915) x AQ991727 (1-749)
Qy 90 GlyArgThrLeuThrLeuAenAspIleGluSerArgProValLeuIleLeuAenAlaThr 109
Db 712 GGTTCNCCTGTCNCCTTAAATATATTGAAGNCCGTCGCTACTACGGGTGNTTGAACA 653
Qy 110 GlyValArgGlnAenHisArgTyrgluAspAenThrProGlyArgLeuLeuAlaIle 129
Db 652 GGGNTTAT-ACAAACTGCCAATATGAANTTTNCCCTGCCCGTNGTTGTATCTGTT 594
Qy 130 ThrGluGlnValGlnAlaGlyGluLysThr-----ThrGluArgLeuIleTrpAla 146
Db 593 GCCGAACAAACACCCGAG--GAAAAACATCCCGTATCACCGAACGCTTGTTGGTT 537
Qy 147 GlyAenThrProGlnGluLysAspTyrgluAenLeuAlaGlyGlnCysValArgHisTyrglu 166
Db 536 GGCAATACCGAAGCAGAGAAGACCAATCTCCCGCAGTGCCTGCTCACTATGAC 477
Qy 167 ThrAlaGlyLeuThrGlnLeuAenSerLeuSerLeuAlaGlyValValLeuSerGlnSer 186
Db 476 ACGCGGGAGTTACCCGGTTANAGAGTTATCACTGACCGGTACTGTTTATCTCAATCC 417
Qy 187 GlnGlnLeuThrAspAenGlnAspAlaAspTrpThrGlyGluAspGlnSerLeuTrp 206
Db 416 AGCCAACATTTGATCGACACTCAAGAGCGAACTGGACAGGTGATAACGAACCGTCTGG 357
Qy 207 GlnGlnLysLeuSerSerAspValTyrlleThrGlnSerAenThrAspAlaThrGlyAla 226
Db 356 CAAACATATGCTGGCTGATGACATCTACACACCTCGAGCACCTTCGATGCCACCGGTGCT 297
Qy 227 LeuLeuThrGlnThrAspAlaLysGlyAenIleGlnArgLeuAlaTyrgluValAlaGly 246
Db 296 TTACTGACTCAGACCGATCGCAAGGGAACATTACAGAGCTGGCTTATGATGTGCCCGGG 237
Qy 247 GlnLeuLysGlySerTrpLeuThrLeuLysGlyGlnAlaGluGlnValIleIleLysSer 266
Db 236 CAGCTAAACGGGAGCTGGCTAAACACTCAAAGCCGACAGCGGAACAGTGATTATCAATCC 177
Qy 267 LeuThrTyrSerAlaAlaGlyGlnLysLeuArgGluGluHisGlyAenGlyIleValThr 286
Db 176 CTGACCTACTCCGCGCGGCAAAATATACGTGAGGAACACCGCAATGATGTTATCACC 117
Qy 287 GluTyrSerTyrgluProGluThrGlnArgLeuIleGlyIleThrArgArgProSer 306
Db 116 GAATACAGTTATGAACCGGAACCAACCGGTGATCGGTATCAAAACCCCGCTCCGTCA 57
Qy 307 AspAlaLysValLeuGlnAspLeuArg 315
Db 56 GACACTAAAGTGCTACAGACCTCGG 30

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RESULT 2
AQ991476
LOCUS
DEFINITION
  rfc02418 Photorhabdus luminescens strain W14 M13 library
  Photorhabdus luminescens genomic clone PLG02418, genomic survey
  sequence.
ACCESSION
  AQ991476
VERSION
  AQ991476.1 GI:9650070
KEYWORDS
  GSS.
SOURCE
  Photorhabdus luminescens
  Photorhabdus luminescens
  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
  Enterobacteriaceae; Photorhabdus.
REFERENCE
  1 (bases 1 to 460)
  ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
  Daborn,P.J., Bowen,D. and Blattner,F.R.
  A genomic sample sequence of the entomopathogenic bacterium
  Photorhabdus luminescens W14: potential implications for virulence
  Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
  10919786
COMMENT
  Contact: ffrench-Constant RH
  Department of Biology and Biochemistry
  University of Bath
  South Building, Bath BA2 7AY, UK
  Tel: (44) 1225 826621
  Fax: (44) 1225 826779
  Email: bssr@bath.ac.uk
  This is one of 2,122 random reads from the M13 library. For
  annotation of identified clones (BLASTX, BLASTN and mapping to E.
  coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
  Acids Res.
  Seq primer: M13 Forward
  Class: shotgun.
FEATURES
  source
    1. .460
    /organism="Photorhabdus luminescens"
    /mol_type="genomic DNA"
    /strain="W14"
    /db_xref="taxon:29488"
    /clone="PLG02418"
    /dev_stage="primary phase variant"
    /clone_lib="Photorhabdus luminescens strain W14 M13
    library"
    /notes="Genomic DNA from strain W14 was size selected (1-2
    kb) and then cloned into M13 Janus."

ORIGIN
Alignment Scores:
Pred. No.: 1.13e-67 Length: 460
Score: 721.50 Matches: 147
Percent Similarity: 94.84% Conservatve: 0
Best Local Similarity: 94.84% Mismatches: 6
Query Match: 15.22% Indels: 3
DB: 9 Gaps: 1

US-10-647-956A-6 (1-915) x AQ991476 (1-460)
Qy 423 AsnArgSerAsnArgGlyValLeuSerThrLeuThrThrAspProAenGlnValAspThr 442
Db 2 AACCGCAGCAATCGGGGTGTTCTCAGTACGCTAACCCACCGATCCAAATCAAGTGATCG 61
Qy 443 LeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIleTrpThr 462
Db 62 TTGTTTATGCCCGTGGTCCACAAACCGAGTTTATATCCCGGACAGACACTTATCTGGACA 121
Qy 463 ProArgGlyGluLeuLysGlnValAenAsnGlyProGlyAsnGluTyrTyrgluTyrglu 482
Db 122 CCACGAGAGAGTTAAAGCAGGTTTAAATATGGCCCGGGAATAGTGGTACCGCTACGAC 181
Qy 483 SerAsnGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAenThrGlnGln 502
Db 182 AGCAACGGCATGAGACAACTGAAAGTGAGTGAACAGCAACCCACCAATACTACGACGAA 241

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QY 503 GlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAlaThrThr 522
 DB 242 CAACGGGTAAATCTATTTCGGGACTGGAGCTACGCACACACCCAGAGCAACGCCACAACA 301
 QY 523 ThrGluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArgValLeu 542
 DB 302 ACCGAAGAGTATACACGTATATACACATCGGTGAAGCCGGTCGCCACAGGT-CGGGTGTG 360
 QY 543 HisTrpGluSerGlyLysProGluAspValAsnAsnGlnLeuArgTyrSer-TyrAs 562
 DB 361 CACTGGGAGCGGTAAAGCAGAGATGTCAACATAATCACTACTGT---TCAGCTCGA 417
 QY 562 pAsnLeuIleGlySerSerGlnLeuGluLeuAspAsnGlnGly 576
 DB 418 TAATCTGATCGGNTTCANCCAGCTTTGACTGGACACCAAGGG 460

RESULT 3
 AQ990411 605 bp DNA linear GSS 14-AUG-2000
 LOCUS Rf001179 Photorhabdus luminescens strain W14 M13 library
 DEFINITION Photorhabdus luminescens genomic clone PLG01179, genomic survey sequence.
 ACCESSION AQ990411 GI:9649005
 VERSION AQ990411.1
 KEYWORDS GSS.
 SOURCE Photorhabdus luminescens
 ORGANISM Photorhabdus luminescens
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Photorhabdus.
 REFERENCE 1 (bases 1 to 605)
 AUTHORS fFrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T., Daborn, P.J., Bowen, D. and Blattner, F.R.
 TITLE A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
 JOURNAL 10919786
 PUBMED
 COMMENT Contact: fFrench-Constant RH
 Department of Biology and Biochemistry
 University of Bath
 South Building, Bath BA2 7AY, UK
 Tel: (44) 1225 826621
 Fax: (44) 1225 826779
 Email: bssrfc@bath.ac.uk
 This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see fFrench-Constant et al. 2000, Nucleic Acids Res.
 Seq primer: M13 Forward
 Class: shotgun.

FEATURES
 source
 1..605
 /organism="Photorhabdus luminescens"
 /mol_type="genomic DNA"
 /strain="W14"
 /db_xref="taxon:29488"
 /clone="PLG01179"
 /dev_stage="primary phase variant"
 /clone_lib="Photorhabdus luminescens strain W14 M13 library"
 /notes="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

ORIGIN
 Alignment Scores: 6.96e-67 Length: 605
 Pred. No.: 716.00 Matches: 140
 Score: 84.85% Conservative: 28
 Best Local Similarity: 70.71% Mismatches: 24
 Query Match: 15.11% Indels: 6
 DB: 9 Gaps: 1

US-10-647-956A-6 (1-915) x AQ990411 (1-605)

QY 140 ThrGluArgLeuIleTyrTrpAlaGlyAenthPrGlnGlnLysAspTyrAsnLeuAlaGly 159
 DB 3 ACAGAGCGCTTATCTGGCTGGGAATACACCTCGGAGAAAGAGTATAACCTCTCCGCT 62
 QY 160 GlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAsnSerLeuSerLeuAla 179
 DB 63 CTGTGTATACGGCCTACACACAGCGGAGTGACCCCGTTGATGAGTCAGTCACCTGGCG 122
 QY 180 GlyValValLeuSerGlnSerGlnGlnLeuLeuThrAspAsnGlnAspAlaAspTyrThr 199
 DB 123 GGGCCATCTATCCCAATCTCACCATTTGTCGGCGAAGGGCAGGAGCTAACTGGAGC 182
 QY 200 GlyGluAspGlnSerLeuTrpGlnGlnLysLeuSerSerAspValTyrIleThrGlnSer 219
 DB 183 GGTGACGACGAAATCTCTGGCAGGGAATGCTGGCAAGTGAGGTCTTATACGACACAAAGT 242
 QY 220 AsnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGlyValIleGlnArg 239
 DB 243 ACCACTAATGTCATCGGGCTTTTACTGACCCAAACCGATGCGAAGGCAATATTACAGCT 302
 QY 240 LeuAlaTyrAspValAlaGlyGlnLeuLysGlySerTrpLeuThrLeuLysGlyGlnAla 259
 DB 303 CTGGCTTATGACATTCGCGGTCACTTAAAGGGAGTTGGTTGACGGTGAAGGCCAGAGT 362
 QY 260 GluGlnValIleIleLysSerLeuThrTyrSerAlaAlaGlyGlnLysLeuArgGluGlu 279
 DB 363 GAACAGGTGATTGTTAAGTCCCTGAGTCGTGAGCGCAGGTCAATAATTCGCTGAAGAG 422
 QY 280 HisGlyAsnGlyIleValThrGluTyrSerTyrGlu-ProGluThrGlnArgIleGlu 299
 DB 423 CACGGTAACCGCGGTGTTACCGAGTACAGTTATGAGCCCGGAAATCAACGTCGTATAGG 482
 QY 299 YIleThrThrArgArgPro-----SerAspAlaLysValLeuGlnAspLeuAr 315
 DB 483 TATACACCGCGCGTCCCAANGAGTCAATCANGAGCCAGAGTATTCAGAGATCTACG 542
 QY 315 gTyrGlnTyrAspProVal-GlyAsnValIleAsnIleArgAsnAspAla 331
 DB 543 CTATAAGTATGATCCCGTGGGGGAATGGTATCAGTATTCAGTATTCATAATGATGCC 592

RESULT 4
 CZ547320/c 878 bp DNA linear GSS 13-MAY-2005
 LOCUS SRAA-aad73b07.b1 Strongyloides ratti whole genome shotgun library
 DEFINITION (SRAAGSS 004) Strongyloides ratti genomic, genomic survey sequence.
 ACCESSION CZ547320
 VERSION CZ547320.1 GI:64683141
 KEYWORDS GSS.
 SOURCE Strongyloides ratti
 ORGANISM Strongyloides ratti
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Panagrolaimoidea; Strongyloidea; Strongyloides.
 REFERENCE 1 (bases 1 to 878)
 AUTHORS Mitreva, M., McCarter, J.P., Thompson, F., Viney, M., Pape, D., Ritter, E., Martin, J., Wylie, T., Dante, M., Waterston, R.H., Clifton, S.W. and Wilson, R.
 TITLE Genome Survey sequences from the rat parasitic nematode Strongyloides ratti
 JOURNAL Unpublished (2005)
 COMMENT Contact: Mitreva M
 Washington University in St. Louis
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: nematode@watson.wustl.edu
 Genomic DNA was provided by Fiona Thompson (F.Thompson@bristol.ac.uk) and Mark Viney (Mark.Viney@bristol.ac.uk) at the University of Bristol, Bristol, UK.
 Class: shotgun.
 Location/Qualifiers

FEATURES
 Location/Qualifiers


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LOCUS      AQ990055              406 bp      DNA      linear      GSS 14-AUG-2000
DEFINITION RfC00763 Photorhabdus luminescens strain W14 M13 library
            Photorhabdus luminescens genomic clone PLG00763, genomic survey
            sequence.
ACCESSION  AQ990055
VERSION    AQ990055.1 GI:9648649
KEYWORDS   GSS.
SOURCE     Photorhabdus luminescens
            Photorhabdus luminescens
ORGANISM   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Photorhabdus.
REFERENCE  1 (bases 1 to 406)
AUTHORS    ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
            Daborn,P.J., Bowen,D. and Blattner,F.R.
TITLE      A genomic sample sequence of the entomopathogenic bacterium
            Photorhabdus luminescens W14: potential implications for virulence
JOURNAL    Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
PUBMED     10919786
COMMENT     Contact: ffrench-Constant RH
            Department of Biology and Biochemistry
            University of Bath
            South Building, Bath BA2 7AY, UK
            Tel: (44) 1225 826621
            Fax: (44) 1225 826779
            Email: bsrfc@bath.ac.uk
            This is one of 2,122 random reads from the M13 library. For
            annotation of identified clones (BLASTX, BLASTN and mapping to E.
            coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
            Acids Res.
            Seq primer: M13 Forward
            Class: shotgun.

FEATURES             Location/Qualifiers
     source           1..406
                     /organism="Photorhabdus luminescens"
                     /mol_type="genomic DNA"
                     /strain="W14"
                     /db_xref="taxon:29488"
                     /clone="PLG00763"
                     /dev_stage="primary phase variant"
                     /clone_lib="Photorhabdus luminescens strain W14 M13
                     library"
ORIGIN
Alignment Scores:      5.67e-44      Length:      406
Pred. NO.:            503.00      Matches:      100
Score:                88.80%      Conservative: 11
Percent Similarity:   80.00%      Mismatches:   12
Best Local Similarity: 10.61%      Indels:       2
Query Match:          9           Gaps:        0
DB:

US-10-647-956A-6 (1-915) x AQ990055 (1-406)

Qy      483  SerAsnGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAsnThrThrGlnGln 502
Db      1   AGCAACGGCATACCGCCAGCTAAAGTGTAATGAACAACTCAGATATATCCCGCAACAA 60
Qy      503  GlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAlaThrThr 522
Db      61  CAAAGGGTAACTTATCTACCGGGGTGGAATACGTACAAACCCAGAACCGCCACAACA 120
Qy      523  ThrGluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArgValLeu 542
Db      121  ACAGAAGAGTTTACACGTTTATCACACTCGGTAAAGCCGGCCGCGCAAGTCGAGTATTG 180
Qy      543  HisTrpGluSerGlyLysProGluAspValAsnAsnGlnLeuArgTyrSerTyrAsp 562
Db      181  CATTGGGAGACGGTAAACGAGAGATATATATACATCATAGCTTCGTTACAGTACGAT 240
Qy      563  AsnLeuIleGlySerSerGlnLeuGluLeuAspAsnGlnGlyGlnIleIleSerGlu-Gl 582

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Db      241  AATCTTTATTGGTCCACCAACTTCAATTAGATAGACGACGGCAAAATTATCAAGTGAAAGA 300
Qy      582  uGluTyrTyrProPheGlyGlyThr-AlaLeuTirPalaLaAAsnSerGlnThrGluAlaAs 602
Db      301  AGAATATTATTCATTGTTGGTGATACAGCGCTGTGGCGGNAGAGGATTAAACCGCAACCAG 360
Qy      602  erTyrLysThr 605
Db      361  CTNTTAAACA 371

RESULT 8
LOCUS     AQ990688/c
DEFINITION RfC01498 Photorhabdus luminescens strain W14 M13 library
            Photorhabdus luminescens genomic clone PLG01498, genomic survey
            sequence.
ACCESSION  AQ990688
VERSION    AQ990688.1 GI:9649282
KEYWORDS   GSS.
SOURCE     Photorhabdus luminescens
            Photorhabdus luminescens
ORGANISM   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Photorhabdus.
REFERENCE  1 (bases 1 to 594)
AUTHORS    ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
            Daborn,P.J., Bowen,D. and Blattner,F.R.
TITLE      A genomic sample sequence of the entomopathogenic bacterium
            Photorhabdus luminescens W14: potential implications for virulence
JOURNAL    Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
PUBMED     10919786
COMMENT     Contact: ffrench-Constant RH
            Department of Biology and Biochemistry
            University of Bath
            South Building, Bath BA2 7AY, UK
            Tel: (44) 1225 826621
            Fax: (44) 1225 826779
            Email: bsrfc@bath.ac.uk
            This is one of 2,122 random reads from the M13 library. For
            annotation of identified clones (BLASTX, BLASTN and mapping to E.
            coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
            Acids Res.
            Seq primer: M13 Forward
            Class: shotgun.

FEATURES             Location/Qualifiers
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                     /organism="Photorhabdus luminescens"
                     /mol_type="genomic DNA"
                     /strain="W14"
                     /db_xref="taxon:29488"
                     /clone="PLG01498"
                     /dev_stage="primary phase variant"
                     /clone_lib="Photorhabdus luminescens strain W14 M13
                     library"
ORIGIN
Alignment Scores:      5.78e-42      Length:      594
Pred. NO.:            487.00      Matches:      111
Score:                64.00%      Conservative: 17
Percent Similarity:   55.50%      Mismatches:   68
Best Local Similarity: 10.27%      Indels:       5
Query Match:          9           Gaps:        0
DB:

US-10-647-956A-6 (1-915) x AQ990688 (1-594)

Qy      428  GlyValLeuSerThrLeuThrThrAspProAsnGlnValAspThrLeuPheAspAlaGly 447
Db      593  GGTTCGTCNTCAGACCCCTAACAAAGGATCCCAATCTGTTGATTCATTCATTTCCTTTCAGGT 534
Qy      448  GlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIleTrpThrPro--ArgGlyGluL 467

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Db 533 GGTCAATCAACCCAGTTTGTATCAGGCATTCTTTAAGCTGNNACCCCGGNAGAACTCCAC 474
Qy eulyserGlnValAsnAsnGlyProGlyAsnGluTyrArgTyrAspSerAsnGlyMetA 487
Db 473 CNANTGACCAAGGGTAAACAGCGCGCGAATGGTC-CGCTATGACAGTGATGGAATGC 415
Qy 487 rg-GlnLeuIysValSerGluGlnProThrGlnAsnThrThrGlnGlnGlnArgValile 506
Db 414 GGCTATTGTAATAAATGACAGCAACCAACCCATATGCCACTGTCACCAACACGCGAGTCNCT 355
Qy 507 TyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAlaThrThrThrGluGluLeu 526
Db 354 TACTTCGACGGTGGAAATACAWACCCTCAAGCGCGCCCAATATACCGAAGACTTG 295
Qy 527 HisValile-ThrLeuGlyGluAlaGlyArgAlaGlnValArgValLeuHisTrpGluSe 546
Db 294 CAAGTTATTGCTGTCGACAGCAAGCAGNAGACGACAAAGTACGCGTTCTACANTGNAAAA 235
Qy 546 rGlyLysProGluAspValAsnAsnGlnLeuArgTyrSerTyrAspAsnLeuIleG1 566
Db 234 AGGCCANCCNCTGGNATAGATNACNATCAGTACAGTACAGTACAGTATCTTNCACA 175
Qy 566 ySerSerGlnLeuGluLeuAspAsnGlnGlyGlnIleIleSerGluGluGluTyrTrpPr 586
Db 174 CAGCAGCGAATAGAACTGNATATGACGGGTAAATATCAGTTGGNAGAGTATACCC 115
Qy 586 oPheGlyGlyThrAlaLeuTrpAlaAlaAsnSerGlnThrGluAlaSerTyrLysThr11 606
Db 114 CTATGCCGCGCACCATATGNGCNCAGAAATCAGTTGAGCTGTWACAAACCAT 55
Qy 606 eArgTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyrTrpGlyTyr 623
Db 54 TCGTTATTACGCAAGAGCGTGATGCAACAGGACTGTACTATTACGGCTAC 3

RESULT 9
LOCUS AQ990013 547 bp DNA linear GSS 14-AUG-2000
DEFINITION Rf00707 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG00707, genomic survey
sequence.
ACCESSION AQ990013.1 GI:9648607
VERSION AQ990013.1
KEYWORDS GSS.
SOURCE Photorhabdus luminescens
ORGANISM Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE 1 (bases 1 to 547)
AUTHORS ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.
TITLE A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
PUBMED 10919786
COMMENT Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bsrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: shotgun.
FEATURES
source
1..547
Location/Qualifiers
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
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/clone="PLG00707"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
/notes="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."

ORIGIN
Alignment Scores:
Pred. No.: 1,39e-33 Length: 547
Score: 409.50 Matches: 73
Percent Similarity: 88.89% Conservatives: 7
Best Local Similarity: 81.11% Mismatches: 7
Query Match: 8.64% Indels: 3
DB: 9 Gaps: 1

US-10-647-956A-6 (1-915) x AQ990013 (1-547)

Qy 585 TyrProPheGlyGlyThrAlaLeuTrpAlaAlaAsnSerGlnThrGluAlaSerTyrLys 604
Db 1 TATCCGTATGGCGGTACGGCGATATGGCGGCAGAAATCAGACAGAAAGCCAGCTACAAA 60
Qy 605 ThrIleArgTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyrGlyTyrArg 624
Db 61 TTTATTGCTTACTCCCGTAAAGAGCGGATGCCACTGGATTGTATTATTACGGCTACCGT 120
Qy 625 TyrTyrGlnProTrpAlaGlyArgTrpLeuSerAlaAspProAlaGlyThrIleAspGly 644
Db 121 TATTATCAACCTTGGTGGTGCATGTTGAGTCTGATCCGCGGGAACCGTGGATGGG 180
Qy 645 LeuAsnLeuTyrArgMetValArgAsnAsnProValSerLeuGlnAspGluAsnGlyLeu 664
Db 181 CTGAATTTGTACCGAATGGTGAGGAATAACCCCATCATTGACTGACCATGACGGATTA 240
Qy 665 AlaProGlu-----LysGlyLysTyr 671
Db 241 GCACCCGCTCTCCAATAGAAATCGAAATAC 270

RESULT 10
LOCUS AQ990147 312 bp DNA linear GSS 14-AUG-2000
DEFINITION Rf00869 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG00869, genomic survey
sequence.
ACCESSION AQ990147.1 GI:9648741
VERSION AQ990147.1
KEYWORDS GSS.
SOURCE Photorhabdus luminescens
ORGANISM Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE 1 (bases 1 to 312)
AUTHORS ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.
TITLE A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
PUBMED 10919786
COMMENT Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bsrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: shotgun.
FEATURES
source
1..312
Location/Qualifiers
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/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clones="PLG00869"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13 library"
/note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

ORIGIN

Alignment Scores:
Pred. No.: 8,71e-30 Length: 312
Score: 371.00 Matches: 73
Percent Similarity: 80.77% Conservative: 11
Best Local Similarity: 70.19% Mismatches: 17
Query Match: 7.83% Indels: 3
DB: 9 Gaps: 1

US-10-647-956A-6 (1-915) x AQ990147 (1-312)

Qy 326 AsnIleArgAsnAspAlaGluAlaThrArgPheTrpArgAsnGlnLysValAla-ProG1 345
Db 2 AATATTCGTAATGATGACGAAGCAACTCGATTCTGGCGTAATCAGAAATAGTACCCGGA 61
Qy 345 uAsnSerTyThrTrpSerLeuTyGlnLeuIleSerAlaThrGlyArgGluMetAl 365
Db 62 AAATGCGGTATACCTATGATTCCTGTGACCACTTATCATAGCAACCGCGCGGAAATGGC 121
Qy 365 aAsnIleGlyGlnGlnAsnGlnLeuProSer-----ProAlaLeuProSerAspAs 383
Db 122 TAACTATAGTCAGCAAGGACGAGCTCCCTCTTAGTTACCCCTCTTCTACCGATGA 181
Qy 383 nAsnThrTyThrAsnTyThrArgSerTySerTyAspHisSerGlyAsnLeuThrG1 403
Db 182 CAATACCTATTAATCTATACCTGACCTTATACCTAGCAGATAGCGCAACCTGACACA 241
Qy 403 nIleArgHisSerProAlaThrGlnAsnAsnTyThrValAlaIleThrLeuSerAs 423
Db 242 AATCCCGCATAAACGCTTCGGCCAGGNACAACTAATCNCNCACGATATTACCATTTNAA 301
Qy 423 nArgSerAsn 426
Db 302 CCGCAATAC 311

RESULT 11
AW901491
LOCUS RCO-NN1012-270300-031-h01 NN1012 Homo sapiens cDNA, mRNA sequence.
DEFINITION AW901491
ACCESSION AW901491
VERSION AW901491.1 GI:8065696
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 644)
Dias Neto,E., Garcia Correa,R., Vertovski-Almeida,S., Briones,M.R.,
Nagai M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P.,
Goldman,G.H., Carvalho,A.P., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

PUBMED 10737800

CONTACT: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=at2=RCO-NN1012-270
300-031-h01&t3=2000-03-27&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 31

High quality sequence stop: 644.

Location/Qualifiers

FEATURES
source

1..644

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_lib="NN1012"

/note="Organ: nervous normal; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)

Profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Alignment Scores:
Pred. No.: 1,39e-22 Length: 644
Score: 309.50 Matches: 83
Percent Similarity: 49.78% Conservative: 32
Best Local Similarity: 35.93% Mismatches: 89
Query Match: 6.53% Indels: 27
DB: 1 Gaps: 7

US-10-647-956A-6 (1-915) x AW901491 (1-644)

Qy 387 ThrAsnTyThrArgSerTySerTyArgHisSerGlyAsnLeuThrGlnIleArgHis 406
Db 3 TCAACTATGTCTACGAGCTGG-----CGGCAT 29
Qy 407 ---SerSerProAlaThrGlnAsnAsnTyThrValAla---IleThrLeuSerAsnArg 424
Db 30 TGCTCGAGCTGATCCACCACGCGCACAGCAACATGGCGGTGTGTAGCAGCGCGCAAGCAC 89
Qy 425 SerAsnArgGlyValLeuSerThrLeuThrAspProAsnGlnValAsp-----Thr 442
Db 90 AGTAATCGCTGCTGCCCGAGGTGGCGGAGGCCACCGACCGAGCTGAGATTGCCGAA 149
Qy 443 LeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIleTrpThr 462
Db 150 GCCTTCGATGCCAACGCAACCTGTTGATGTTGGACCGGGCGGCAACACTGAGTTGGAT 209
Qy 463 ProArgGlyGluLeuLysGlnValAsn-----AsnGlyProGlyAsn 476
Db 210 GCAGGTAACCACTAGCCATGTGTCATATGGTGAGCGCACGTTGGCCCTCAATGACACC 269
Qy 477 GluTrpTyThrArgTyArgSerAsnGlyMetArgGlnLeuLysValSerGluGlnProThr 496
Db 270 GAGCGCTACCTCTACGCTGCCGCGCAGCGCATGCGCGCAAGGTGGCGACGACGCAAAACC 329
Qy 497 GlnAsnThrThrGlnGlnArgValIleTyLeuProGlyLeuGluLeuArgThrThr 516
Db 330 AAGCCCGCACCTTGGTCACTGAGACCCGATATCTACCGGCTGGAAACGCGCGATGG 389
Qy 517 GlnSerAsnAlaThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGlyArg 536
Db 390 GATGGC-----GAGAACTGCACGTGTCACCGTC---CAGGCGGCGCGC 431
Qy 537 AlaGlnValArgValLeuHisTrpGluSerGlyLysProGluAspValAsnAsnGln 556
Db 432 ACCACGCTGAGGTGTTGCATTGGGAAGCGCGCGCGCGCGCGCAACTGGCGAATGATCAA 491


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Qy 557 LeuArgTyrSerTyrAspAsnLeuIleGlySerSerGlnLeuGluLeuAspAsnGlnGly 576
Db 492 TACCGTTACACCCCTTACGATCATCTGGGCTCTTGTTCGCTGAACCTGGACAGTGAAGCG 551
Qy 577 GlnIleIleSerGluGluGluTyrTyrProPheGlyGlyThrAlaLeuTrrpAlaAlaAsn 596
Db 552 AGGATCATCATCGCGAGAGCTATCATCCGTTGGTACGAGCGCCCTTCACGAGAGGGGT 611
Qy 597 SerGlnThrGluAlaSerTyrLysThrIleArg 607
Db 612 GATTCGAGCGAAGAGAGTTATCGCACGTTGCGT 644

RESULT 12
LOCUS C2532972/c 795 bp DNA linear GSS 13-MAY-2005
DEFINITION SRRA-aac82c03.g1 Strongyloides ratti whole genome shotgun library
(SRAAGSS 004) Strongyloides ratti genomic, genomic survey sequence.
ACCESSION C2532972
VERSION C2532972.1 GI:64646528
KEYWORDS GSS.
SOURCE Strongyloides ratti
ORGANISM Strongyloides ratti
Panagrolaimoidea; Nematoda; Chromadorea; Rhabditida;
Eukaryota; Metazoa; Strongyloidea; Strongyloidea.
REFERENCE 1 (bases 1 to 795)
AUTHORS Mitreva,M., McCarter,J.P., Thompson,F., Viney,M., Pape,D.,
Ritter,E., Martin,J., Wyllie,T., Dante,M., Waterston,R.H.,
Clifton,S.W. and Wilson,R.
TITLE Genome Survey sequences from the rat parasitic nematode
Strongyloides ratti
JOURNAL Unpublished (2005)
COMMENT Contact: Mitreva M
Washington University in St. Louis
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: nematode@watson.wustl.edu
Genomic DNA was provided by Fiona Thompson
(F.Thompson@bristol.ac.uk) and Mark Viney
(Mark.Viney@bristol.ac.uk) at the University of Bristol, Bristol,
UK.
Class: shotgun.
FEATURES
    source
        Location/Qualifiers
            1..795
                /organism="Strongyloides ratti"
                /mol_type="genomic DNA"
                /strain="Isotemale line ED321 heterogonic"
                /db_xref="taxon:34506"
                /dev_stage="infective larval stage (iL3)"
                /lab_host="GS10"
                /clone_lib="Strongyloides ratti whole genome shotgun
                library (SRAAGSS 004)"
                /notes="vector: pOTW13; Site 1: BstXI; Site 2: BstXI;
                Strongyloides ratti genomic DNA was randomly sheared,
                end-repaired and size fractionated to enrich for 2-4 kb
                fragments. Genomic DNA was provided by Fiona Thompson
                (F.Thompson@bristol.ac.uk) and Mark Viney
                (Mark.Viney@bristol.ac.uk) at the University of Bristol,
                Bristol, UK. Sequencing by Washington University Genome
                Sequencing Center, St. Louis, MO."

ORIGIN
Alignment Scores:
Pred. No.: 2.45e-08 Length: 795
Score: 180.00 Matches: 69
Percent Similarity: 32.90% Conservative: 33
Best Local Similarity: 22.26% Mismatches: 80
Query Match: 3.80% Indels: 128
DB: 10 Gaps: 12

US-10-647-956A-6 (1-915) x C2532972 (1-795)

```

```

Qy 368 GlyGlnGlnAsnAsnGlnLeuProSerProAlaLeuProSerAspAsnAenThrTyr--- 386
Db 668 GGAGGCAAGCTGAGAAAGAGAGCCCTTAACCTTCCAAAACAGGAGTGGTTCGGTTATACC 609
Qy 387 -----ThrAsnTyrThrArgSerTyrSerTyrAspHisSerGlyAsnLeuThrGlnIle 404
Db 608 TCAATTACGGATTATCTGGATGGTTCCCAATAC----- 576
Qy 405 ArgHisSerSerProAlaThrGlnAsnAenTyrThrValAlaIleThrLeuSerAsnArg 424
Db 576 ----- 576
Qy 425 SerAsnArgGlyValLeuSerThrLeuThrAspProAsnGlnValAspThrLeuPhe 444
Db 575 -----CTGAGTACGGTAGGAAGCAACCCCAATGAGATGGATCCTATT--- 534
Qy 445 AspAlaGlyGlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIleTrrpThrProArg 464
Db 534 ----- 534
Qy 465 GlyGluLeuGlnValAsnAenGlyProGlyAsnGluTrrpTyrArgTyrAspSerAsn 484
Db 533 -----GAGTATGCCTATGAACAGGAA 513
Qy 485 GlyMetArgGlnLeuLysValSerGluGlnProThrGlnAsnThrThrGlnGlnGlnArg 504
Db 512 GCCTTTCTAGAGCAACAGCAGTCGCGAGCAGCCG-----AATCCAACGCTCCAC--- 465
Qy 505 ValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAlaThrThrGlu 524
Db 464 -----TTTTTCCCA-----ACTGCGGAA 447
Qy 525 GluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArgValLeuHisTrp 544
Db 446 GGATTTTAT----- 438
Qy 545 GluSerGlyLysProGluAspValAsnAsnAenGlnLeuArgTyrSerTyrAspAsnLeu 564
Db 437 -----GATTATGAAATAATAGTATATTTACCAGTACAAAGATCAT 396
Qy 565 IleGlySerSerGlnLeuGluLeu-----AspAenGlnGlyGlnIleIleSer 580
Db 395 TTGGGAATGTACGGTAAGCTATATAAAGAGGCTCTGTGCTTGCACAGATTACCGAC 336
Qy 581 GluGluGluTyrTyrProPheGly-----GlyThrAlaLeuTrpAla 594
Db 335 CAGATGATTACTATCTCTTCGGGATGAATATTTCCAAGGGAAGAGCGGCTTTGGG 276
Qy 595 AlaAsnSerGlnThrGluAlaSerTyrLysThrIleArgTyrSerGlyLysGluArgAsp 614
Db 275 ACCAATAGTTTA-----TACAACATAAG-----TACAACGGTAAGGAACCTCA 231
Qy 615 AlaThrGluLeuTyrTyrTyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTrpLeu 634
Db 230 GAGACAGGAATGTATGATTATGAGCGGAGATTATATGCGGATATTGGGAGATGGGT 171
Qy 635 SerAlaAspPro---AlaGlyThrIleAspGlyLeuAsnLeuTyrArgMetValArgAsn 653
Db 170 GTGGTGATCCGCTGCGGGAAGAAATATACAGNATGCTCTCCATATACTATATGTTGGAAT 111
Qy 654 AsnProValSerLeuGlnAspGluAenGly 663
Db 110 AACCTTCAATATTTGTTGATTATGATGCT 81

RESULT 13
CC818388/c 681 bp DNA linear GSS 17-JUL-2003
LOCUS CC818388
DEFINITION 100004D09R Oxytricha plasmid UUGC10 library Sterkiella
histriomuscorum genomic clone UUGC100004D09 R, genomic survey
sequence.
ACCESSION CC818388
VERSION CC818388.1 GI:32897684
KEYWORDS GSS.

```


Db 832 GGGCCGAGCGAGTTCGAGGCCAGTATCATTTACGATCGCTGGCCGCCGAGCCGC 773
Qy LysVal-----SerGluGlnProThrGlnAenThrThrGlnGlnGln 503
Db 772 AAGCGCGTGCCTACAGGGCCAAACGACAGCAGCCGTTCTGTGCGAGGGCTAC 713
Qy ArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGln-SerAenAlaThrThr 523
Db 712 CGGTTGCTG-----CAGGAGCAGCGCAGCAGCGC 683
Qy rGluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArgValLeuHi 543
Db 682 AGCGCGCGAGCTGAGTACGATCCGCCAGCC-----CGTGAGCCCA 638
Qy sTTPGluSerGlyLysProGluAenValAenAenAenGlnLeuArgTyrSerTyrAenAs 563
Db 637 CTGGCGCGCTGGAGCAGCGGGCGCAGCGCTCGGCAGATATT-TACTGGTATCACAC 579
Qy nLeuIleGlySerSerGlnLeuGluLeu---AspAenGlnGlyGlnIleIleSerGluGl 582
Db 578 CGATCTCAACAGCGCGCGCTGGAAGTGACCGAGCGCGCGGCAACCTGTGCTGCTCGG 519
Qy uGluTyrTyrProPhe-----GlyGlyThrAlaLeuTrpAlaAenSerGl 598
Db 518 GCATACGACACCTTCGCGCAAGCTGCAGAGCGCCAGCGTGGCGCGCGGAGCGCA 459
Qy nThrGluAlaSerTyrLysThrIleArgTyrSerGlyLys---GluArgAspAlaThrGl 617
Db 458 GGGTGGCGCATACAGCAGCGCTGCGCTAGCGGGCAATATACAGCAGCAGCAAGCGG 399
Qy yLeuTyrTyrTyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTrpLeuSerAlaAs 637
Db 398 CTGCACTACAACTGTTCCGTACTACGAACCGAGTGGGGGCTTTCACCGCAGGA 339
Qy pProAlaGlyThrIleAspGlyLeuAenLeuTyrArgMetValArgAenProValse 657
Db 338 TCCGATAGGGCTGCGCGCGGTTGAACCTTTATCAGTATGCA---CCGAACCGCTGAT 282
Qy rLeuGlnAspGluAenGluAlaProGluLysGlyLysTyrThrLysGluValAenPh 677
Db 281 GTGGTGGATCCGCTGGGGTTGAGTGTAAAGCCTTTGTAACACAGAAAAGAG----- 230
Qy ePheAspGluLeuLysPheLysLeuAlaAlaLysSerSerHisValValLysTrpAenGl 697
Db 229 -----CCGAAGATTCTTAT----- 215
Qy uLysGluSerSerTyrThrLysAenLysSerLeuLysValValArgValGlyAspSerAs 717
Db 214 -----GAACAAGCTAGGAATAAAGCACTCAA----- 188
Qy pProSerGlyTyrLeuLeuSerHisGluGluLeuLysGlyIleGluLysSerGlnIl 737
Db 188 ----- 188
Qy eileTyrSerArgLeuGluGluAenSerSerLeuSerGluLysSerLysThrAenLeuSe 757
Db 187 -----TGGCTTGAGGAACGTGGTTTCAAGCGGAAAAGTCAATACAGGG---AA 141
Qy rLeuGlySerGluIleSerGlyTyrMetAlaArgThrIleGlnAspThrIleSerGluTy 777
Db 140 ATTTGGCGCAACAGAGGCAACCTGTGCGGAATGACCACCTTGATGGTAAACAGGGTT 81
Qy rAlaGluGluHisLysTyrArgSerAenHisProAspPheTyr-SerGluThrAspPhePh 797
Db 80 TAGGATTGAATATGATGAGAGAAGTGGT-----GCTCATATAAATGTCCTT 36
Qy eAlaLeuMetAspLysSerGlu 804
Db 35 TAGTGGGAAGGATTAAGGAGAG 14

RESULT 15
CC110859

LOCUS CC110859 850 bp DNA linear GSS 16-APR-2003
DEFINITION NDL.20H16.SP6 Notre Dame Liverpool Aedes aegypti genomic clone
NDL.20H16, genomic survey sequence.
VERSION CC110859
ACCESSION CC110859.1 GI:29979914
KEYWORDS GSS.
SOURCE Aedes aegypti (yellow fever mosquito)
ORGANISM Aedes aegypti
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Culicidae; Culicinae; Culicini; Aedes; Stegomyia.
REFERENCE 1 (bases 1 to 850)
AUTHORS Loftus, B., Shetty, J., Knudson, D. and Severson, D.
TITLE BAC end sequencing of Aedes aegypti
JOURNAL Unpublished (2003)
COMMENT Other GSSs: NDL.20H16.T7
Contact: Brendan Loftus
Department of Eukaryotic Genomics
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: enta@tigr.org
Library was provided by David Severson
Seq primer: SP6
Class: BAC ends.
FEATURES
source
1..850
/organism="Aedes aegypti"
/mol_type="genomic DNA"
/strain="Liverpool"
/db_xref="taxon:7159"
/clone_lib="Notre Dame Liverpool"
/note="Vector: pECBAC1, Site_1: Hind III; The library was
prepared from whole body tissue of newly hatched 1st larvae
by David Severson at the University of Notre Dame and
Hongbin Zhang"
ORIGIN
Alignment Scores: 1.79e-07 Length: 850
Pred. No.: 172.50 Matches: 79
Score: 35.67% Conservative: 43
Percent Similarity: 23.10% Mismatches: 118
Best Local Similarity: 3.64% Indels: 102
Query Match: 9 Gaps: 13
DB:
US-10-647-956A-6 (1-915) x CC110859 (1-850)
Qy 329 AenAspAlaGluAlaThrArgPheTrpArgAenGlnLysValAlaProGluAenSerTyr 348
Db 24 AATATTGCGGAACACTGACTGGGCAACACAAAATAGCGGAACACATAAGACCGCTATAGCTAC 83
Qy 349 ThrTyrAspSerLeuTyrGlnLeuIleSerAlaThrGluGluMetAlaAenIleGly 368
Db 84 CAATATGATGGTACTAATCGTTA-----AAGAGAGTAAATTATTGGGCAATGCCGA 137
Qy 369 GlnGlnAenAenGlnLeuProSerProAlaLeuProSerAenAenThrTyrThrAen 388
Db 138 GCT-----ACAGCTGGATCT 152
Qy 389 TyrThrArgSerTyrSerTyrAspHisSerGlyAenLeuThrGlnIleArgHisSerSer 408
Db 153 TATGCGGAGAAATTGAATTATGACTTAAACGGGAATATTACTGGGTTCGCAAGAACAGGT 212
Qy 409 ProAlaThrGlnAenAenTyrThrValAlaIleThrLeuSerAenArgSerAenArgGly 428
Db 213 -----CAGGGTGGCGGA 224
Qy 429 ValLeuSerThrLeu-----ThrThrAspProAenGlnValAenThr 442
Db 225 GTAATGGATCAGCTCAGTTATACCTACGATCAATCGGGGAATAGTAATAAACTGATTAGG 284

GenCore version 5.1.6
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OM protein - nucleic search, using frame plus p2n model

Run on: December 14, 2005, 12:23:18 ; Search time 387 Seconds
(without alignments)
4202.762 Million cell updates/sec

Title: US-10-647-956A-6
Perfect score: 4740
Sequence: 1 MSYNSAIDQKTPSIKVLN.....EAINRRAIAENLGMRTS 915

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10647956 @CGN 1.1 290 @runat_12122005_091818_29634 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DLEXT=7

Database :

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5: /cgn2_6/ptodata/1/ina/H COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4740	100.0	2745	3	US-09-817-514A-5
2	2501.5	52.8	37948	3	US-09-251-645-11
3	2467	52.0	3132	3	US-08-851-567B-60
4	336	7.1	4884	3	US-09-328-352-2478
5	322.5	6.8	2997	3	US-09-252-991A-11853
6	307	6.5	2925	3	US-09-252-991A-7069
7	286.5	6.0	4881	3	US-09-252-991A-7234
8	281	5.9	4320	3	US-09-543-681A-3388
9	273.5	5.8	4281	3	US-09-492-709A-180

10	262	5.5	31960	3	US-09-453-702B-11	Sequence 11, Appl
11	282	5.5	31960	3	US-10-114-170-11	Sequence 11, Appl
12	256	5.4	5519	3	US-09-453-702B-226	Sequence 226, App
13	256	5.4	5519	3	US-10-114-170-226	Sequence 226, App
14	254.5	5.4	4134	3	US-09-711-164-296	Sequence 296, App
15	253.5	5.3	11613	3	US-09-453-702B-42	Sequence 42, Appl
16	253.5	5.3	11613	3	US-10-114-170-42	Sequence 42, Appl
17	248.5	5.2	4791	3	US-09-328-352-1416	Sequence 1416, Ap
18	246	5.2	9717	3	US-09-251-645-1	Sequence 1, Appl1
19	242	5.1	4998	3	US-09-543-681A-304	Sequence 304, App
20	235	5.0	4761	3	US-09-543-681A-1157	Sequence 1157, Ap
21	227.5	4.8	1857	3	US-09-252-991A-11787	Sequence 11787, A
22	219.5	4.6	1857	3	US-09-252-991A-7125	Sequence 7125, Ap
23	216	4.6	7841	3	US-09-902-540-816	Sequence 816, App
24	213.5	4.5	3003	3	US-09-902-540-1863	Sequence 1863, Ap
25	201	4.2	3660	3	US-09-453-702B-12	Sequence 12, Appl
26	201	4.2	3660	3	US-10-114-170-12	Sequence 12, Appl
27	197	4.2	3387	3	US-09-252-991A-14461	Sequence 14461, A
28	184	3.9	1683	3	US-09-252-991A-6977	Sequence 6977, Ap
29	184	3.9	1683	3	US-09-252-991A-11588	Sequence 11588, A
30	183.5	3.9	1035	3	US-09-328-352-2531	Sequence 2531, Ap
31	179	3.8	26012	3	US-09-902-540-1212	Sequence 1212, Ap
32	172.5	3.6	11091	3	US-09-134-001C-2243	Sequence 2243, Ap
33	171.5	3.6	4770	3	US-09-543-681A-826	Sequence 826, App
34	171	3.6	30549	3	US-09-134-001C-322	Sequence 322, App
35	170.5	3.6	2495	3	US-09-668-113A-1	Sequence 1, Appl1
36	169	3.6	1764	3	US-09-252-991A-14908	Sequence 14908, A
37	169	3.6	3840	3	US-09-710-279-3187	Sequence 3187, Ap
38	168.5	3.6	9319	3	US-08-976-259-85	Sequence 85, Appl
39	168.5	3.6	9319	3	US-09-956-004-85	Sequence 85, Appl
40	168.5	3.6	22671	3	US-08-976-259-14	Sequence 14, Appl
41	168.5	3.6	22671	3	US-09-956-004-14	Sequence 14, Appl
42	167	3.5	4453	3	US-09-453-702B-90	Sequence 90, Appl
43	167	3.5	4453	3	US-10-114-170-90	Sequence 90, Appl
44	166.5	3.5	1515	3	US-09-902-540-2019	Sequence 2019, Ap
45	166.5	3.5	3543	3	US-09-710-279-4149	Sequence 4149, Ap

ALIGNMENTS

RESULT 1
US-09-817-514A-5
; Sequence 5, Application US/09817514A
; Patent No. 6639129
; GENERAL INFORMATION:
; APPLICANT: firench-Constant, Richard
; APPLICANT: Bowen, David
; APPLICANT: Rocheleau, Thomas
; APPLICANT: Waterfield, Nicholas
; TITLE OF INVENTION: DNA SEQUENCES FROM PHOTORHABDUS LUMINESCENS
; FILE REFERENCE: 61645
; CURRENT APPLICATION NUMBER: US/09/817,514A
; PRIOR FILING DATE: 2000-03-26
; PRIOR APPLICATION NUMBER: US 60/191806
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 2745
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2745)
US-09-817-514A-5

Alignment Scores:
Pred. No.: 0
Score: 4740.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 3
Length: 2745
Matches: 915
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

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Qy	41	GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro	60
Db	121	GAATTAATACGTTCTATGAGTTCAATATATCCGGGATTTACGGTAAAAAGCACCGATCT	180
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Qy	81	ValLeuArgGluGluSerValAspAlaGlyArgThrIleThrLeuAenAspIleGluSer	100
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Qy	121	ThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGlyGluLysThrThr	140
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Qy	621	TyrGlyTyrArgTyrTyrGlnProTrrAlaGlyArgTrrLeuSerAlaAspProAlaGly	640
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Qy 821 LysValTyrHisAspLeuLysAenLysGlnSerGluLeuHisValAenTyrAlaLeuAla 840
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Qy 841 HisProTyrThrGlnLeuSerAenGluGluArgAlaLeuLeuGlnGluProAla 860
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Qy 861 IleAlaIleAspArgGluTyrAenPheLysGlyValGlyLysPheLeuThrMetLysAla 880
Db 2581 ATTGCAATAGATAGAGAAATATAATTTCAAAGGTGTTCGCAAAATTCCTGACAAATGAAGCA 2640

Qy 881 IleLysLysSerLeuLysGlyHisLysIleAsnArgIleSerThrGluAlaIleAenIle 900
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Qy 901 ArgSerAlaIleAlaGluAenLeuGlyMetArgArgThrSer 915
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RESULT 2
US-09-251-645-11
; Sequence 11, Application US/09251645
; Patent No. 6281413
; GENERAL INFORMATION:
; APPLICANT: Kramer, Vance C.
; APPLICANT: Morgan, Michael K.
; APPLICANT: Anderson, Arne R.
; APPLICANT: Hart, Hope
; APPLICANT: Warren, Gregory W.
; APPLICANT: Dunn, Martha
; APPLICANT: Chen, Jeng S.
; TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
; FILE OF INVENTION: AND NUCLEIC ACID SEQUENCES CODING THEREFOR
; FILE REFERENCE: CCG1963/A
; CURRENT APPLICATION NUMBER: US/09/251,645
; CURRENT FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 37948
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (15171)..(18035)
; OTHER INFORMATION: orf5
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (23768)..(31336)
; OTHER INFORMATION: hph2
; FEATURE:
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; NAME/KEY: CDS
; LOCATION: (31393)..(35838)
; OTHER INFORMATION: orf2
US-09-251-645-11
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Alignment Scores:
Pred. No.: 2,69e-244 Length: 37948
Score: 2501.50 Matches: 505
Percent Similarity: 74.33% Conservative: 103
Best Local Similarity: 61.74% Mismatches: 159
Query Match: 52.77% Indels: 51
DB: 3 Gaps: 13

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Db 15531 TCCCTACCCGGTCTGTGTCTGTTACCGAAACAAATACCA-----GAAAAACATCC 15584

Qy 140 -----ThrGluArgLeuIleTrpAlaGlyAenThrProGlnGluLysAspTyrAenLeu 157
Db 15585 CGTATCACCGAACGCTGATTTGGGTGGCATAGCAAGACAGAGAAACCATATATCTT 15644

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Qy 178 LeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAspAenGlnAspAlaAen 197
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Qy 198 TrpThrGlyGluAenGlnSerLeuTrpGlnGlnLysLeuSerSerAenValTyrIleThr 217
Db 15765 TGGACAGGTGATATGAACCGCTCTGGCAAAACATGCTGGCTGATGACATCTACACAACC 15824

Qy 218 GlnSerAenThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGlyAenIle 237
Db 15825 CTGAGCGCCTTTGATGCCCGCGCTTTACTCACTCAGACCGATCGCAAAAGGAACATTT 15884

Qy 238 GlnArgLeuAlaTyrAspValAlaGlyGlnLeuLysGlySerTrpLeuThrLysGly 257
Db 15885 CAGAGGCTAACCTATGATGTGGCCGGCAGCTAAACGGGAGCTGGTTAACTTAAAGAC 15944

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Db 15945 CAACCGAAACAAGTGAATATCAGATCCCTGACCTATTCCGCCCGCGGACAAATAATACG 16004

Qy 278 GluGluHisGlyAenGlyIleValThrGluTyrSerTyrGluProGluThrGlnArgLeu 297
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Db 16005 GAGGAACACGCAATGGTGTATCACCGAATACAGTTATGAACCGGAAACCCACACGCTT 16064
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Db 16065 ATCCGTTACCAAAACCCACCGTCCTGAGATGCCAAAGTGTGCAAGATCTACGTTATGAG 16124
Qy 318 TyrAspProValGlyAsnValIleAsnIleArgAsnAspAlaGluAlaThrArgPheTyr 337
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Db 16365 GCGGCAATTTGACTAAATCCAGCACACAGTTTCACCGCGACGCAAAACACTACACACA 16424
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Db 16425 AACATCATCGGTTTCTAACCGGAGCAATCGCGCAGTACTCTGACCAAGATCCG 16484
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Qy 458 ThrLeuIleThrProArgGlyGluLeuLysGlnVal-----AsnAsn 472
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Qy 473 GlyProGlyAsn-----GluTyrTyrArgTyrAspSerAsnGlyMetArgGlnLeuLys 490
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Qy 511 LeuGluLeuArgThrThrGlnSerAsnAlaThrThrThrGluGluLeuHisValIleThr 530
Db 16725 TTAGAACTTCGCTAAACAAAAACAGCACGATCACAACCGAAGATTTGCAAGTTATCACA 16784
Qy 531 LeuGlyGluAlaGlyArgAlaGlnValArgValLeuHisTyrGluSerGlyLysProGlu 550
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Qy 551 AspValAsnAsnAsnGlnLeuArgTyrSerTyrAspAsnLeuIleGlySerSerGlnLeu 570
Db 16845 GATATCGACAATAATACGTACGTTATAGCTACCATTAATCTTATCGGTTCAGTCAACTT 16904
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Qy 591 AlaLeuTrpAlaAlaAsnSerGlnThrGluAlaSerTyrLysThrIleArgTyrSerGly 610
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Db 17025 ANAGCGGGATGCCACCGGACTATATTATACGGTTACCGATATATACGCCTTGGGTA 17084
Qy 631 GlyArgTrpLeuSerAlaAspProAlaGlyThrIleAspGlyLeuAsnLeuTyrArgMet 650
Db 17085 GGACGATGTTAAGTGCCGATCCGCGAGAACAGTACAGTGGTTGAAATTTATATACGGATG 17144

Qy 651 ValArgAsnAsnProValSerLeuGlnAspGluAsnGlyLeuAlaPro----- 666
Db 17145 GTAAGGAATAATCCGGTTACTCTGCTTGATCTCTGATGGATTATGTCACCAAAATTCAGAA 17204
Qy 667 -----GluLysGlyLysTyr-----ThrLysGlu 674
Db 17205 CGCATAGCAGCACTGCAAAAAAATAAAGTAGCAGATTTCAGCGCTTCGCCAACAAATGCC 17264
Qy 675 ValAsnPhePheAspGluLeuLysPheLysLeuAlaLysSerSerHisValValLys 694
Db 17265 ACAACGTAGCAGTAAACATCCGCCCGCGGTAGCACCAAAACCTACC---TTACCCAAA 17321
Qy 695 TrpAsnGluLysGluSerSerTyrThr-----LysAsnLysSerLeuLysValVal 711
Db 17322 GCATCAGAGTAGCCAACTCACTATACCCCATCAATCTCAAGCATAAACCCACG 17381
Qy 712 ArgValGlyAspSer-----AspProSerGlyTyrLeuLeuSerHisGlu 726
Db 17382 ACCTCGGATCATCCATTACTGCTCCACTGAGTCCAGTAGGAAATAAATCTACTCTCTGAA 17441
Qy 727 GluLeuLeuLysGlyLleGluLysSerGlnIleIleTyrSerArgLeuGluGluAsnSer 746
Db 17442 ATATCTCTTCCA-----GAAAGCACTCAA-----AGC 17468
Qy 747 SerLeuSerGluLysSerLysThrAsnLeuSerLeuGlySerGluIleSerGlyTyrMet 766
Db 17469 AATCTTCAAGCCCTATTTCAACAAATCTACAGAAAAAGTCA---TTTACTTTATATAGA 17525
Qy 767 Ala-----ArgThrIleGlnAspThrIleSerGluTyrAlaGluGluHisLys 782
Db 17526 GCGGATAATAGATCCCTTTGAAGACATGCAGAGTAAATTCCTCGAAGGATTTAAA 17579

RESULT 3

US-08-851-567B-60
; Sequence 60, Application US/08851567B
; Patent No. 6528484
; GENERAL INFORMATION:
; APPLICANT: Ensign, Jerald C
; APPLICANT: Bowen, David J
; APPLICANT: Petell, James
; APPLICANT: Fatig, Raymond
; APPLICANT: Schoonover, Sue
; APPLICANT: ffrench-Constant, Richard
; APPLICANT: Rocheleau, Thomas A.
; APPLICANT: Blackburn, Michael B.
; APPLICANT: Hey, Timothy D.
; APPLICANT: Orr, Gregory L.
; APPLICANT: Roberts, Jean L.
; APPLICANT: Strickland, James A.
; APPLICANT: Guo, Lining
; APPLICANT: Ciche, Todd A.
; APPLICANT: Sukhapiinda, Kitiseri
; APPLICANT: Merlo, Donald J.
; APPLICANT: Orr, Gregory L.
; APPLICANT: Roberts, Jean L.
; APPLICANT: Strickland, James A.
; APPLICANT: Guo, Lining
; APPLICANT: Ciche, Todd A.
; APPLICANT: Sukhapiinda, Kitiseri
; TITLE OF INVENTION: Insecticidal Protein Toxins From Photorhabdus
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dow Agrosciences Patent Department
; STREET: 9330 Zionsville Road
; CITY: Indianapolis
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/851,567B
; APPLICATION NUMBER: 05-MAY-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:


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/ APPLICATION NUMBER: US 08/063,615
/ FILING DATE: 18-MAY-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/395,497
/ FILING DATE: 28-FEB-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/007,255
/ FILING DATE: 06-NOV-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/608,423
/ FILING DATE: 28-FEB-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/705,484
/ FILING DATE: 28-AUG-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Seay, Nicholas J
/ REGISTRATION NUMBER: 27386
/ REFERENCE/DOCKET NUMBER: 960296.93804
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 608-251-5000
/ TELEFAX: 608-251-9166
/ INFORMATION FOR SEQ ID NO: 60:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3132 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ US-08-851-567B-60

Alignment Scores:
Pred. No.: 1,61e-242 Length: 3132
Score: 2467.00 Matches: 470
Percent Similarity: 81.25% Conservative: 89
Best Local Similarity: 68.31% Mismatches: 111
Query Match: 52.05% Indels: 18
DB: 3 Gaps: 5

US-10-647-956A-6 (1-915) x US-08-851-567B-60 (1-3132)
QY 1 MetSerSerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn 20
DB 1 ATGAGTCCGCTCGAGACTACTCTTTATCTCAAAACCCCAACAGTCAGCGGTGTAGATAAT 60
QY 21 ArgLysLeuAsnValArgThrLeuArgThrLeuArgThrGlnAlaAspGluAsnSerAsp 40
DB 61 CCGCGTCTGTCATTCGTATGTTGGTTTCACCGTATTGTAATCGGGGGGATCTGAC 120
QY 41 GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro 60
DB 121 ACCCGGTCACCGCTCACCATGATGATGCCGTGGACACCTGAACCTACAGATTGACCCA 180
QY 61 Arg-----LysAsnLysAsnGlnSerGlyProAsnPheIleArgValPhe 75
DB 181 CGCTTGTATGATGCAAGCAGCGCTGATACTCAGTAAAGCCTAATTTGTCTGGCAGCAT 240
QY 76 AsnLeuAlaGlyGlnValLeuArgGluGluSerValAspAlaGlyArgThrIleThrLeu 95
DB 241 GATCTGGCGGTCATCCCTCGCGACAGAGAGTGTGATGCTGCTGCTACTGTGTGCAATG 300
QY 96 AsnAspIleGluSerArgProValLeuIleAsnAlaThrGlyValArgGlnAsnHis 115
DB 301 AATGATATTGAAGTCTTCGGTAAATGACAATGAATGCGACCGCTGTCGTACAGCCCGT 360
QY 116 ArgTyrGluAspAsnThrLeuProGlyArgLeuLeuAlaIleThrGluGlnVal----- 133
DB 361 CGCTATGAAGCAACACCTTGCCTCGCTGCTTTATCTGTGAGCAGCAAGTTTCAAC 420
QY 134 GlnAlaGlyGluLysThrThrGluArgLeuIleThrPheAlaGlyAsnThrProGlnGluLys 153
DB 421 CAAGAGAGTGTAAAGTGACAGAGCCGTTATCTGGGCTGGGAAATACACCTCGGAGAAA 480
QY 154 AspTyrAsnLeuAlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeu 173
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DB 481 GAGTATAACCTCTCCGGTCTGTGTATACGCCACTACGACACAGCGGAGTGACCCGGTTG 540
QY 174 AsnSerLeuSerLeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAspAsn 193
DB 541 ATGAGTCACTGCTGGCGGCGCCATGCTATCCCAATCTCACCATAATGCTGGCGGAAGG 600
QY 194 GlnAspAlaAspTrpThrGlyGluAspGlnSerLeuTrpGlnGlnLysLeuSerSerAsp 213
DB 601 CAGGAGGCTAACTGGAGCGGTGACGACGAACTGTCTGGCAGGAAATGCTGCAAGTGAG 660
QY 214 ValTyrIleThrGlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAla 233
DB 661 GTCTATACACACAAAGTACCCTAATGCCATCGGGGCTTTACTGACCCCAACCGATGCG 720
QY 234 LysGlyAsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLeuLysGlySerTrpLeu 253
DB 721 AAAGGCNATATTTCAGGCTCTGGCTTATGACATTGCGGTGAGTTAAAGGAGTGGTTG 780
QY 254 ThrLeuLysGlyGlnAlaGluGlnValIleLysSerLeuThrTyrSerAlaAlaGly 273
DB 781 ACGGTAAAGGCGCAGAGTGAACAGGTGATTGTTAAGTCCCTGAGCTGTCAGCGCAGGT 840
QY 274 GlnLysLeuArgGluGluHisGlyAsnGlyIleValThrGluTyrSerTyrGluProGlu 293
DB 841 CATAAATTCGCTGAAGAGCAGCGTAACGCGGTGTTACGGAGTACAGTTATGAGCCGGA 900
QY 294 ThrGlnArgLeuIleGlyIleThrThrArgArg-----ProSerAspAlaLys 309
DB 901 ACTCAAGTCTGATAGTATACACCCCGCGTCCGAAAGGAGTCAANTCAGGAGCCAGA 960
QY 310 ValLeuGlnAspLeuArgTyrGlnTyrAspProValGlyAsnValIleAsnIleArgAsn 329
DB 961 GTATTGAGGATCTACGCTATAAGTATGATCGGTGGGAAATGTTATCAGTATCCATAAT 1020
QY 330 AspAlaGluAlaThrArgPheTrpArgAsnGlnLysValAlaProGluAsnSerTyrThr 349
DB 1021 GATGCCAAGCTACCGCTTTTGGCGTAATCAGAAAGTGGAGCGCGAGAAATCCGCTATGT 1080
QY 350 TyrAspSerLeuTyrGlnLeuIleSerAlaThrGlyArgGluMetAlaAsnIleGlyGln 369
DB 1081 TATGATTCTCTGTATCAGCTTATGATGCGACAGCGCGTGAATGCTAATATCGGTGAG 1140
QY 370 GlnAsnAsnGlnLeuProSerProAlaLeu-----ProSerAspAsnAsnThrTyrThr 387
DB 1141 CAAAGCAACCAACTTCCCTCACCGTTATACCTGTTCTTACTGACGACGACACTTATACC 1200
QY 388 AsnTyrThrArgSerTyrSerTyrAspHisSerGlyAsnLeuThrGlnIleArgHisSer 407
DB 1201 AATTACCTTCGTACCTTATCTTATGACCGTGGCGTAATTTGGTTCCAAATCCGACACAG 1260
QY 408 SerProAlaThrGlnAsnAsnTyrThrValAlaIleThrLeuSerAsnArgSerAsnArg 427
DB 1261 TCACCCGCGCATCAAAATAGTTACACACAGATATCCCGTTTCAAGCGCAGTAACCGG 1320
QY 428 GlyValLeuSerThrLeuThrThrAspProAsnGlnValAspThrLeuPheAspAlaGly 447
DB 1321 GCGGTATTGATACATTAAACGACAGATCCAAACCGAGTGGATGCGCTATTGATTCCGGC 1380
QY 448 GlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIleThrProArgGlyGluLeu 467
DB 1381 GGTGTCATCAGAAGATGTTAATACCGGGGCAAAATCTGGATTGGAATATTCCGGGTGAATG 1440
QY 468 LysGlnVal-----AsnAsnGlyProGlyAsnGluTrpTyrAsgTyrAsp 482
DB 1441 CAACGAGTCAACCCGCTGAGCCGTAAGAAATAGCAGTACAGTGAATGTTATCCCTATAGC 1500
QY 483 SerAsnGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAsnThrThrGlnGln 502
DB 1501 AGTGATGGCATCGCGCTGCTAAAGTGAGTGAACACGACGACGCGGCAACAGTACTCAAG 1560
QY 503 GlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAlaThrThr 522
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736 GAATACGACGTCGACACCAAGGGCAATCGCACCGCCAGCGCATCAAGGACCGCAGCGGC 795
Qy
160 GlnCysValArgHis-----TyrAspThrAlaGlyLeuThrGlnLeuAsnSer 175
Db
796 AGCCTGGTGGCCGACGACGCAATGGCGCTACGACGAGCTTGGC-----CGGCTGCTCCGTGGC 852
Qy
176 LeuSerLeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAspAsnGlnAsp 195
Db
853 GTCCGGCCGGCCGACAGACACGCGAGCTTGCCTACGAC-----CTCAACGACAAATCCG--- 906
Qy
196 AlaAspTrpThrGlyGluAspGlnSerLeuTrpGlnGlnLysLeuSerSerAspValTyr 215
Db
907 -----GTCGGCGAAACCAACCCG-----CGCCAGTTGCGCCACGACGAGCGCTTC 951
Qy
216 IleThrGlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGly 235
Db
952 -----GAGCCCTCGACCGGCTGTCGGCCAGACGATCCCTCGGC 993
Qy
236 AsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLeu-----Lys 249
Db
994 GGCAGACCCGACTCGGCTACGACGCCGACGACAACTCACCGAGGTCAAGGACCCCGCGC 1053
Qy
250 GlySerTrpLeuThrLeuLys-----GlyGlnAlaGluGlnValIle 263
Db
1054 GGC-----GTCACCAACCGCTACGAATACGACGGCTCGGCAACCTGACCGACTGGTC 1107
Qy
264 -----IleLysSerLeuThrTyrSerAlaAlaGlyGlnLysLeuArgGlu 278
Db
1108 AGCCCGACGACGACACCCACCTTCGAGCAGACGCCCGCGCAACGTCATCCGCGCGC 1167
Qy
279 GluHisGlyAsnGlyIleValThrGluTyrSerTyrGluProGluThrGlnArgLeuIle 298
Db
1168 ACCGACCTCGGTGGTCCGTCACCGAGTATCGTACGAC---GCCCTCAATCGGCTG--- 1221
Qy
299 GlyIleThrThrArgArgProSerAspAlaLysVal----- 310
Db
1222 --GTCGAGCGCGCTCGCGAGCGACCCGAGCGCTCGAGGTACAGTACCGCTACGACCTC 1278
Qy
311 -----LeuGlnAsp 313
Db
1279 ACCCGCAGCGCAACGAGGCGATCGCGCGCTGGCGGCCCATCGAAGTGGCCGACAGC 1338
Qy
314 LeuArgTyrGlnTyrAspProValGlyAsnValIle-----AsnIleArgAsn 329
Db
1339 CTGGTGTACCGCTACGACGAGCGCGCAACCTGTGTGAGCAGGTACGCGATCCGCGCTC 1398
Qy
330 AspAlaGlu----- 332
Db
1399 GACCAGCAGACCTGTCTCGACCGGCTGACCTACCGCTACGACGGCGCAACCACTGTGTG 1458
Qy
333 -----AlaThrArgPheTrpArgAsn----- 339
Db
1459 GAGATCGGCTACCCCTCGGCGCTCGCCATCGGCTACCGCGCAACGCGCGCGCCAGGTC 1518
Qy
339 ----- 339
Db
1519 GCCAGGTGACCCCTGGCAGTGGCGCAGCAAGCGCGGAGCACCCCTGGTTGGGCATCGCC 1578
Qy
340 -----GlnLysValAlaProGluAsnSerTyrThr----- 349
Db
1579 TACCTGCCCTTCGGCCCGCTGACGCGCTGACCTGGGGCAACGCGCATCTCTCAGCGCGC 1638
Qy
350 ---TyrAspSerLeuTyrGlnLeuIleSerAlaThrGlyArgGluMetAlaAsnIleGly 368
Db
1639 GAGTACGACCAAGGACTACCAACTGCTGCG-GCAGAAAGTGGCGCCCTGGCA----- 1688
Qy
369 GlnGlnAsnGlnLeuProSer----- 376
Db
1689 -----GAGCGACTACGACGAGTGGCAATGGCAATATCCAGCAGCACCCGCCACAG 1739
Qy
377 -----ProAlaLeuProSerAspAsnThrTyr 386
Db
1740 CCTCTGGGGCACCCCTGGACTACCACTACGACCCCGCTGGACCGCTGACCGAGGAACGCGG 1799

Qy
387 -ThrAsnTyrThrArgSerTyrSerTyrAspHisSerGlyAsnLeuThrGlnIleArgHis 406
Db
1800 CGTCCAGGGCGGCGGACGCTACGCTACGACGGCGTGGCAACCGCACCCCAA---CGCAG 1856
Qy
406 sSerSerPro-----AlaThrGlnAsnAsnTyrThrValAlaIleThrLe 421
Db
1857 CGACAACCCCGCCTCAGCGGGCACCCGACGACGACGAGTACCGAGTACGCG----- 1908
Qy
421 uSerAsnArgSerAsnArgGlyValLeuSerThrLeuThrThrAspProAsnGlnValAs 441
Db
1909 -----CCGACGACGACCGA-----TTACCGCATCGGCGCGCAAGCGGT 1949
Qy
441 pThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIleTr 461
Db
1950 GACC---AGCGACCGCGCGCAACCTCACCGAGGACCGCGCGGCAACTGGGCTA 2006
Qy
461 pThrProArgGlyGluLeuLysGlnValAsn---AsnGlyProGlyAsnGluTrpTyrAr 480
Db
2007 CGACGCCAGGCGCGCTGCAAGCGTCAGCCTCGACGGCCAGCGAGTCCGCAATACCG 2066
Qy
480 gTyrAspSerAsnGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAsnThrTh 500
Db
2067 CTACAACGCGCTCGCGCAGCGCATCTCAAGCTCAC---CCCGAGAGCATCACAC 2120
Qy
500 xGlnGlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAl 520
Db
2121 C-----TACTCTACCGTCCGACGGCCAGTTG----- 2148
Qy
520 aThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGly----- 535
Db
2149 -----CTCGCGAAGCCGACACACGACGCGCAGCGG 2177
Qy
536 -----ArgAlaGlnValArgValLeuHisTrpGluSerGlyLysPro----- 549
Db
2178 CCGGAAACTCGAGCGCCAGTACTACCTG-----TGGCTGGACAGCTGCGCTGGCCAC 2231
Qy
550 -----GluAspValAsnAsnGlnLeuArgTyrSerTy 561
Db
2232 CATCGACGCGCATACGACCCCGAGGCAAGTGGCAACCCGACCTGTCTTACTCTCCA 2291
Qy
561 rAspAsnLeuIleGlySerSerGlnLeuGluLeuAspAsnGlnGlyGlnIleLeuSerG 581
Db
2292 TGGCGACCACTCGACACCGCGCGCTGGCTACCGACGCGCGCGCAGATCGCTGGCA 2351
Qy
581 uGluGluTyrTyrProPheGly---GlyThrAlaLeuTrpAlaAlaAsnSerGlnThrG 600
Db
2352 GTGGCAGTCCGACCGCTTCGGCGCGCGGCAAGCGCTGAGCCAGGCGACGCCAGGTC-- 2409
Qy
600 uAlaSerTyrLysThrIleArgTyrSerGlyLysGluArgAspAla---ThrGlyLeuTy 619
Db
2410 -----AACCCTGGCTTCCCGGCGAGTACTACGATCGGAGAGCGGCTGCA 2456
Qy
619 rTyrTyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTrpLeuSerAlaAspProAl 639
Db
2457 CTACAACCTACTTCGCGACTATGATCCGAGACTGCGGCGGTATGTGGAGAGTATCGGAT 2516
Qy
639 aGlyThrIleAspGlyLeuAsnLeuTyrArgMetValArgAsnAsnProValSerLeuG 659
Db
2517 TGGACTAAGTGGGGAGTGAACACATACGATATGTACAGGAGGCCCGCCCTCAACCGTAT 2576
Qy
659 nAspGluAsnGlyLeuAla 665
Db
2577 TGATCCTTTAGTCTAGCA 2595

RESULT 6

US-09-252-991A-7069
; Sequence 7069, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

```

; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7069
; LENGTH: 2925
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7069

Alignment Scores:
Pred. No.: 7,66e-21 Length: 2925
Score: 307.00 Matches: 212
Percent Similarity: 33.22% Conservative: 91
Best Local Similarity: 23.25% Mismatches: 280
Query Match: 6.48% Indels: 331
DB: 3 Gaps: 43

US-10-647-956A-6 (1-915) x US-09-252-991A-7069 (1-2925)
QY 46 TyrGluPheAsnIleProGlyPheGlnValLysSerThrAspProArgLysAsnLysAsn 65
DB 349 TACAGCTACAAACCGCTCGGCTGATCAAGCGCGGAGCGGTCCGGCCACCGATGTGCAG 408
QY 66 -----GlnSerGlyProAsnPheIleArgValPheAsnLeuAla 78
DB 409 GAGCTCACCTCTATGCTTACGACAGTCGCGGCAACCTGACCGAGTGACCAAGCGCCCTC 468
QY 79 GlyGlnValLeuArgGluSerValAspAlaGlyArgThrIleThrLeuAsnAspIle 98
DB 469 GGCAGGTACCCGC-----CTCGCGGACTAT 495
QY 99 GluSerArg-----ProValLeuIleAsnAlaThrGlyValArgGlnAsnHisArg 116
DB 496 GACGAGCGGGCAAGCCCGGCGAGCATCACCGATGCCAACCGCGCTACCGACGACCTCGCC 555
QY 117 TyrGlu-----GluGlnValGlnAlaGlyGluLysThrThrGluArgLeu 143
DB 556 TACACCGCGGTGACGCGCTGCTGCGCTCGTCAGCACCGCGCGGACACCAACCTCGGCGAAGCGCTC 735
QY 144 IleTyr-----AlaGlyAsnThrProGlnGluLysAspTyrAsnLeuAlaGly 159
DB 736 GAATACGACGTCGACACCAAGGCAATCGCACCGCCCGCGCATCAAGGACGCGCGCGC 795
QY 160 GlnCysValArgHis-----TyrAspThrAlaGlyLeuThrGlnLeuAsnSer 175
DB 796 AGCTGTGTGGCCGACGAGCAATGGGCTACGAGAGCTTGGC---CGGTGCTCGGTGGC 852
QY 176 LeuSerLeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAspAsnGlnAsp 195
DB 853 GTCGCGCGCGCGCGGCGGACGACGACGCTTCGCTACGAC---CTCAACGACATCCG--- 906
QY 196 AlaAspTyrThrGlyGluAspGlnSerLeuTyrGlnGlnLysLeuSerSerAspValTyr 215
DB 907 -----GTGCGCGAACAACCGC-----CGCCAGTTCGCCACACGACGCGGCTTC 951
QY 216 IleThrGlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGly 235
DB 952 -----GATGCCCTCGACCGCTGTGCGCGGACGAGCGATCCCTCGCG 993
QY 236 AsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLeu-----Lys 249

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DB 994 GGCAAGACCCGAGCTCGCTTACGACGCCAGGACAACTCACCAGGTCAAGGACCCCGCGC 1053
QY 250 GlySerTrpLeuThrLeuLys-----GlyGlnAlaGluGlnValIle 263
DB 1054 GGT-----GTCAACACCGCTACGAATACGACGGCTCGGCAACCTGACCCGACTGGTC 1107
QY 264 -----IleLysSerLeuThrTyrSerAlaAlaGlyGlnLysLeuArgGlu 278
DB 1108 AGCCCGGACAGCGGACCAACCACTTCGAGACGACGACCGCGCGCAACGTATCCGCGCGC 1167
QY 279 GluHisGlyAsnGlyIleValThrGluTyrSerTyrGluProGluThrGlnArgLeuIle 298
DB 1168 ACCGAGCTCGCGGTGCGGTACCGAGTATCGTACGAC---GCCCTCAATCGGCTG--- 1221
QY 299 GlyIleThrThrArgArgProSerAspAlaLysVal----- 310
DB 1222 ---GTGAGCGCGCTCGCGAGGACCGAGGCTCGAGCTACGCTACCGCTACGACCTC 1278
QY 311 -----LeuGlnAsp 313
DB 1279 ACGCGCGACGCAACAAAGGCGCATCGGCGCGCATCGATGGCGCTCGCGCAGC 1338
QY 314 LeuArgTyrGlnTyrAspProValGlyAsnValIle-----AsnIleArgAsn 329
DB 1339 CTGGTGATCCGCTTACGACGAGCGCGCAACCTGTGTCGAGAGGTGCGAGCATCCGCTC 1398
QY 330 AspAlaGlu----- 332
DB 1399 GACCAGACACCTGCTCGACCGGTGACTACCGGTACGACGCGCGCAACCAACTGCTG 1458
QY 333 -----AlaThrArgPheTrpArgAsnGln----- 340
DB 1459 GAGATCGGCTACCCCTCGCGCTCGGCATCGGCTACCGCGCAACCGCGCGCGCAGGTC 1518
QY 341 -----LysValAlaProGluAsn----- 346
DB 1519 GCCAGGTGACCTGCGAGTGGGCGACAGGCGCGCAGCACCTGCTCGGCGAGATCGCC 1578
QY 347 -----SerTyr 348
DB 1579 TACCTCCCTTGGCCCGCTGCTGCGCTGACCTGGGGCAACGGCATCATCTCAGCGCGC 1638
QY 349 ThrTyrAspSerLeuTyrGlnLeuIleSerAlaThrGlyArgGluMetAlaAsnIleGly 368
DB 1639 GAGTACGACGAGGACTACCACTGCTGCG- GCAGAAGGTGCGGCCCTCGGCA----- 1688
QY 369 GlnGlnAsnAsnGlnLeuProSer----- 376
DB 1689 -----GAGCGACTACGACGACGATGCCAATGGCAATATCCAGCAGCACGCCACAG 1739
QY 377 -----ProAlaLeuProSerAspAsnAsnThrTyr 386
DB 1740 CCTCTGGGACACCTGGATACACGATACACCGCTGGACCGCTCACCAGGAGAACGCGG 1799
QY 387 -ThrAsnTyrThrArgSerTyrSerTyrAspHisSerGlyAsnLeuThrGlnIleArgH1 406
DB 1800 CGTCCAGGCGGGCGGAGCTATGCTTACGACGCGGTGCGCAACCGCACCCAA---CGCAG 1856
QY 406 sSerSerPro-----AlaThrGlnAsnAsnTyrThrValAlaIleThrLe 421
DB 1857 CGACAACCCCGCTCAGGCGGACCGCACCGACGACGACGACGACTACAGTACGCG----- 1908
QY 421 userAsnArgSerAsnArgGlyValLeuSerThrLeuThrThrAspProAsnGlnValAs 441
DB 1909 -----CCGACGACCAACCGA-----TTGACCGCATCGGCGCGCAAGCGGT 1949
QY 441 pThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIleTr 461
DB 1950 GACC---ACGACCGCGCGGCAACCTCACCAGGACCGCGCGCGCAACTGGCCTA 2006
QY 461 pThrProArgGlyGluLeuLysGlnValAsn---AsnGlyProGlyAsnGluTrpTyrAr 480

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Db 2007 CGACGCCAGCGCGCTGCAAAAGCGTCAGCCTCGACGCCAGCGGTCCGCAATACCG 2066
Qy 480 gTyrAspSerAsnGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAsnThrTh 500
Db 2067 CTAAACGCCCTCGGCAGCGCATCGCAAGCTCACCC-----CCGAGAGCGTCCACC 2120
Qy 500 rGlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAl 520
Db 2121 C-----TACCTCATGGTCCGAGCGCCAGTTG-----2148
Qy 520 aThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGly-----535
Db 2149 -----CTCGCGAAGCCGCAACACGACGCGCAGCGG 2177
Qy 536 -----ArgAlaGlnValArgValLeuHisTyrGluSerGlyLysPro-----549
Db 2178 CCGGAAACTCGGAGCCAGTACTACTG-----TGGCTGGACAGCCTGCGCTGGGCCAC 2231
Qy 550 -----GluAspValAsnAsnGlnLeuArgTyrSerTy 561
Db 2232 CATCGACGCCGACTACAGCCCGAGGCAAGTCCGCAACCCGACCTGTCTACTCTCCA 2291
Qy 561 rAspAsnLeuIleGlySerSerGlnLeuGluLeuAspAsnGlnGlyGlnIleIleSerGl 581
Db 2292 TGGCGACCACTCGACACCCCGCGCTGGCCACCGACGCCGCGCAGATCGCCTGGCA 2351
Qy 581 uGluGluTyrTyrProPheGly---GlyThrAlaLeuTrpAlaAlaSerGlnThrGl 600
Db 2352 GTGCGACTCGGACGCTTCGCGCGCGGAGCGCTGAGCCAGCGCCAGCCACCCAGTGC-- 2409
Qy 600 uAlaSerTyrLysThrIleArgTyrSerGlyLysGluArgAspAla---ThrGlyLeuTy 619
Db 2410 -----AACCTGCGCTTCGCCGGCGACTACTAGATCGGAGAGCGGCTGCG 2456
Qy 619 rTyrTyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTrpLeuSerAlaAspProAl 639
Db 2457 CTAAACTCTAAGAAAGCTCAACAACTGAGACTGCGGAGCTGGCGGTATGTGGAGAGTGATCCTGT 2516
Qy 639 aGlyThrIleAspGlyLeuAsn-----646
Db 2517 AGAAACTCTAAGAAAGCTCAACAACTGAGACTGCGGAGCTGGCGGTATGTGGAGAGTGA 2576
Qy 647 -----LeuTyrArgMetVa 651
Db 2577 GCTCAAGCCACTCCGTATTGGGAACATGGATTACCGCGGATCACTAATCACTACTC 2636
Qy 651 lArgAsnAsnProValSerLeuGlnAspGluAsnGlyLeuAlaProGluLysGlyLys-- 670
Db 2637 CGATAACATCCAACTGCNAAAGCGACAGCATGGTCTTTCACCAACCCCTACGGACAA 2696
Qy 671 -----TyrThrLysGluValAsnPheAspGluLeuLysPheLys-----684
Db 2697 CTTGATCTACACACTGACACCAACTGCATGATGATATAGAGTGCAAGAAAAAATTATC 2756
Qy 685 -----LeuAlaLysSerSerHisValVally 694
Db 2757 TGGAAATGGAAAGTCTTTCCTGTGGAGCTCTATGTAGCAAAAGCCAC-CACCCCGTCT 2815
Qy 694 sTrpAsnGluLysGluSerSerTyrThrLysAsn 705
Db 2816 TTGGGGGAGTAGTATGCATAGCACATAGTAAT 2849

RESULT 7
US-09-252-991A-7234
; Sequence 7234, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
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; PRIOR APPLICATION NUMBER: US 60/074,789
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7234
; LENGTH: 4881
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7234

Alignment Scores:
Pred. No.: 2,24e-18 Length: 4881
Score: 286.50 Matches: 178
Percent Similarity: 35.63% Conservative: 91
Best Local Similarity: 23.58% Mismatches: 239
Query Match: 6.04% Indels: 250
DB: 3 Gaps: 34

US-10-647-956A-6 (1-915) x US-09-252-991A-7234 (1-4881)

Qy 8 IleAspGlnLysThrProSerIleLysValLeuAspAsnArgLysLeuAsnValArgThr 27
Db 2581 ATAGAAGAACAGCTTCCGACGCGTAGCGTG-----CGCGCTATCGCTACGCACACA 2631
Qy 28 LeuGluTyrLeuArgThrGlnAlaAspGluAsnSerAspGluLeuIleThrPheTyrGlu 47
Db 2632 CTGGGTAGACAGTACCCGCCAGGACGAAGCGGC-----GCCATCACCCGGTTCACAA 2685
Qy 48 PheAsnIleProGlyPheGlnValLysSerThrAspProArgLysAsnLysAsnGlnSer 67
Db 2686 TGGGATGACAGCAGCGCGCTGAGCCAGATCACCTGCC-----GGT 2727
Qy 68 GlyProAsnPheIleArgValPheAsnLeuAlaGlyGlnValLeuArgGlu-----Glu 85
Db 2728 GCGCGCCAGCGCATGTACCGCTACAAACGCTTACGCAAGGTCAACCAGCGAGTGGCAGCAA 2787
Qy 86 SerValAspAlaGlyArgThrIleThrLeuAsnAspIleGlu-----SerArgProVal 103
Db 2788 CAGGCGCGATGATCCCGTACGAAATATCTTGACGACTGCACCTGTGTCAGCCGCGGCGG-- 2844
Qy 104 LeuIleIleAsnAlaThrGlyValArgGlnAsnHisArgTyrGluAspAsnThrLeuPro 123
Db 2845 -----ATCAACCCGCGAGCGCAGTCAGCTGCGCTACCGCTACGAAAC-----2886
Qy 124 GlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGlyGluLysThrThrGluArgLeu 143
Db 2887 GCGCGGCTACTGCTCAGCGAGATCGAGAACGAACGCGCGCAACGC-----TATCGCCTC 2940
Qy 144 IleTrpAlaGlyAsnThrProGlnGluLysAspTyrAsnLeuAlaGlyGlnCysValArg 163
Db 2941 GATTACACGGCAACCGCGCTGATCAGCAGAAACCGGCTTCAGCGCCCGCCGACCGCC 3000
Qy 164 His-----TyrAspThrAlaGlyLeuThrGlnLeuAsnSerLeuSerLeuAlaGlyVal 182
Db 3001 TATCGCTACGCTCAAGGC-----3021
Qy 183 LeuSerGlnSerGlnGlnLeuLeuThrAspAsnGlnAspAlaAspTrpThrGlyGluAsp 202
Db 3022 -----CAGCTTCTGGAGAAAAACGAGTACGCGCAGCAGCGCAGCGCAACTG 3066
Qy 203 GlnSerLeuTrpGlnGlnLysLeuSerSerAspValTyrIleThrGlnSerAsnThrAsp 222
Db 3067 CGCACCATCTACGAGCGC-----GAC 3087
Qy 223 AlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGlyAsnIleGlnArgLeuAlaTyr 242
Db 3088 AGTACCGGGCGCTGTGGCGAAGACACTCTCCCGCAGCGCAATCGGGTCGACTACCGGTAC 3147
Qy 243 AspValAlaGlyGlnLeu-----LysGlySerTrp---LeuThrLeuLysGly 257
Db 3148 GATACGCTCGAGCGCTGGTGGCGTTCGACGAGCGCACCTGGCGCTGGCGTACGAAATAC 3207
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QY 258 GlnAlaGluGlnValIleIleIleSer-----LeuThrTyr 269
Db 3208 GACCTACGGAGCCGCTGTCGCGAGCACACAGGGCTGGGCCACCCTTCACTACGCGCTAC 3267
QY 270 SerAlaAlaGlyGlnLysLeu----- 276
Db 3268 GACGCCCTCGGCACGTTGATTCACCTCCGACTCCGACGCGGACCGCGTCGACTACCGC 3327
QY 277 -----ArgGlu 278
Db 3328 TACCAGACGGGGCCACCCTCTCGGCAATCATCTCAACGGCCAGTCCCTGACCCGGCAC 3387
QY 279 GluHisGlyAsnGly-----IleValThrGluTyrSer 289
Db 3388 CAGTTCGTAGCGGTCCGGAACGCCAGCGCCAGCGGCAACTGCTCAGCCAATACCCAC 3447
QY 290 TyrGluProGluThrGlnArgLeuIleGlyIleThrThrArgArgProSerAspAlaLys 309
Db 3448 TAGCATGACGAGGGCCGCTGCTGGCCACCAGGTCAAGTCAGTCAGCGG-----CAGCGC 3498
QY 310 ValLeuGlnAspLeuArgTyrGlnTyrAspProValGlyAsnValIleAsnIleArgAsn 329
Db 3499 CATCTCTACGAGCGCCAGTACCGCTATGAGCTAGCGGCAACTGCGCCCATCGAGGAC 3558
QY 330 AspAlaGluAlaThrArgPheTrpArgAsnGlnLysValAlaProGluAsnSerTyrThr 349
Db 3559 AGCGCAAGGGCAATCGC-----AGCTTCCAC 3585
QY 350 TyrAspSerLeuTyrGlnLeuIleSerAlaThrGlyArg----- 362
Db 3586 TAGCACCCGCTGACCGCTGCTCGCGGTACGCGTGAAACCCCGGAAAGCTTCGTGGCAC 3645
QY 363 ---GluMetAlaAsnIleGlyGlnGlnAsnGlnLeuProSerProAlaLeuPro--- 380
Db 3646 GACCCCGCGCAACTGTCGCCAGGGCGCAATTCAGCGCGCACAGTGGAGTT 3705
QY 381 SerAspAsnAsnThrTyrThrAsnTyrThrArgSerTyrSerTyrAspHisSerGlyAsn 400
Db 3706 CGCGGAATCGCCTGTCTGACGAGGCGCACCGCAATTCGACTACGACGCCCGCCGCAAT 3765
QY 401 LeuThrGlnIleArgHisSerSerProAlaThrGlnAsnAsnTyrThrValAlaIleThr 420
Db 3766 CTCGTT----- 3771
QY 421 LeuSerAsnArgSerAsnArgGlyValLeuSerThrLeuThrThrAspProAsnGlnVal 440
Db 3772 -----CGCAAGCCCGCGCACCGCGCAGACGCTGTCACCAATACACG----- 3816
QY 441 AspThrLeuPheAspAlaGlyGlyHisGln-----ThrSerLeuLeuProGlyGln 457
Db 3817 -----TACGACTGC---CAACACCGCCTGATCGGGCTCAGCCTGCGGAGCGGCGC 3864
QY 458 ThrLeuIleTrpThrProArgGlyGluLeuLysGlnValAsnAsnGlyProGlyAsnGlu 477
Db 3865 CAGGTCGTC----- 3873
QY 478 TrpTyrArgTyrAspSerAsnGlyMetArgGlnLeuLysVal-----Ser 492
Db 3874 ---TACCGCTACAGCGCTTCGGCCGACGATCCGCAAGCAGTCCGCGGCGCAATATCC 3930
QY 493 GluGlnProThrGlnAsnThrThr-----GlnGlnGlnArgValIleTyrLeuProGly 510
Db 3931 GAGTT-CTCTGCTCGCGCAAGCCTGCTCGCGGAGAGCGGCGCGCACTACCGCAC 3989
QY 511 LeuGluLeuArgThr----- 515
Db 3990 CTATCTCTACGAACCGCACAGCTTCGCGCCGCTGCTCGACGGCGAAGCGCCGGA 4049
QY 516 ThrGlnSerAsnAlaThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGly 535
Db 4050 ACAGG-TCGAACCCCTGCTACTACCAACTCGAC-CACCTCGGTACCCCGCGAAGTACG 4107
QY 536 ArgAlaGlnValArgValLeuHisTrpGluSerGlyLysProGluAspValAsnAsn 555
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Db 4108 CCGCCGATGGCGC---CTCTGCTGGTCGGC----- 4137
QY 556 GlnLeuArgTyr---SerTyrAspAsnLeuIleGlySerSerGlnLeuGluLeuAspAsn 574
Db 4138 -----CGTACCGGGCTTACGCAATGCTCAAGCTCGACATCCCGAAGTGGATAAC 4191
QY 575 GlnGlyGlnIleSerGluGluTyrTyrProPheGlyGlyThrAlaLeuTrpAla 594
Db 4191 ----- 4191
QY 595 AlaAsnSerGlnThrGluAlaSerTyrLysThrIleArgTyrSerGlyLysGluArgAsp 614
Db 4192 -----CCACTGCGCTTCAGGGCCAGTATTCGAC 4221
QY 615 Ala---ThrGlyLeuTyrTyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTrp 633
Db 4222 GCCGACCGGCTGCACTACAACCCCATCGTACTACAATCCAAGCACGGGACGCTAC 4281
QY 634 LeuSerAlaAspProAlaGlyThrIleAspGlyLeuAsnLeuTyrArgMetValArgAsn 653
Db 4282 CTGACCCCGATCCGATCAGGCTGGCAGGTGGTGAACAGCTACCGGTACGTG---CCG 4338
QY 654 AsnProValSerLeuGlnAspGluAsnGlyLeuAlaProGluLys 668
Db 4339 AATCCGACGGGTGGGTGGACCCGTTGGGGCTGGCCTCAATAAA 4383

RESULT 8
US-09-543-681A-3388
; Sequence 3388, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 3388
; LENGTH: 4320
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-3388

Alignment Scores:
Pred. No.: 6,75e-18 Length: 4320
Score: 281.00 Matches: 169
Percent Similarity: 37.16% Conservative: 122
Best Local Similarity: 21.58% Mismatches: 286
Query Match: 5.93% Indels: 206
DB: 3 Gaps: 40

US-10-647-956A-6 (1-915) x US-09-543-681A-3388 (1-4320)
QY 32 ArgThrGlnAlaAspGluAsnSerAspGluLeuIleThrPheTyr----- 46
Db 1819 CGTTGCAATATCAGAAATGAACGCGCGCCTTATCCTGATTTTGGCGCGGATAACACA 1878
QY 47 -----GluPheAsnIleProGlyPheGlnValLysSerThrAspPro----- 60
Db 1879 GAGTCGCGTTTAGCGTATGACAGTTTGGGCGCGACTGATTAAAGAAATTTCTCCCTCAT 1938
QY 61 -----ArgLysAsn 63
Db 1939 CAGATCACCGAATACCGCTATGACTTTAAACCACATTCGCGCCCACTATACGCAATTGAT 1998
QY 64 LysAsnGlnSerGlyProAsnPheIleArgValPheAsnLeuAlaGlyGlnValLeuArg 83
Db 1999 GCCAAGCAAGGACGACGTAGTGTTC------TGGAAACAAACGTCGGCAATTACTGCGC 2052
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Qy 84 GluGluSerValAspAlaGlyArgThrIleThrLeuAsnAspIleGluSerArgProVal 103
Db 2053 CATACTGATGCTCAGCAACAACATATTTGGTGTATGATGACGAAGCCGCTGTTGTT 2112
Qy 104 LeuIleIleAsnAlaThrGlyValArgGlnAsnHisArgTyrGluAspAsnThrLeuPro 123
Db 2113 TCTCAAAACCAACGCTTTCAGGAAGCCACCGAGTACCAGTACGATGAG-----GTG 2163
Qy 124 GlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGlyGluLysThrThrGluArgLeu 143
Db 2164 GGAACACCTCGCTCGCATATA-----TTGCCCGCATATTTACCGTGCAACTG 2211
Qy 144 IleTyr-----AlaGly-----AsnThrProGlnGlu 152
Db 2212 GCATGGAAATCCGCGAGGATTTACTCATCATCAACGCAATGACATACCCCATGTCAA 2271
Qy 153 LysAspTyrAsnLeuAlaGlyGlnCysValArg----- 163
Db 2272 TGGCAATACAAACGCTTTGGTCGTGTCCACACAGAAATTGATAAATCTCGCTCGGCATATC 2331
Qy 164 -----HisTyrAspThrAlaGlyLeuThrGlnLeuAsnSerLeuSerLeuAlaGlyVal 181
Db 2332 CACTACCATTTACATGACCAAGGT-----GCATTAATTTCAATT 2370
Qy 182 ValLeuSerGlnSerGlnGlnLeuLeuThrAspAsnGlnAspAlaAspTyrThrGlyGlu 201
Db 2371 GAAATCCCAATGGCGGGGTATCTCTC-----AACCGTATGCC-----GAA 2415
Qy 202 AspGlnSerLeuTyrGlnGlnLysLeuSerSerAspValTyrIleThrGlnSerAsnThr 221
Db 2416 GATCGGTTAGTC-----GAAGAAATACGTCCTCATGAGAGCTACTCCAATACACCTAT 2469
Qy 222 AspAlaThrGlyAlaLeuLeuThrGln----- 248
Db 2470 AACCTCGCTGGACACTGGTTGAAGAAAGCTCACTTAGCGCGACCGAGTCTTCACATCTGCA 2529
Qy 234 LysGlyAsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLeu----- 248
Db 2530 CCAGCGACATA-----TTACTCGACTATGATCGCGGGTAACTTGTCAAACGTGAGACC 2586
Qy 249 -----LysGlySerTyr----- 252
Db 2587 TTAACGTATCGCTATCAATATGATGATAGTATGAACCGCTTATTTGGTCGCGACAAA 2646
Qy 253 -----LeuThrLeuLysGlyGlnAlaGluGlnValIleIleLysSer 266
Db 2647 CAACCTAATCAACGTGTCTTTGAAATGGGTTTGAAGCGAATCAAGTC-----CAC 2697
Qy 267 LeuThrTyrSerAlaAlaGlyGlnLysLeuArgGluGluHisGlyAsnGlyIleValThr 286
Db 2698 TTTACCTACGATGACACTGGCGGATTTATTCGTGAACAAACAGCGGAGGATATCGTC--- 2754
Qy 287 GluTyrSerTyrGluProGluThrGlnArgLeuIleGlyIleThrThrArgArgProSer 306
Db 2755 GAATTTAATATGAT---GAACTCAATAACCTAAGCCGCTCTGACGTTACCTCAAGGT--- 2808
Qy 307 AspAlaLysValLeuGlnAspLeuArgTyrGlnTyrAspProValGlyAsnValIleAsn 326
Db 2809 -----GACAGCCTCAACTGGCTCTATTATGGCTCTCGGCGATGCCCGCT 2853
Qy 327 IleArgAsnAspAlaGluAlaThrArgPheThrArgAsnGlnLysValAlaProGluAsn 346
Db 2854 ATCAACCACTTGTGTATAGT-----CGTCTCATGTTAAT-----ACT 2892
Qy 347 SerTyrThrTyrAspSerLeuTyrGlnLeuIleSerAlaThr----- 360
Db 2893 GAATTTGAACGTGACACCTACCGTGAATCAGTCGAATCAAGGAGAGCTCACCCAA 2952
Qy 361 -----GlyArgGluMetAlaIleGlyGlnGlnAsnGln 373
Db 2953 TATCGGCAATACGATAAATCGGGCGAACCTATAGCACTTTTCAGCTCGCGTGAAGCAA 3012
Qy 374 LeuProSerProAlaLeuProSerAspAsnAsnThrTyrThrAsnTyrThrArgSerTyr 393

Db 3013 CATCCATAAATGGTATT-----ACTTTATGGCTGAAGTGG 3048
Qy 394 SerTyrAspHisSerGlyAsnLeuThrGlnIleArgHisSerSerProAlaThrGlnAsn 413
Db 3049 TTTTATGATCCCAAGGTATCTTGGCGCCATGGAAGAC-----ACCTATCGA 3096
Qy 414 AsnTyrThrValAlaIleThrLeuSerAsnArgSerAsnArgGlyValLeuSerThrLeu 433
Db 3097 GGTGGGTAGATACTGTATGACTCAGAGCAACGTTTAAAAAAGTCGCAGCAGTGAA 3156
Qy 434 ThrThrAspPro-----AsnGlnValAspThrLeuPheAspAlaGlyGlyHis 449
Db 3157 AACCTCGATGCTATGCTGTTTACGATCGCGGATAAATCTACTCGAAACCCCAATCC 3216
Qy 450 GlnThrSerLeuLeuProGlyGlnThrLeuIleTyrThrProArgGlyGlu---LeuLys 468
Db 3217 GAAATCGATGCTGAACACTCCCTACTTTAGAACTAAGTCCCAAGGGATAGTACGT 3276
Qy 469 GlnValAsnAsnGlyProGlyAsnGluTyr---TyrArgTyrAspSerAsnGly----- 485
Db 3277 CAATTTCAAGGC-----TGGCACTATCAGTATGCTATGCTATGCTATGCTATGCT 3321
Qy 486 ---MetArgGlnLeuLysValSerGluGlnProThrGlnAsnThrThrGlnGlnArg 504
Db 3322 ATTGCTCGCGTTACCGTAACCAATCATCAAAACCTATGCTTATGATGCTGATAATCGT 3381
Qy 505 ValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAlaThrThrThrGlu 524
Db 3382 CTGTTATCGCTCATATCAAGCATATAAAGCTCAATACACCTACGATGCCCTAGGCCGT 3441
Qy 525 GluLeuHis---ValIleThrLeuGlyGluAlaGlyArgAlaGlnValArgValLeuHis 543
Db 3442 CGTATTCACAAACCGTTGAAACCCGAGAAAGTGGCAAGTTAAACGACAGAGCCAT 3501
Qy 544 -----TrpGluSerGlyLys-----ProGluAspValAsnAsnAsnGlnLeuArg 558
Db 3502 TTTATTTGGCAAGGGCTACGGTTACTGCAAGAGCAGGATATCAACACCGGTAAACACCA 3561
Qy 559 ---TyrSerTyrAspAsnLeu----- 564
Db 3562 ACTTATTTGCTACGAAGAGCAGCGAGTATACCCCTCTTGGCCGTTATCGTGAACAAATCC 3621
Qy 565 -----IleGlySerSerGlnLeuGluLeuAsp 573
Db 3622 AGCGTTTTCATTATTACTGGCACCACTGTGATATTAAACAGCGCCCACTTGAAGTACC 3681
Qy 574 Asn---GlnGlyGlnIleIleSerGluGluTyrTyrProPheGly----- 588
Db 3682 AATGCACAAGCAATACGATATGTCAGGGAAATATGAACGCTTTGGCTTTGTTTCGCAGT 3741
Qy 589 ---GlyThrAlaLeuTrpAlaAlaAsnSerGlnThrGluAlaSerTyr---LysThrIle 606
Db 3742 AGCCCTCTGAGTTTATTCAGTCCCTGAACGCTGTGATGGCTCTTTGAGCAAAATCTA 3801
Qy 607 ArgTyrSerGlyLysGluArgAsp---AlaThrGlyLeuTyrTyrTyrGlyTyrArgTyr 625
Db 3802 CGTATGCCGCAATATTTTGAATGAACCGGATACATTTTATACCTTTAGATTC 3861
Qy 626 TyrGlnProTrpAlaGlyArgTyrProLeuSerAlaAspProAlaGlyThrIleAspGlyLeu 645
Db 3862 TACGACCCACAGATAGCCCGTTTATCATCGCTGACCAATTTGGATTATTGGGTGGGATT 3921
Qy 646 AsnLeuTyrArgMetValArgAsnAsnProValSerLeuGlnAspGluAsnGlyLeuAla 665
Db 3922 AATCTGTATCAATATGCG---CCGAATCCGTTGGATGGATTGATCCGCGGGGTTGTCA 3978
Qy 666 ProGluLys 668
Db 3979 TCTCAGGAA 3987
RESULT 9
US-09-492-709A-180


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; Sequence 180, Application US/09492709A
; Patent No. 6720139
; GENERAL INFORMATION:
; APPLICANT: Zyskind, Judith
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Trawick, John
; APPLICANT: Forevth, R. Allyn
; APPLICANT: Froelich, Jamie M.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
; TITLE OF INVENTION: ESCHERICHIA COLI
; FILE REFERENCE: ELITRA.001A
; CURRENT APPLICATION NUMBER: US/09/492,709A
; CURRENT FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 485
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 180
; LENGTH: 4281
; TYPE: DNA
; ORGANISM: E. Coli
US-09-492-709A-180

Alignment Scores:
Pred. No.: 3,91e-17 Length: 4281
Score: 273.50 Matches: 220
Percent Similarity: 30.66% Conservative: 136
Best Local Similarity: 18.95% Mismatches: 352
Query Match: 5.77% Indels: 453
DB: 3 Gaps: 52

US-10-647-956A-6 (1-915) x US-09-492-709A-180 (1-4281)
Qy 3 SerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsnArgLys 22
Db 1141 AGTACCGCTATCTTTATGAGCAG-----GACCGATACCGTACCAGACAGC----- 1188
Qy 23 LeuAsnValArgThrLeuGluTyrLeuArgThrGlnAla----- 35
Db 1189 CTGAACCGCGCT-----GAGGTGCTGCATACAGAGGCGGGCGCGGTGAAACGCGGTG 1242
Qy 36 -----AspGluAsnSerAspGluLeuIleThrPheTyrGluPheAsnIleProGlyPhe 53
Db 1243 GTGAAAAAAGAACTGGCGGAGCCGACGCGTCACGCGCAGCGGTATGACGCGGAGGAAGG 1302
Qy 54 GlnValLysSerThrAspProArgLysAsnLysAsnGlnSerGlyProAsnPheIleArg 73
Db 1303 CTCACGGCGCAGACGCGCGCGCGGACGCGGAGCAGAGTACCGTCTGAATGTGGTG--- 1359
Qy 74 ValPheAsnLeuAlaGlyGlnValLeuArgGluSerValAspAlaGlyArgThrIle 93
Db 1360 -----TCGGCGATATACCGGACATCACACACCGGACCGGCGGAGACGAAA 1407
Qy 94 ThrLeuAsnAspIleGluSerArgProValLeuIleAsnAlaThrGlyValArgGln 113
Db 1408 TTTTACTATAACGACGGAACAGCTGACGCGGTGGTGTCCCGCGACGCGCTGGAGAGC 1467
Qy 114 AsnHisArgTyrGluAspAsnThrLeuProGlyArgGluLeuAlaIleThrGluGlnVal 133
Db 1468 CGCGGGAAATATGATGAA-----CCGGGCGAGGCTG-----GTATCGGAGACATCG 1512
Qy 134 GlnAlaGlyGluLys----- 138
Db 1513 CGCAGCGGGAGACAGTACCTACCGCTACGATCAGCGGCACAGTACGAGTTACCGGCGACG 1572
Qy 139 -----ThrThrGluArgLeuIleTrpAla----- 146
Db 1573 ACAACGATGCGAGCGGACGACCGCGCAGATACCTGGAGCGCTACGCGGCGGTGCTG 1632
Qy 147 -----GlyAsnThrProGlnGluLysAspTyrAsnLeuAlaGlyGlnCys 161
Db 1633 GCCTTACCGACTGCTCGGGCTACACAGCCCGTTATGAATACGACCGCTTCGCGCCAGATG 1692
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Qy 162 Val-----ArgHisTyrAspThrAlaGlyLeu 170
Db 1693 ACGCGGTCCACCGCGAGGAAGCATCAGCTTTTACCGCGCTATGACAAACCGTGGC--- 1749
Qy 171 ThrGlnLeuAsnSerLeuSerLeuAla----- 179
Db 1750 ---CGGTTAACCTCGGTGAAGACGACAGGGCGGTGAAACGGGTATGATACACACGCC 1806
Qy 179 ----- 179
Db 1807 GCAGGCGACTGACTCGCTTATCACCCCGGACGCAACCGGAGCGAGACACAGTACGAT 1866
Qy 180 -----GlyValValLeuSerGlnSerGlnLeuLeuThrAspAsnGlnAspAlaAsp 197
Db 1867 GCGTGGGAAAGCGGTGACACACGACGAGGCGGCTGACGCGCATGTGGAGTACGAT 1926
Qy 198 TprThrGlyGluAspGlnSerLeuTprGlnGlnLysLeuSerAspValTyrIleThr 217
Db 1927 GCTGCCGAGCTGTCTATCAGCTGACCAACGAGACGCGGACGACAGCGTCTTC----- 1980
Qy 218 GlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGlyAsnIle 237
Db 1981 -----AGTTACGATCGCTGGACCGCTGGTACACGACGCGGCGCTTTGACGCGGACG 2034
Qy 238 GlnArgLeuAlaTyrAspValAlaGlyGlnLeuLysGlySer----- 251
Db 2035 CAACGTTATATTATGACCTGACCGGAAACTCACACAGAGTGGAGTGGAGGACTTGTG 2094
Qy 251 ----- 251
Db 2095 ATCCTCTGGTACTACGATGAATCGGACCGTATCATCTACCGCAGCGTGAACGCGGAACCG 2154
Qy 252 -----TrpLeuThr----- 254
Db 2155 GCAGACGAGTGGCAGTATGATGCCACCGCTGCTGCACAGACATCAGCCACCTGAGCGAA 2214
Qy 255 -----LeuLysGlyGlnAla 259
Db 2215 GGCCACCGTGTTCCTCCACTATGCTATGACGATAAAGCGCGCTGACCGCGAATGC 2274
Qy 260 GluGlnVal----- 262
Db 2275 CAGACGCTGGAGAACCCGAGAGCGGGGAACTCTCTGTGGCAGCATGAGACAAACACGCA 2334
Qy 262 ----- 262
Db 2335 TACAACGACGAGGGGTGGCAAAACCGCTCACGCCGACAGCCTGCCCGGTGGAGTGG 2394
Qy 262 ----- 262
Db 2395 CTGACGTATGGCAGCGTTACCTGGCGGAATGAAGCTGGCGGAGCGCGCTGGTTCGAG 2454
Qy 263 -----IleLysSerLeu----- 267
Db 2455 TATACCGGGACAGGTGTCACCGTACAGCGTGGCAGCTTCGGCAGCATGGCAGGAGT 2514
Qy 268 -----ThrTyrSerAlaAlaGlyGlnLysLeuArgGluGlu 279
Db 2515 AATGCCGCATACGAACCTGACACACATACACCCCGCGAGGCCAG---TTACAGAGCCAG 2571
Qy 280 HisGlyAsnGlyIleVal----- 285
Db 2572 CACCTGAACAGCGCTGTATATGACTACGGTGGAGTGAGTGAACACGCGACCTGGTG 2631
Qy 286 -----ThrGluTyrSerTyrGluProGluThrGlnArgLeu 297
Db 2632 CGCATCAGCGGCCCGCAGACGCGGGGAATACGGTACAGC---GCCACGGCAGGCTG 2688
Qy 298 IleGlyIleThrThrArgArgProSerAspAlaLysValLeuGlnAspLeuArgTyrGln 317
Db 2689 GAGAGTGTGGCAACCTTCGCACACGAC-----CTGGACATCCGATCCCG 2733
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QY 318 Tyr-----AspProValGlyAsnValIle-----AsnIleArgAsnAspAlaGlu 332
Db 2734 TATGCCACGACCGCGCGGACACCGCTCCGCGACCGGAGCTGCACCGCGACAGTACA 2793
QY 333 AlaThrArgPheTrpArgAsnGlnLysValAlaProGluAsnSerTyrThrTyrAspSer 352
Db 2794 CTCACA---GTGTGGCGGATACCGCATCCGCGAGGATGCGCACTATGTCTAC----- 2844
QY 353 LeuTyrGlnLeuIleSerAlaThrGlyArgGluMetAlaAsnIleGlyGlnGlnAsnAsn 372
Db 2845 -----CGCCACGATGAATACCGCAGGCTGCAGGAGACGAGACGCGAC 2883
QY 373 GlnLeuProSerProAlaLeuProSerAspAsnAsnThrTyrThrAsnTyrThrArgSer 392
Db 2884 CGATCCCGCGGGGTGTATACCGACGAGCAGCAGCGG-----ACCCACCAC 2931
QY 393 TyrSerTyrAspHisSerGlyAsnLeu-----ThrGlnIleArgHisSerSerPro 409
Db 2932 TACCACCTACGACGACCGACCGCTGTGTCTTCTACACGCGGATACAGCATGGCGAGCCA 2991
QY 410 AlaThrGlnAsnAsnTyr-----ThrValAlaIleThrLeuSerAsnArgSer----- 415
Db 2992 CTGCTCAGAGCGCTACTCTACACCGCTGGACCGCGCAATGGCAAAACGGTCTGG 3051
QY 416 -----ThrValAlaIleThrLeuSerAsnArgSer----- 425
Db 3052 CGCGCGGAGGTGACCTGACGCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3111
QY 426 -----AsnArgGlyValLeuSerThrLeuThrThrAspProAsnGlnValAspThr 442
Db 3112 TATGGCTGGGACGAGACGCTGACGACGCTGACGACGCTGACACACACGATCCACAGC 3171
QY 443 LeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIleTrpThr 462
Db 3172 GTATACGAGCGGGAAGCTTC---ACGCGCTCATCCGGTCCGAGACA----- 3216
QY 463 ProArgGlyGluLeuLysGlnValAsnAsnGlyProGlyAsnGluTrpTyrArgTyrAsp 482
Db 3216 ----- 3216
QY 483 SerAsnGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAsnThrThrGlnGln 502
Db 3217 GAGAACCGCGAGCGGAA---AAGCGCGAGCGCGGCGCTGCGGACGAGCGCTCCACAGC 3273
QY 503 Gln-----ArgValIleTyrLeuProGlyLeuGluLeuLeuArgThrThrGln 517
Db 3274 GAAGGAGTGAGAACCGCCACGCGCTGTGTCTCCCGCTGAACCTGGTGGCGCTCTCGAC 3333
QY 518 SerAsnAlaThrThrThrGluGluHisValIleThrLeuGlyGluAlaGlyArgAla 537
Db 3334 -----AGGCTGGAGGAAGAAATCGGGCAGCAGCGGTGACAGTGAAGCCGGCG 3384
QY 538 GlnValArgValLeuHisTrp-----GluSerGlyLysProGluAspValAsnAsn 555
Db 3385 -----TGCTTGGCAGCGCGGCTGACGCGGAGCAACTGGCCAGA 3426
QY 556 GlnLeuArgTyrSerTyrAspAsnLeuIleGlySerSerGlnLeuGluLeuAspAsnGln 575
Db 3427 CAGGTGGAGCGGAATACACACCGCGCGAAAGCTCATCTTTATCATCTGCGACACCGG 3486
QY 576 Gly-----GlnIleIleSerGluGluGluTyrTyrProPheGlyGlyThrAlaLeu 592
Db 3487 GGACTCGCGCTGGCGCTTATCAGCGAAGAC-----GGCAATACGGCG 3528
QY 593 TrpAlaAla-----AsnSerGlnThrGluAlaSer----- 602
Db 3529 TGGAGCGGAATATGATGAATGGGCAACACGCTTAATGAGGAGAACCCCGCATCATGTG 3588
QY 603 TyrLysThrIleArgTyrSerGlyLysGluArgAsp---AlaThrGlyLeuTyrTyr 621
Db 3589 TATCAGCGGTACCGCTCTGCCAGGCGCAGCATGATGAGGAATCAGGGCTGTACTATAAC 3648
QY 622 GlyTyrArgTyrTyrGlnProTrpAlaGlyArgTrpLeuSerAlaAspProAlaGlyThr 641
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Db 3649 CGTCACCGCTACTACGATCCGTTGAGGGCGGTATATTACTCAGACCGCATGGGTTG 3708
QY 642 IleAspGlyLeuAsnLeuTyrArgMetValArgAsnAsnProValSerLeuGlnAspGlu 661
Db 3709 AAAGGGGATGGAATTTATATCAGTATCCTTTA---AATCCACTACAACAATTGACCT 3765
QY 662 AsnGlyLeu----- 664
Db 3766 ATGGGATTTATGCAGACTTGGGATGATGCCAGATCTGGAGCATGTACGGGGGAGTTGT 3825
QY 665 -----AlaProGluLysGlyLysTyrThrLysGluValAsnPhe 677
Db 3826 GGTGTTCTTTTACGTATAATAGGACCAAGTAAATTTGATAGTACTGCAGATGCT---GCG 3882
QY 678 PheAspGluLeuLysPheLysLeuAlaLysSerSerHisValValLysTrpAsnGlu 697
Db 3883 TTAGATGCTTTGAAA----- 3897
QY 698 LysGluSerSerTyrThrLysAsnLysSerLeuLysValValArgValGlyAspSerAsp 717
Db 3898 -----GAAACGCAGATAGATCTCTA-----TGTAAATGATATGGAA 3933
QY 718 ProSerGlyTyrLeuSerHisGluGluLeuLysGlyLysGlyLysSerGlnIle 737
Db 3934 TACTCTGTTATGCTCTGTAAGATATACTAATGGAAATATTTTGCATCTTAAGCGAGAACT 3993
QY 738 IleTyrSerArgLeuGluAsnSerSerLeuSerGluLysSerLysThrAsnLeuSer 757
Db 3994 GATAATTTAAGA---AAGGAGTCATATCTCTGAAAAGAAATGTCCCACAGTACAGAT 4050
QY 758 LeuGlySerGluIleSerGlyTyrMetAlaArgThrIleGlnAspThrIleSerGluTyr 777
Db 4051 AGAGTTGCTGCTTATCATCTACGCTGCGAGATAGTCATGCGCATTTGTTGATGATTT 4110
QY 778 -----AlaGluGluHisLysTyrArgSer-----AsnHisProAspPheTyr 791
Db 4111 TTTTCAAGTAGCGATAAAATCTTGAAGAAGTAAAGATAATAATCTTGAAGCATTTTAT 4170
QY 792 SerGluThrAsp-----PhePheAlaLeuMetAspLysSerGlu----- 804
Db 4171 CTGCGCAACACCTGATGCGACGATTTGAGCGCTTAAATAAAGAGAGAATATATTTTATC 4230
QY 805 LysAsnAspTyrSerGlyGluArgLysIleTyrAlaAlaMetGluValLysValTyrHis 824
Db 4231 AGAAATAGTCTCCCGGATTGAGTTGATGATGATACCG-----TATCAT 4275
QY 825 Asp 825
Db 4276 GAT 4278
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RESULT 10

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US-09-453-702B-11
; Sequence 11, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; Burland, Valerie
; Perna, Nicole T.
; Plunkett, Guy
; Welch, Rod
; TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 31960
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-453-702B-11

Alignment Scores:
Pred. No.: 1,57e-14 Length: 31960
Score: 262.00 Matches: 184
Percent Similarity: 29.83% Conservative: 97
Best Local Similarity: 19.53% Mismatches: 287
Query Match: 5.53% Indels: 374
DB: 3 Gaps: 41

US-10-647-956A-6 (1-915) x US-09-453-702B-11 (1-31960)

QY 23 LeuAsnValArgThrLeuGluTyrLeu-----ArgThrGlnAla 35
DB 26734 CTGAACCGCGGAGGTGTGTACACGAGCGCGGTGGCTGAAACCTGTGTGAAG 26793
QY 36 AspGluAsnSerAspGluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnVal 55
DB 26794 AAGAAATCATCGGACGGGAGCATCACCGCAGCGAGTATGATGAGCGGGAGGCTGAAG 26853
QY 56 LysSerThrAspProArgLysAsnLysAsnGlnSerGlyProAsnPheIleArgValPhe 75
DB 26854 GCACACGCGATCGCGCGGACCGCGCGGAGTACAGC-----CTG 26895
QY 76 AsnLeuAlaGlyGlnValLeuArgGluSerValAspAlaGlyArgThrIleThrLeu 95
DB 26896 CATATGCGTGGGTGCGGTGACAGCGGTGACCGGGCGGACGAGGACGGTGGCTAT 26955
QY 96 AsnAspIleGluSerArgProValLeuIleIleAsn---AlaThrGlyValArgGlnAsn 114
DB 26956 GGCTATAACAGCCAGCGCGGAGGTGACGTGAGTACGTACCGGACCGGCTGCGCAGCAGC 27015
QY 115 HisArgTyrGluAspAsnThrLeuProGlyArgAlaIleThrLeuGluGln----- 132
DB 27016 CGGGAGTATGATGAGAAG-----GGNAGCTGGCGCGGAGACCTCGCGCAGCGGA 27066
QY 133 -----ValGlnAla 135
DB 27067 GAGACGACGCGGTACAGTATGATGATACCGCGGAGTGAGTGGCGACAGGATACAGGAC 27126
QY 136 GlyGluLysThrThrGluArgLeuIleThrAlaGly----- 147
DB 27127 GCGACGGCGAGTACAAACAGATGGCATGGACCGGTTACGGTCAGCTGCTGACCTTTACG 27186
QY 148 -----AsnThrProGlnGluLysAsp----- 154
DB 27187 GACTGCTCGGGGTACAGCAGCGCGGTATGATGATGATGATGATGATGATGATGATGATG 27246
QY 155 -----TyrAsnLeuAlaGlyGlnCysValArg 163

DB 27247 CACCGGGAAGAAGGCATCAGCACTTACAGAGGTATAACCCGCGTGGCCAACTGGTCAGT 27306
QY 164 HisTyrAspThrAlaGlyLeuThrGlnLeuAsnSerLeuSerLeuAla----- 179
DB 27307 CAGAAGATGCGCAGGGGCGTGAACCCCGTTATGAGTACAGCGCCGCGGACCTCACC 27366
QY 180 -----GlyValVal 182
DB 27367 GCTATCGTTCCCGGACGCGCAGCGCAGTACAGTATGATGATGATGATGATGATGATG 27426
QY 183 LeuSerGlnSerGlnGlnLeuLeuThrAspAsnGlnAspAlaAspTrpThrGlyGluAsp 202
DB 27427 GTCAGCACCCAGCAGGGCGGTCTGACGCGCAGCATGGGTATGACGCTCGCGGCGCATC 27486
QY 203 GlnSerLeuTrpGlnGlnLysLeuSerSerAspValTyrIleThrGlnSerAsnThrAsp 222
DB 27487 ACCGTGCTGACCAACGAGAACGCGCAGCAGTCCACGTTG-----CGGTATGAC 27534
QY 223 AlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGlyAsnIleGlnArgLeuAlaTyr 242
DB 27535 CCGGTGGACAGGCTGACTGAACAGCGCGGTGTTGATGGCGGACGACGACGTTACCACTAT 27594
QY 243 AspValAlaGlyGlnLysGlySer----- 251
DB 27595 GACCTGACCGGAAACTCACGAGAGTGAAGACGAGGGGCTTGTACCTCTCGGCATAC 27654
QY 251 ----- 251
DB 27655 GATGCGTCGACCGCATCAGCACCGGACGGTGAACCGGACCCGCGCAGAGCAGTGGCAG 27714
QY 252 -----TrpLeuThr----- 254
DB 27715 TATGATGACGACGGGTGGCTTAACCACTCAGCATACCACTGAGGCGCACCGGGTGTG 27774
QY 255 -----LeuLysGlyGlnAlaGluGlnVal----- 262
DB 27775 GTCCACTACGGCTATGACGATAAGSCCGCTGACGGGTGAACGGCAGACGGTGGAGAAC 27834
QY 262 ----- 262
DB 27835 CCGGACACGGGGAGNATGCTGTGGAGCATGAGACGGGGCAGCGCTACAGCGAACAGGGG 27894
QY 263 -----IleIleLysSerLeuThrTyrSerAla 271
DB 27895 CTGGGACCCGTCAGGACCGGACGGTCTGCGCGGTAGAGTGGCTGACGTATGGCAGC 27954
QY 272 -----AlaGlyGlnLys----- 275
DB 27955 GGTATCTTTGCGGGATGAAGCTGGGCGGAGCCCACTGTCGAGTACATGCGGAGCCGG 28014
QY 275 ----- 275
DB 28015 CTGACCGTGAGACGCGCCGCGAGCTTCGCGGGGAGGATATGAACTTGCACCGCGCTGG 28074
QY 276 -----LeuArgGluGluHis----- 280
DB 28075 AATACCAGCGGCAGCTCCGGAGCAGGCACCTTCCGCGAGCTTGACCGTGACTAC 28134
QY 281 -----GlyAsnGlyIleVal-----ThrGluTyr 288
DB 28135 GACTGGAACGACACGAGCAGCTAATCCGCATCAGCGCGCGCAGGAGAGCCGCGAGTAC 28194
QY 289 SerTyrGluProGluThrGlnArgLeuIleGlyIleThrThrArgArgProSerAspAla 308
DB 28195 CGTTACAGT---GACACGGGAAGGCTGACGGCGCTCCACACC-----ACGGCAGCG 28242
QY 309 LysValLeuGlnAspLeuArgTyrGlnTyrAspProValGlyAsnValIle----- 325
DB 28243 AACCTGGATATCGATATCCGTATGCAACGGACCCCGCAGGAAACCGGCTCGCGGACCG 28302
QY 326 AsnIleArgAsnAspAlaGluAlaThrArgPheTyrArgAsnGlnLysValAlaProGlu 345

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Db 28303 GAATGTCACCGGACAGCACCTCACGGCA---TGGCCGGATAACCCGATCGCGAAGAT 28359
Qy 346 AsnSerTyrThrTyrAspSerLeuTyrGlnLeuIleSerAlaThrGlyArgGluMetAla 365
Db 28360 GCGCACTATGCTAC-----CGCTACGAT-----GAATACGGC 28392
Qy 366 AsnIleGlyGlnGlnAsnGlnLeuProSerProAlaLeuProSerAspAsnAsnThr 385
Db 28393 AGCTGGCGGAGAGACGGACCGGATCCCGAAGGGGTATC-----CGGATG 28440
Qy 386 TyrThrAsnTyrThrArgSerTyrSerTyrAspHisSerGlyAsnLeu-----Thr 402
Db 28441 CACGACGAGCGACCCACCACTACTACTAGCACGACGACCGCTGGTGTCCACACG 28500
Qy 403 GlnIleArgHisSerSerProAlaThrGlnAsnAsnTyrThrValAlaIleThrLeuSer 422
Db 28501 CGGATACAGCAGCGCAACCAAGTGGAGCGGTAC----- 28539
Qy 423 AsnArgSerAsnArgGlyValLeuSerThrLeuThrThrAspProAsnGlnValAspThr 442
Db 28539 ----- 28539
Qy 443 LeuPheAspAlaGlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIleTyrThr 462
Db 28540 CTCTATGACCGCTGGCGCGCGACGGGA-----AAACGGGTGTGGCG 28584
Qy 463 ProArgGlyGluLeu-----LysGlnValAsnAsnGlyProGlyAsnGluTyrTyr 479
Db 28585 CGGAGCGTGACCTGACCGGGTGGATGCTGCTGCGCTAAACCGGAGGACCTGTATC 28644
Qy 480 ArgTyrAspSerAsnGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAsnThr 499
Db 28645 GGTGGGACGGTGACAGCTG-----ACCACGTGTACG 28677
Qy 500 ThrGlnGlnGlnArgVal-----IleTyrLeuProGly----- 510
Db 28678 ACCCAACAGACAAGATACAGACGGTATACAGCGCGGAAGCTTCACGCGCTCCTCGAGA 28737
Qy 511 -----LeuGluLeuArg 514
Db 28738 ATCGAAACAGAGAAATGTTGAACAGCGGAAGCGCGCACCGTACCGTGGCGGAGGTGTG 28797
Qy 515 ThrThrGlnSerAsnAlaThrThrGluGlnLeuHisValIleThrLeuGly----- 532
Db 28798 CAGGAGACACGGGTGTGACGCTACCGCGGAGCTGGCGGTGAG-----CTGGGAGAGCTG 28854
Qy 533 -----GluAlaGlyArgAlaGlnValArgValLeuHisTyr-----GluSer 546
Db 28855 GAGCGGAGCTGCGCGAGGCGAGCTGAGTGAAGAAAGCCAGCAGCTGCTGCGCAGTGC 28914
Qy 547 GlyLysProGluAspValAsnAsnGlnLeuArgTyrSerTyrAspAsnLeuIleGly 566
Db 28915 GGGCTGACGGCGGAGCAGATGCGCGCAGCTGGAGCGGAATAC-----ATCCCG 28965
Qy 567 SerSerGlnLeuGluLeu-----AspAsnGlnGly-----GlnIleIleSer 580
Db 28966 GAGAGGAAACTTCATCTTTACCATCTGCAGCACCGCGGAGCTGCGCTGGCGCTCATCAGC 29025
Qy 581 GluGlu-----GluTyrTyrProPheGlyThrAlaLeuTyr 593
Db 29026 CCGGAAGGGGAAACCGCGTGGCAGGGGAGTATGACGAGTGGGGAAACCTGCTG----- 29079
Qy 594 AlaAlaAsnSerGlnThrGluAlaSerTyr-----LysThrIleArgTyrSerGlyLys 611
Db 29080 -----GGCGAAACCGCGCGCAGCACCTTCAACACAGTCACTCCGCTCCCGGGCGAG 29130
Qy 612 GluArgAsp-----AlaThrGlyLeuTyrTyrGlyTyrArgTyrTyrGlnProTyrAla 630
Db 29131 CAGTATGATGAGGAGTCGGGGCTGTACTACACCGCAACCGGTACTATGATCCGTTGCAG 29190
Qy 631 GlyArgTyrLeuSerAlaAspProAlaGlyThrIleAspGlyLeuAsnLeuTyrArgMet 650
Db 29191 GGGAGATATATACCCAGGACCCGATAGGGCTGGAGGGGGGATGGAACTGTATCAGTAC 29250
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Qy 651 ValArgAsnAsnProValSerLeuGlnAspGluAsnGlyLeuAlaProGluLysGlyLys 670
Db 29251 CCACCTC---AATCCTATTGAACATAGATCCGTTGGGGTTAGCACTTGATTGAATTAT 29307
Qy 671 TyrThr 672
Db 29308 TATTCT 29313
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RESULT 11

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US-10-114-170-11
; Sequence 11, Application US/10114170
; Patent No. 6855814
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; Burland, Nicole T.
; Plunkett, Guy
; Welch, Rod
; TITLE OF INVENTION: No. 6855814e1 Sequences of E. coli O157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/114,170
; FILING DATE: 01-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/453,702
; FILING DATE: 03-DEC-1999
; APPLICATION NUMBER: 60/110,955
; FILING DATE: 04-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.95017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31960
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-114-170-11
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Alignment Scores:
Pred. No.: 1.57e-14 Length: 31960
Score: 262.00 Matches: 184
Percent Similarity: 29.83% Conservative: 97
Best Local Similarity: 19.53% Mismatches: 287
Query Match: 5.53% Indels: 374
DB: 3 Gaps: 41
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US-10-647-956A-6 (1-915) x US-10-114-170-11 (1-31960)
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Qy 23 LeuAsnValArgThrLeuGluTyrLeu-----ArgThrGlnAla 35
Db 26734 CTGAACCGCGGGAGGTGTGTACACGAGGCGGCTGGCTGAAG 26793
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Db 28738 ATCGAAACAGAGAATGCTGAACAGCGGAGCGCGCACCGTAGCTGCGGAGGTGTG 28797
Qy 515 ThrThrGlnSerAsnAlaThrThrThrGluGluLeuHisValIleThrLeuGly----- 532
Db 28798 CAGGAGCACCGGTGTGACGCTACCGCGCGAGCTGCGGTGATG---CTGGGAAGCGTG 28854
Qy 533 -----GluAlaGlyArgAlaGlnValArgValLeuHisTrp-----GluSer 546
Db 28855 GAGCGGAGCTGCGGAGGAGCGGTGAGTGAAGAAAGCAGCAGTGGCTGGCGAGTGC 28914
Qy 547 GlyLysProGluAspValAsnAsnGlnLeuArgTyrSerTyrAspAsnLeuIleGly 566
Db 28915 GGGCTGACGGCGGAGCAGATGGCGCGCAGCTGGAGCGGAATAC-----ATCCCG 28965
Qy 567 SerSerGlnLeuGluLeu-----AspAsnGlnGly-----GlnIleIleSer 580
Db 28966 GAGAGGAAACTTCATCTTACCAGTGCAGCACCGGGGAGCTGCGGTGGCGCTCATCAGC 29025
Qy 581 GluGlu-----GluTyrTyrProPheGlyGlyThrAlaLeuTrp 593
Db 29026 CCGGAGGGGAAACCGGCTGGCAGGGGAGTATGACAGTGGGGAACCTGCTG----- 29079
Qy 594 AlaAlaAsnSerGlnThrGluAlaSerTyr-----LysThrIleArgTyrSerGlyLys 611
Db 29080 -----GGCGAAACACGCGCAGCAGCACCTTCAACAGTCACTCCGTCTGCCGGGCGAG 29130
Qy 612 GluArgAsp---AlaThrGlyLeuTyrTyrTyrGlyTyrArgTyrTyrGlnProTrpAla 630
Db 29131 CAGTATGATGAGGAGTGGGGCTGTACTACAAACCGCAACCGGTACTATGATCGGTTCAG 29190
Qy 631 GlyArgTrpLeuSerAlaAspProAlaGlyThrIleAspGlyLeuAsnLeuTyrArgMet 650
Db 29191 GGGGATATATCACCCAGGACCCGATAGGGCTGAGGGGGGATGGAACTGTATCAGTAC 29250
Qy 651 ValArgAsnAsnProValSerLeuGlnAspGluAsnGlyLeuAlaProGluLysGlyLys 670
Db 29251 CCACTC---AATCCTATTGAACATATAGATCCGTTGGGTTAGCACTTGATTTGAATTAT 29307
Qy 671 TyrThr 672
Db 29308 TATTCT 29313

RESULT 12

US-09-453-702B-226
Sequence 226, Application US/09453702B
Patent No. 6365723

GENERAL INFORMATION:

APPLICANT: Blattner, Frederick R.
Burland, Valerie
Perna, Nicole T.
Plunkett, Guy
Welch, Rod

TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Quarles & Brady

STREET: 1 South Pinckney Street

CITY: Madison

STATE: WI

ZIP: 53701-2113

COUNTRY: US

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 8.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/453,702B

FILING DATE: 03-Dec-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/110,955

FILING DATE: 04-DEC-1998

ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 226:
SEQUENCE CHARACTERISTICS:
LENGTH: 5519
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 226:
US-09-453-702B-226

Alignment Scores:

Pred. No.: 3.7e-15 Length: 5519
Score: 256.00 Matches: 191
Percent Similarity: 33.98% Conservative: 126
Best Local Similarity: 20.47% Mismatches: 347
Query Match: 5.40% Indels: 270
DB: 3 Gaps: 45

US-10-647-956A-6 (1-915) x US-09-453-702B-226 (1-5519)

Qy 1 MetSerSerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn 20
Db 1809 CTGAGTCAGTACGCG---GCATACGACGACGCGGTGAGCACTTAATTCGCGTGAAGAC--- 1862
Qy 21 ArgLysLeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAsnSerAsp 40
Db 1863 -----ACGCGGGCCATGAA----- 1877
Qy 41 GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro 60
Db 1878 -----ACGCGGTATGAATACAAACGCGCGGTGACCTGACCACTGCGTTCATTCGCCCG 1928
Qy 61 ArgLysAsnLysAsn----- 66
Db 1929 GACGCGCAGCAAGAAACGGGACACAGTACGATCGGTGGGAAAGCCATCTGTACACGCGAG 1988
Qy 67 SerGlyProAsnPheIleArgValPheAsnLeuAlaGlyGlnValLeuArgGluGluser 86
Db 1989 GCGGTCTGACGCGCAGTATGGAAATGATGCTGCGGACGGGTATCCCGCTGACCACT 2048
Qy 87 ValAspAlaGlyArgThrIleThrLeuAsnAspIleGluSerArgProValLeuIleIle 106
Db 2049 GAAACGCGGACACACCACTTCCTGTTACGATGTACTCGACCGG-----CTGATA 2099
Qy 107 AsnAlaThrGlyValArgGlnAsnHisArgTyrGluAspAsnThrLeuProGlyArgLeu 126
Db 2100 CAGGAAACCGGCTTTCACGCGCGCACACAGCGTATATCACCACTGACCGCGCAACTT 2159
Qy 127 LeuAlaIleThrGluGln-----ValGlnAlaGlyGluLysThr 139
Db 2160 ATCCGACGAGGATGAGGGGTGTCACCACTGGCACTATACGAGGACGACCGGCTC 2219
Qy 140 ThrGluArgLeuIleTrpAlaGlyAsnThrProGlnGluLysAspTyrAsnLeuAlaGly 159
Db 2220 ACGCAGCGCACCGTG---AAGGGTGAACCGCAGAGCGCTGGCAGTATGACGAACGCGGC 2276
Qy 160 GlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAsnSerLeuSerLeuAla 179
Db 2277 -----TGGCTGCACACATCATGCCATATATCAGCGAAGGG 2309
Qy 180 GlyValVal-----LeuSerGlnSerGlnGlnLeuLeuThrAspAsnGln 194
Db 2310 CACGGGTGACGCTGATACGGGTATGATGAAGAGCGCGGTGACCGGTGACGCTCAG 2369
Qy 195 AspAlaAspTrpThrGlyGluAspGlnSerLeuTrpGlnGlnLysLeuSerSerAspVal 214
Db -----

Db 2370 ACGTGCATCACCGCAGACGGAAGCACTGCTCTGGCAGCATGAG----- 2414
Qy 215 TyrIleThrGlnSerAsnThrAspAlaThrGly---AlaLeuLeuThrGlnThrAspAla 233
Db 2415 -----ACCACACAGCTTACAAACGCGCAGCGCTGGCGAACCGCTGTATACCGGACAGC 2468
Qy 234 LysGlyAsnIleGlnArgLeuAlaTyrAsp-----ValAlaGlyGlnLeuLysGly 250
Db 2469 CTCGCCCGCGTGAATGGCTGACCTATGGCAGCGCTGGCTGGCAGCATGAAGCTCGGC 2528
Qy 251 SerTrpLeuThrLeuLysGlyGlnAlaGluGlnValIleIleLysSerLeu----- 267
Db 2529 GACACACCGCTGTGGATTTCACCGCGGACCGCTGCACCGGAAACGCTGCCAGATTC 2588
Qy 268 -----ThrTyrSerAlaAlaGlyGlnLysLeuArgGluGluHis 280
Db 2589 GCGCGTTATGAACCTACCAACCGCTTATACCCCTGCCGGGAG--TTACAGAGCCAGCAC 2645
Qy 281 GlyAsnGlyIle----- 284
Db 2646 CTGAACAGCCTGCAGTATGACCGCATTTACCTGGAAACGACACGCGCAACTCATCCGC 2705
Qy 285 -----ValThrGluTyrSerTyrGluProGluThrGlnArgLeuIle 298
Db 2706 ATCAGCAGCCCGCCAGACCCCGAGTTACAGCTACAGC---GACTCCGGCAGGCTGACC 2762
Qy 299 GlyIle---ThrThrArgArgProSerAspAlaLysValLeuGlnAspLeuArgTyrGln 317
Db 2763 GCGGTTACACACCCAGCAGCATCTGGATATCCGCATC-----CCGTATGCC 2810
Qy 318 TyrAspProValGlyAsnValIle-----AsnIleArgAsnAspAlaGluAlaThr 334
Db 2811 ACGGACCCCGCAGTAACCCCTGCCCGACCCGAGCTGCACCGGACAGCACCCCTCAGC 2870
Qy 335 ArgPheTrpArgGlnLysValAlaProGluAsnSerTyrThrTyrAspSerLeuTyr 354
Db 2871 ---ATGTGGCGGATACCGCTTCGCGCTGCGCGCACCTATCTTTAC----- 2915
Qy 355 GlnLeuIleSerAlaThrGlyArgGluMetAlaAsnIleGlyGlnGlnAsnAsnGlnLeu 374
Db 2916 ---CGGTATGACCGTCAGCGCAGG-----CTGACAGAGAAACCGACTCATC 2960
Qy 375 ProSerProAlaLeuProSerAspAsnAsnThrTyrThrAsnTyrThrArgSerTyrSer 394
Db 2961 CCGGAAGGGGTTATCCGACAGGATGATGAGCGG-----ACTCACCGGTACCAT 3008
Qy 395 TyrAspHisSerGlyAsnLeu-----ThrGlnIleArgHisSerProAlaThr 411
Db 3009 TAGCAGTCAGCACCGCGCTGGTGCACTACACCGGACACAATATGAAGAGCCGCTGGTC 3068
Qy 412 GlnAsnAsnTyrThrValAlaIleThrLeuSerAsnArgSerAsnArgGlyValLeuSer 431
Db 3069 GAAAGCGCTAT----- 3080
Qy 432 ThrLeuThrThrAspProAsnGlnValAspThrLeuPheAspAlaGlyHisGlnThr 451
Db 3081 -----CTTTACGACCGCTGGCGCCGAGGGTG 3107
Qy 452 SerLeuLeuProGlyGlnThrLeuIleTrpThrProArgGlyGluLeu-----Lys 468
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Qy 469 GlnValAsnAsnGlyProGlyAsnGluTrpTyrArgTyrAspSerAsnGlyMetArgGln 488
Db 3153 TCCTGTACGGAACCGCAAGTGACCTGTGTAGCGGTGGACCGGACCGGCTGACCACA 3212
Qy 489 LeuLysValSerGluGlnProThrGlnAsnThrThrGlnGlnGlnArgValIleTyrLeu 508
Db 3213 ATA-----CAGAACGACAGAACCCGCATCCAGACGATTTATCAG 3251
Qy 509 ProGly-----LeuGluLeuArgThrThrGlnSerAsnAlaThrThr 523
Db 3252 CCGGGGAGCTTCACGCCCATCATCAGGGTTGAACCCGCCACCGCTGAGCTGGCGAAACG 3311

RESULT 13

US-10-114-170-226

; Sequence 226, Application US/10114170

; Patent No. 6855814

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Db 3312 CAGCGCCGC-----AGCCTGGCGATGGCT-TCAGCAGCTCGGCGGCGAAGACGG 3361
Qy 544 TrpGluSerGlyLysProGluAspValAsnAsnGlnLeu-ArgTyr-SerTyrAspAs 563
Db 3362 TGGCAGTGGGTGTTCCCGCGGTGTGTGTGCAGATGCTCGACCGGCTGGAAAGTGAAT 3421
Qy 563 nLeuIleGly----- 566
Db 3422 CCTGGCTGACCGGTGAGTGAGMAAGCCGCGCTGGTGGCATCGTGGCGCTGACTGT 3481
Qy 567 -----SerSerGlnLeuGlu----- 571
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Qy 572 ----LeuAspAsnGlnGly-----GlnIleIleSerGluGluGluTyrTyrProPh 587
Db 3542 CCACCTCGACCATCGCGGCTCGCGCTGGCCCTTATCAGTAAGGAA----- 3587
Qy 587 eGlyGlyThrAlaLeuTrpAlaAla-----AsnSerGlnThrGluAl 601
Db 3588 ----GGGGCAACAGATGTCGCGCAATACGATGAGTGGGCAACCTGCTGAATGAAGA 3643
Qy 601 aSer-----TyrLysThrIleArgTyrSerGlyLysGluArgAsp---AlaTh 616
Db 3644 GAACCGCATCAGCTGCAGCAGCTTATCGCCCTGCGCGGCGCAGCATGATGAGGATC 3703
Qy 616 xGlyLeuTyrTyrTyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTrpLeuSerAl 636
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Qy 636 aAspProAlaGlyThrIleAspGlyLeuAsnLeuTyrArgMetValArgAsnAsnProVa 656
Db 3764 GATCCGATTGGCTGAGGGGGGAGTGAACCTGTATATATATATATATATATATATAT 3820
Qy 656 lSerLeuGlnAspGluAsnGlyLeuAlaProGluLysGlyLysTyrThrLysGluValAs 676
Db 3821 GAATGCATGGATCCATTAGGATTATTAATTTAAATCAAAAAATATAGATGATATGG 3880
Qy 676 nPhePhe-----AspGluLeuLysPh 683
Db 3881 AATATTTCATGGCAATGTAAATGGAGAATCAATTAAACGAGAATAAAGAATATGGTGG 3940
Qy 683 eLysLeuAlaAlaLysSerSerHisValValLysTrpAsnGluLysGluSerSerTyrTh 703
Db 3941 ACTAATATGAAGACGACAGGTGAATATTTCCTCCATGAATCCGATAGTTCAATGATAA 4000
Qy 703 xLysAsnLysSerLeuLysValVal-----ArgValGlyAspSe 716
Db 4001 TGATAGTGTAGACTTGGGAAATATAAATGCTCGTGAAGGTTTCAGAGAGAGTAGCGGATTA 4060
Qy 716 rAspProSerGlyTyrLeuLeuSerHisGluGluLeuLysGly-----IleGluLys 734
Db 4061 TCACACTACCGGTTTTTACTCTGACGAT-----AAAGSAAATAAGTAACAAA 4108
Qy 734 sSerGlnIleIleTyrSerArgLeuGluGluAsnSerSerLeuSerGluLysSerLysTh 754
Db 4109 AGMAAATGATGTTTATGATAGTCTA-----AATTTTCAAGCAAGATTAAAC 4156
Qy 754 xAsnLeuSerLeuGly-----SerGluIleSerGlyTyrMetAlaArgThrI 770
Db 4157 GAATTCCTATATGAATGGAATGGGAAAAAAGAAATGCAGTAGTTACTTGGGA---ACACC 4213
Qy 770 eGlnAspThrIleSerGluTyrAlaGluGluHisLys 782
Db 4214 AAATAACACCTATCTAAAAATATAATATCCCAAGCTAAA 4250


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Db 2961 CCGAAGGGGTTATCCGCCGATGATGACGG-----ACTCACCGGTACCAT 3008
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QY 412 GlnAsnAsnTyrThrValAlaIleThrLeuSerAsnArgSerAsnArgGlyValLeuSer 431
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QY 452 SerLeuLeuProGlyGlnThrLeuIleThrProArgGlyGluLeu-----Lys 468
Db 3108 GCA-----AAACCGGTGGCGAGCTGAACCGGACCTGACGGGCTGGATG 3152
QY 469 GlnValAsnAsnGlyProGlyAsnGluTyrArgTyrAspSerAsnGlyMetArgGln 488
Db 3153 TCCTGTGCAGGAAACCGCAAGTGACCTGTGACGGCTGGCGACCGCGCTGACCACA 3212
QY 489 LeuLysValSerGluGlnProThrGlnAsnThrThrGlnGlnArgValIleTyrLeu 508
Db 3213 ATA-----CAGAACGACAGAACCCGCTCCAGACGATTTATCAG 3251
QY 509 ProGly-----LeuGluLeuArgThrThrGlnSerAsnAlaThrThrThr 523
Db 3252 CCGGGAGCTTCAGCCACATCATCAGGTGTGAACCGCCACCGGTGAGCTGGCGAAACG 3311
QY 524 GluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArgValLeuHis 543
Db 3312 CAGCGCGC-----ACCTGGCGGATGGCT-TCACGACTCGCGCGCGAAGACGG 3361
QY 544 TrpGluSerGlyLysProGluAspValAsnAsnGlnLeu-ArgTyrSerTyrAspAs 563
Db 3362 TGGCAGTGTGTGTTCCTCCCGCGTGTGTGTGCAGATCTCGACCGGCTGGAAGTGAAT 3421
QY 563 nLeuIleGly-----566
Db 3422 CCTGGCTGACCGGTGAGTGAGGAAGCCCGCTGGCTGGCATCTGGCGCCTGACTGT 3481
QY 567 -----SerSerGlnLeuGlu-----571
Db 3482 GCGCAGATCAAAAGCCAGATGACCCGGTATACACCGCGCGGAAATCCACCTGTA 3541
QY 572 -----LeuAspAsnGlnGly-----GlnIleLeuSerGluGluGluTyrTyrProPh 587
Db 3542 CCACTGCGACCATCGCGCGCTTCGCGCTGGCCCTTATCAGTAAGGAA-----3587
QY 587 eGlyGlyThrAlaLeuTrpAlaIa-----AsnSerGlnThrGluAl 601
Db 3588 -----GGGGCAACAGATGGTGGCGAGAAATACGATGAGTGGGCAACCTGCTGAATGA 3643
QY 601 aSer-----TyrLysThrIleArgTyrSerGlyLysGluArgAsp---Alath 616
Db 3644 GAACCCGCATCAGCTGCAGCAGCTTATCCGCTGCCCGGCGCAGCAGTATGATGAGGATC 3703
QY 616 rGlyLeuTyrTyrTyrGlyTyrArgTyrTyrGlnProTyrAlaGlyArgTrpLeuSerAl 636
Db 3704 CGGCGCTGATTACAAACCGCACCGCTATTATGACCCGCTGCAGGGGAGGTATATCACTCA 3763
QY 636 aAspProAlaGlyThrIleAspGlyLeuAsnLeuTyrArgMetValArgAsnAsnProva 656
Db 3764 GATCCGATTGGGCTGAAGGGGGATGGAACCTGTATACATATCCCGCTG---AGCCCGGT 3820
QY 656 lSerLeuGlnAspGluAsnGlyLeuAlaProGluLysGlyLysTyrThrLysGluValAs 676
Db 3821 GAATGGCATGATCCATTAGGATTTATGATTTAAATCAAAAATATAGATGATATGG 3880
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Db 3881 AATATTTGCATTGGCAATGTGTAATGGAGAATCAATTAACGAGAATAAAGAATATGTTGG 3940
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QY 754 rAsnLeuSerLeuGly-----SerGluIleSerGlyTyrMetAlaArgThrIl 770
Db 4157 GAATTCCTTATGAAATGGAATGGAAAAAAGAAATCGAGTAGTTACTTGGGA---ACACC 4213
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Db 4214 AATAACACCTATCTAAATATATAATCCCAAGCTAAA 4250
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RESULT 14

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US-09-711-164-296
; Sequence 296, Application US/09711164
; Patent No. 6589738
; GENERAL INFORMATION:
; APPLICANT: Forsyth, R. Allyn
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERET
; FILE REFERENCE: ELITRA.008A
; CURRENT APPLICATION NUMBER: US/09/711,164
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/164415
; PRIOR FILING DATE: 1999-11-9
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 296
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(4134)
US-09-711-164-296
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Score: 254.50 Matches: 167
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Best Local Similarity: 21.14% Mismatches: 279
Query Match: 5.37% Indels: 237
DB: 3 Gaps: 41
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US-10-647-956A-6 (1-915) x US-09-711-164-296 (1-4134)

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QY 1 MetSerSerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn 20
Db 1705 CTGAGTCAGTACCGC---GCATACGACAGCGCGTGGACAGTTAATTCGCGTGAAGAC--- 1758
QY 21 ArgLysLeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAsnSerAsp 40
Db 1759 -----ACGACGGGCCCATGAA----- 1773
QY 41 GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro 60
Db 1774 -----ACGCGGTATGAATACACATCGCCGGTGACCTGACCGCGCTCATTCGCCCG 1824
QY 61 ArgLysAsnLysAsn-----Gln 66
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Search completed: December 14, 2005, 20:09:52
Job time : 562 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame plus_p2n model

Run on: December 14, 2005, 20:15:22 ; Search time 1433 Seconds
(without alignments)
5280.168 Million cell updates/sec

Title: US-10-647-956A-6
Perfect score: 4740
Sequence: 1 MSYNSAIDQKTPSIKVLN.....EAINRSAAIAENLGMRRTS 915

Scoring table: BLOSUM62 Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : Published Applications NA_Main.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	4686	98.9	2748	7	US-10-609-113-45
3	2960	62.4	2817	7	US-10-609-113-48
4	2956	62.4	2817	7	US-10-706-424-15
5	2956	62.4	2817	8	US-10-754-115-57
6	2537.5	53.5	2883	7	US-10-706-424-11
7	2537.5	53.5	2883	7	US-10-609-113-46

8	2537.5	53.5	2883	8	US-10-754-115-46
9	2512	53.0	2850	7	US-10-706-424-13
10	2512	53.0	2850	7	US-10-609-113-47
11	2467	52.0	3132	7	US-10-262-794A-60
12	2467	52.0	3132	7	US-10-609-113-44
13	2467	52.0	3132	8	US-10-754-115-25
14	2187.5	46.1	2889	8	US-10-754-115-50
15	2187.5	46.1	2889	10	US-11-020-848-3
16	2187.5	46.1	2947	8	US-10-754-115-53
17	2187.5	46.1	2947	10	US-11-020-848-8
18	2187.5	46.1	7508	8	US-10-754-115-54
19	2187.5	46.1	7508	10	US-11-020-848-9
20	2168	45.7	3048	8	US-10-753-901-15
21	2168	45.7	3048	8	US-10-754-115-21
22	2168	45.7	3051	7	US-10-609-113-21
C 23	2168	45.7	39005	8	US-10-753-901-6
C 24	2168	45.7	39005	8	US-10-754-115-6
25	2025.5	42.7	38258	6	US-10-365-319-1
26	1558.5	32.9	2793	7	US-10-609-113-12
27	1558.5	32.9	2793	8	US-10-754-115-41
28	1558.5	32.9	2862	8	US-10-754-115-55
29	1558.5	32.9	33521	7	US-10-609-113-1
30	1219	25.7	2823	6	US-10-365-742-63
31	643.5	13.6	858	7	US-10-609-113-40
32	366.5	7.7	70922	6	US-10-156-761-284
C 33	366.5	7.7	9025608	6	US-10-156-761-1
34	339	7.2	2802	7	US-10-282-122A-8433
35	309	6.5	3957	6	US-10-369-493-34930
36	296.5	6.3	3750	6	US-10-156-761-22
37	285	6.2	4539	7	US-10-282-122A-42202
38	291	6.1	2832	7	US-10-282-122A-11622
39	290	6.1	7158	6	US-10-156-761-201
40	286	6.0	4716	7	US-10-282-122A-33231
41	281	5.9	4695	7	US-10-282-122A-8374
42	274	5.8	4095	7	US-10-282-122A-39125
43	273.5	5.8	4281	3	US-09-912-020-180
44	273.5	5.8	4281	7	US-10-282-122A-6433
45	273.5	5.8	4281	8	US-10-771-241-180

ALIGNMENTS

RESULT 1
US-09-817-514A-5
; Sequence 5, Application US/09817514A
; Patent No. US20020078478A1
; GENERAL INFORMATION:
; APPLICANT: ffrrench-Constant, Richard
; APPLICANT: Bowen, David
; APPLICANT: Rocheleau, Thomas
; APPLICANT: Waterfield, Nicholas
; TITLE OF INVENTION: DNA SEQUENCES FROM PHOTORHABDUS LUMINESCENS
; FILE REFERENCE: 61645
; CURRENT APPLICATION NUMBER: US/09/817,514A
; PRIOR FILING DATE: 2000-03-26
; PRIOR APPLICATION NUMBER: US 60/191806
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 5
; LENGTH: 2745
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2745)
US-09-817-514A-5

Alignment Scores:
Pred. No.: 0
Score: 4740.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Length: 2745
Matches: 915
Mismatch: 0

Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0
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Qy	1	MetSerTyrAenSerAlaileAspGlnLysThrProSerIleLysValLeuAspAsn	20
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Qy	21	ArgLysLeuAenValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAenSerAsp	40
Db	61	AGGAAATTAATATGATGACGTACTTTAGAAATATCTAGCCACTCAAGCTGACGAAAAACAGTGAT	120
Qy	41	GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro	60
Db	121	GAATTAATATTCAGTTCTATGAGTTCAATATTCGGGATTTTCAGGTAAAGACCCGATCCT	180
Qy	61	ArgLysAenLysAenGlnSerGlyProAenPheIleArgValPheAenLeuAlaGlyGln	80
Db	181	CGTAAATAAACCAGAGCGGCCCAATTTCAATTCGTGCTTTAATCTTGCCCGGTCAA	240
Qy	81	ValLeuArgGluGluSerValAspAlaGlyArgThrIleThrLeuAenAspIleGluSer	100
Db	241	GTTTTACGTGAAGAAAGTGTGATCGCGTCCGACTATTACCCCTCAATGATATTGAAAGT	300
Qy	101	ArgProValLeuIleIleAsnAlaThrGlyValArgGlnAenHisArgTyrGluAspAsn	120
Db	301	CGCCCGGTGTGATCATCAATGCAACCCGGTGTCCGCCAAAACCATTCGTTATGAAGATAAC	360
Qy	121	ThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGlyGluLysThr	140
Db	361	ACCCTTCCCGTCTGCTGCTGCTATCACCAGAACAGTACAGCGAGGAGAAACCGACC	420
Qy	141	GluArgLeuIleTrpAlaGlyAsnThrProGlnGluLysAspTyrAenLeuAlaGlyGln	160
Db	421	GAACGCTTATCTGGCGCGCAATACGCCGCAAGAAAAAGATTACAACCTCGCCGCTCAG	480
Qy	161	CysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAenSerLeuSerLeuAlaGly	180
Db	481	TGTCGCGCCCAATACGATACCCGCGGACTTACTCAACTCAATAGCCCTTCTCGGCTGGC	540
Qy	181	ValValLeuSerGlnSerGlnGlnLeuLeuThrAspAenGlnAspAlaAspTrpThrGly	200
Db	541	GTCTGTCTATCACAACTCTCAACACTGCTTACCGATAACAGGATGCCGACTGGACAGGT	600
Qy	201	GluAspGlnSerLeuTrpGlnGlnLysLeuSerSerAspValTyrIleThrGlnSerAsn	220
Db	601	GAAGACCAAGACCTCTGGCAACAAAACTGAGTAGTGATGTCTATATCACCCAAAGTAAAC	660
Qy	221	ThrAepAlaThrGlyAlaLeuLeuThrGlnThrAepAlaLysGlyAenIleGluArgLeu	240
Db	661	ACTGATGCCACCGGGGCTTTACTGACCCAGACCGATGCCAAAGGCAACATTCAGCGGCTG	720
Qy	241	AlaTyrAspValAlaGlyGlnLeuLysGlySerTrpLeuThrLeuLysGlyGlnAlaGlu	260
Db	721	GCCTATGATGTGGCGGCGCAGCTAAAGGGAGTGTGTTAACTCAAGGTTCAGCGGAA	780
Qy	261	GlnValIleIleLysSerLeuThrTyrSerAlaAlaGlyGlnLysLeuArgGluGluHis	280
Db	781	CAGGTGATTATCAAACTCAACCTACTCTCCGCGCGGCGCAAAAAATTAACGTGAAGAGCAC	840
Qy	281	GlyAenGlyIleValThrGluTyrSerTyrGluProGluThrGlnArgLeuIleGlyIle	300
Db	841	GGTAACGGGATGTCTCACTGAATACAGCTACGAACCGGAAACCCAAACGGCTTATCGGCATT	900
Qy	301	ThrThrArgArgProSerAspAlaLysValLeuGlnAspLeuArgTyrGlnTyrAspPro	320
Db	901	ACCCTCGCGCTCCATCAGACGCCAAGGTGTGCAAGACCTACGCTATCAATATGACCCA	960
Qy	321	ValGlyAenValIleAsnIleArgAenAspAlaGluAlaThrArgPheTrpArgAenGln	340
Db	961	GTAGCAATGTCAATTAATATCCGTAATGATCGGAAGCCACTCGCTTTTGGCGCAATCAG	1020
Qy	341	LysValAlaProGluAenSerTyrThrTyrAspSerLeuTyrGlnLeuIleSerAlaThr	360
Db	1021	AAAGTAGCCCGGAGAAATAGCTATATCTACGATTCCCTGTATCAGCTTATCAGCGCCACC	1080
Qy	361	GlyArgGluMetAlaAenIleGlyGlnAenAenGlnLeuProSerProAlaLeuPro	380
Db	1081	GGCGCGAAATGGCCAATATCGGTACGAAAAACAACCAACTTCCTCCCTCCCTGGGTACCT	1140
Qy	381	SerAspAenAsnThrTyrThrAenTyrThrArgSerTyrSerTyrAepHisSerGlyAen	400
Db	1141	TCGCAACAATAATACCTACACTACTATCTCGCAGCTACAGCTATGATCAAGTGGTAAT	1200
Qy	401	LeuThrGlnIleArgHisSerSerProAlaThrGlnAenAsnTyrThrValAlaIleThr	420
Db	1201	CTGACGCAAAATTCGGCACAGCTCGCCAGCTACCCAGACAACTACACCGTGGCTATCACC	1260
Qy	421	LeuSerAenArgSerAenArgGlyValLeuSerThrLeuThrThrAspProAenGlnVal	440
Db	1261	CTCTCAAAACCGCAGCAATCGGGTGTCTCAGTAGCTAACCCACCGATCCAAATCAAGTG	1320
Qy	441	AspThrIleuPheAspAlaGlyGlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIle	460
Db	1321	GATACGTTGTTGATCCGGTGTCCACAAACAGTTTATTACCCGACAGACACTTATC	1380
Qy	461	TrpThrProArgGlyGluLeuLysGlnValAenAenGlyProGlyAenGluTyrTyrArg	480
Db	1381	TGACACACAGAGAGAGTTAAAGCAGGTTAATAATGGCCCGGGAATAGTGGTACCGC	1440
Qy	481	TyrAspSerAenGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAenThrThr	500
Db	1441	TACGACAGCAACCGCATGAGCAACTGAAAGTCAGTGAAACAGCAACCCAGAAATCTACG	1500
Qy	501	GlnGlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAenAla	520
Db	1501	CAGCAACACCGGTAAATCTATTTGCGCGGACTCGAGCTACGCACAAACCCAGAGCAACGCC	1560
Qy	521	ThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArg	540
Db	1561	ACAAACAGGAAGTTTACAGTTATCACACTCGGTGAACCGGTCCGCGCACAGGTACGG	1620
Qy	541	ValLeuHisTrpGluSerGlyLysProGluAspValAenAenAenGlnLeuArgTyrSer	560
Db	1621	GTGTTGCACTGGGAGAGCGGTAAGCCAGAGAGATGTCAACAATAATCAACTACGTTCACGC	1680
Qy	561	TyrAspAenLeuIleGlySerSerGlnLeuGluLeuAenAenGlnGlyGlnIleIleSer	580
Db	1681	TACGATAATCTGATCGGCTCCAGCCAGCTTGAACCTGGACAAACCAAGGACAAATTTATCAGC	1740
Qy	581	GluGluGluTyrTyrProPheGlyGlyThrAlaLeuTrpAlaAlaAenSerGlnThrGlu	600
Db	1741	GAGGAAGATTTATTCATTTGGCGGACAGCGCTGTGGGACGAAACAGCAACAGCAACAGAA	1800
Qy	601	AlaSerTyrLysThrIleArgTyrSerGlyLysGluArgAspAlaThrGlyLysTyrTyr	620
Db	1801	GCCAGCTATAAAACGATTCGCTATTCGCGCAAGAACAGAGATGCCACCGGTTGTATTAT	1860
Qy	621	TyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTrpLeuSerAlaAenProAlaGly	640
Db	1861	TACGGTTATCGTTATTAACCAACCGTGGCGGGCAGATGGTTAAGCGCGGACCCCGCAGGA	1920
Qy	641	ThrIleAspGlyLeuAenLeuTyrArgMetValArgAenAenProValSerLeuGlnAsp	660
Db	1921	ACCATGATGGCTGATCTATACCGAATGTTAAGAAATAATCTCTGTGAGTTTACAAGAT	1980
Qy	661	GluAenGlyLeuAlaProGluLysGlyLysTyrThrLysGluValAenPheAenGlu	680
Db	1981	GAAATGCAATAGCGCCAGAAAAAGGAAATATACCAAGAGAGGTAAATTTCTTTGATGAA	2040
Qy	681	LeuLysPheLysLeuAlaAlaLysSerSerHisValValLysTrpAenGluLysGluSer	700
Db	2041	TTAAATTTCAAAATGGCAGCCAAAAGTTTCATGTTCTCAATGGAAACGAGAAAGAGAGC	2100
Qy	701	SerTyrThrLysAenLysSerLeuLysValValArgValGlyAspSerAspProSerGly	720

Db	2101	AGTTATACAAAAATAAATCAITGAAGTGGTTCGGTCCGGATTCCTCGATCCGTCGGT	2160
Qy	721	TyrLeuLeuSerHisGluGluLeuLeuLeuGlyIleGluLeuSerGlnIleIleTyrSer	740
Db	2161	TATTTGCTAAGCACCAAGAGTACTAAAGGTATAGAAAAAGTCAATCATATATAGC	2220
Qy	741	ArgLeuGluGluAenSerSerLeuSerGluLeuSerLysThrAenLeuSerLeuGlySer	760
Db	2221	CGACTTGAAGAAAAACAGCTCCCTTTTCAGAAAAATCAAAAAACGAATCTTTCTTAGGATCT	2280
Qy	761	GluIleSerGlyTyrMetAlaArgThrIleGlnAenThrIleSerGluTyrAlaGluGlu	780
Db	2281	GAAATATCCGGTTATATGGCAAGAACCATACAGATACCATATCAGAAATATGCCGAAGAG	2340
Qy	781	HisLysTyrArgSerAenHisProAenPheTyrSerGluThrAenPheAlaLeuMet	800
Db	2341	CATAATATAGAAAGTAATCACCTGATTTTATTCAGAAACCGATTTCTTCGGTTAATG	2400
Qy	801	AspLysSerGluLysAenAspTyrSerGlyGluArgLysIleTyrAlaAlaMetGluVal	820
Db	2401	GATAAAGTCAAAAAATGATTTATCCGGTGAAGAAAAAATTTATGCGCAATGCGAGTT	2460
Qy	821	LysValTyrHisAspLeuLysAenLysGlnSerGluLeuHisValAenTyrAlaLeuAla	840
Db	2461	AAGGTTTATCATGATTTAAAAATAAACCAATCAGAAATACATGTCAACTATGCAATGGCC	2520
Qy	841	HisProTyrThrGlnLeuSerAenGluAlaArgAlaLeuLeuGlnGluThrGluProAla	860
Db	2521	CATCCCTATACCAATTTAGTAATGAAGAAGAGCGCTGTTGCAAGAACAGACCCGCT	2580
Qy	861	IleAlaIleAspArgGluTyrAenPheLysGlyValGlyLysPheLeuThrMetLysAla	880
Db	2581	ATTGCAATAGATAGAGAAATAAATTTCAAAAGGTGTTGGCAAAATTCCTGACAATGAAAGCA	2640
Qy	881	IleLysLysSerLeuLysGlyHisLysIleAenArgIleSerThrGluAlaIleAenIle	900
Db	2641	ATTAATAAAATCATTTGAAGGACATAAAATTAATAGGATATCAACAGAGCTTAAATATT	2700
Qy	901	ArgSerAlaAlaIleAlaGluAenLeuGlyMetArgArgThrSer	915
Db	2701	CGCTCTCGCGCTATCGCTGAGAAATTTAGGAATGCGGAGAACTTCA	2745
RESULT 2			
US-10-609-113-45			
; Sequence 45, Application US/10609113			
; Publication No. US20040110184A1			
; GENERAL INFORMATION:			
; APPLICANT: Bintrim, Scott			
; APPLICANT: Bevan, Scott			
; APPLICANT: Zhu, Baolong			
; APPLICANT: Merlo, Donald J.			
; TITLE OF INVENTION: Pesticidally Active Proteins and Polynucleotides Obtainable from			
; FILE OF INVENTION: Paenibacillus Species			
; FILE REFERENCE: DAS-101XC2			
; CURRENT APPLICATION NUMBER: US/10/609,113			
; CURRENT FILING DATE: 2003-06-27			
; PRIOR APPLICATION NUMBER: US 60/392,633			
; PRIOR FILING DATE: 2002-06-28			
; PRIOR APPLICATION NUMBER: US 60/441,647			
; PRIOR FILING DATE: 2003-01-21			
; NUMBER OF SEQ ID NOS: 49			
; SOFTWARE: PatentIn version 3.2			
; SEQ ID NO 45			
; LENGTH: 2748			
; TYPE: DNA			
; ORGANISM: Photorhabdus strain W14			
US-10-609-113-45			
Alignment Scores:			
Pred. No.:	0	Length:	2748
Score:	4686.00	Matches:	902
Percent Similarity:	99.23%	Conservative:	6

Best Local Similarity: 98.58%		Mismatches: 7
Query Match: 98.86%		Indels: 0
DB:		Gaps: 0
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DB	1	ATGACAGATTACAATTCGCAATTGACCAAAAGACCCCTCGATTAAAGGTATTAGATAAC 60
QY	21	ArgLysLeuAenValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAenSerAap 40
DB	61	AGCAAAATTAATTAATGTAGTACTTTAGAAATATCTACGCACCTCAAGCTGACGAAACAGTGAT 120
QY	41	GluLeuIleThrPheTyrGluPheAenIleProGlyPheGlnValLysSerThrAapPro 60
DB	121	GAATTAATTTACGTTCTATGAGTTCAATATTCGGGATTTTCAGGTAAAAAGCACCGGATCCT 180
QY	61	ArgLysAenLysAenGlnSerGlyProAenPheIleArgValPheAenLeuAlaGlyGln 80
DB	181	CGTAATAAATAAAACAGAGCGGCCCAATTTTCATTCTGTCCTTTAATCTTCCCGGTCAA 240
QY	81	ValLeuArgGluGluSerValAaspAlaGlyArgThrIleThrLeuAenAaspIleGluSer 100
DB	241	GTITTTACGTGAAGAAGTGTGATGCCGTCGACTATTACCCCTCAATGATTTGAAAGT 300
QY	101	ArgProValLeuIleAenAlaThrGlyValArgGlnAenHisArgTyrGluAapAen 120
DB	301	CGCCCGGTGTTGATCATCAATGCAACCGGTGCCCAAAACCATCGTTATGAAGATAAC 360
QY	121	ThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGlyGluLysThrThr 140
DB	361	ACCCTTCCCGTCGTCGCTCATCAACGAAACAAAGTACAGGCAGGAGAGAAAACGACC 420
QY	141	GluArgLeuIleTyrAlaGlyAenThrProGlnGluLysAapTyrAenLeuAlaGlyGln 160
DB	421	GAACTGCTTTATCTGGCGCGCAATACGCGCAAGAAAAAGATTACAACTCTCGCGGTGAG 480
QY	161	CysValArgHisTyrAaspThrAlaGlyLeuThrGlnLeuAenSerLeuSerLeuAlaGly 180
DB	481	TGTGTCGGCCATTCAGATACCGGGGACTTACTCAACTCAATAGCCTTTCTCTGGCTGGC 540
QY	181	ValValLeuSerGlnSerGlnLeuThrAaspAenGlnAaspAlaAaspThrThrGly 200
DB	541	GTCTGCTATCAACAATCTCAGCAACTACTCTGTCGATGATAAAATGCTCACTGGACAGGT 600
QY	201	GluAapGlnSerLeuTyrGlnGlnLysLeuSerSerAapValTyrIleThrGlnSerAen 220
DB	601	GAAGACCAAAAGCCTCTGGCAGCAAAACTGAGCAGTGATGCTATACCAACCCCAATAAA 660
QY	221	ThrAapAlaThrGlyAlaLeuLeuThrGlnThrAaspAlaLysGlyAenIleGlnArgLeu 240
DB	661	GCCGATGCCACCGGGCTTTATTGACCCAGACCGATGCCAAAGGCACATCCAGCGCTCTG 720
QY	241	AlaTyrAaspValAlaGlyGlnLysGlySerTyrLeuThrLeuLysGlyGlnAlaGlu 260
DB	721	GCCTACGACGTAGCCGGCAGCTAAAGGCTGTTGGTTGACACTCAAAAGCTCAGGCCGAG 780
QY	261	GlnValIleLysSerLeuThrTyrSerAlaAlaGlyGlnLysLeuArgGluGluHis 280
DB	781	CAAGTGATTTATCAAAATCGCTGACCTACTCCGCGCGCGGACAAAAATTCAGCGAAGACAC 840
QY	281	GlyAenGlyIleValThrGluTyrSerTyrGluProGluThrGlnArgLeuIleGlyIle 300
DB	841	GGTAACGGGGTTATCACTGAATACAGCTATGAAACCAAGAAACCCACGGCTTATCGGTATT 900
QY	301	ThrThrArgProSerAaspAlaLysValLeuGlnAaspLeuArgTyrGlnTyrAapPro 320
DB	901	GCCACCGCGCTCCGTCCAGACGCCAAAGTGTGCAAGACTTACGCTATCAATATGACCCG 960
QY	321	ValGlyAenValIleAenIleArgAenAaspAlaGluAlaThrArgPheTyrArgAenGln 340
DB	961	GTAGGCAATGTGATCAATATCCGTAATGATGCGAAGCCACCCGCTTTTGGCGCAATCAG 1020

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Db 1021 AAAGTGTCCGGAGAAATAGCTATACCTAGACTCCCTGTATCAGCTTATCAGTGCACCC 1080
QY 361 GlyArgGluMetAlaAenIleGlyGlnGlnAenGlnLeuProSerProAlaLeuPro 380
Db 1081 GGGCGGAATGGCTAATATAGGTACAGAAATTAACCAACTGCCCTCCCTCGCGTACCT 1140
QY 381 SerAspAenAenThrTyrThrAsnTyrThrArgSerTyrSerTyrAspHisSerGlyAen 400
Db 1141 TCTGACAACAATACCTACCTAACTATACCTCGCAGCTACAGCTATGATCACTAGTGGTAAT 1200
QY 401 LeuThrGlnIleArgHisSerSerProAlaThrGlnAenAenTyrThrValAlaIleThr 420
Db 1201 CTGACGCAAAATTCGCACAGCTCCGCCAGCTACCCAGAACCACTACACCGTGGCTATCACC 1260
QY 421 LeuSerAenArgSerAenArgGlyValLeuSerThrLeuThrThrAspProAenGlnVal 440
Db 1261 CTCTCAAAACCGCAGCAATCGGGTGTCTCAGTACGCTAACCCACCGATCCAAATCAAGTG 1320
QY 441 AspThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIle 460
Db 1321 GATACGTTGTTGATCGCGTGGTCCACCAACCACTGTTTATTTACCCGACAGACACTTATC 1380
QY 461 TrpThrProArgGlyGluLeuLysGlnValAenAenGlyProGlyAenGluTyrTyrArg 480
Db 1381 TGGACACACGAGAGAGTAAAGCAGGTTAAATATGCGCCGGGAAATGAGTGATCCGC 1440
QY 481 TyrAspSerAenGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAenThrThr 500
Db 1441 TACGACAGCAACGCGATGAGACAACTGAAAGTGAAGTGAACGCCAACCCAGATACCTACG 1500
QY 501 GlnGlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAenAla 520
Db 1501 CAGCAACAACGGGTAACTATTTCCCGGACTGAGCTACGCAACAACCCAGAGCAACGCC 1560
QY 521 ThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArg 540
Db 1561 ACAACAACGGAAGAGTTACACGTTTATCACCTCGGTGAAGCCGCTCGCGCACAGGTACGG 1620
QY 541 ValLeuHisTrpGluSerGlyLysProGluAspValAenAenAenGlnLeuArgTyrSer 560
Db 1621 GTGTTGCACTGGGAGAGCGGTAAAGCCAGAGATGTCAACAATATCAACTACGTTACAGC 1680
QY 561 TyrAspAenLeuIleGlySerSerGlnLeuGluLeuAspAenGlnGlyGlnIleIleSer 580
Db 1681 TACGATAATCTGATCGGCTCCAGCCAGCTTGAACCTGGACAAACCAAGGACAAATTTATCAGC 1740
QY 581 GluGluGluTyrTyrProPheGlyGlyThrAlaIleuTrpAlaAlaAenSerGlnThrGlu 600
Db 1741 GAGGAAGAGTATTATCACTTTGGCGGGACAGCGCTGTGGGCGAGCAAAACAGCCAAACAGAA 1800
QY 601 AlaSerTyrLysThrIleArgTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyr 620
Db 1801 GCCAGCTATAAAGCATTCGCTATTTCGGCAAGAACAGAGATGACCGCGGTTGTATTAT 1860
QY 621 TyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTrpLeuSerAlaAspProAlaGly 640
Db 1861 TACGGTTATCGTTATTTACCAACCGTGGCGGCGAGATGGTTAAGCGCGACCCCGCAGGA 1920
QY 641 ThrIleAspGlyLeuAenLeuTyrArgMetValArgAenAenProValSerLeuGlnAsp 660
Db 1921 ACCATTGATGGCTGAAATCTATACCGAATGTAAGAAATAATCTCTGTGAGTTTCAAGAT 1980
QY 661 GluAenGlyLeuAlaProGluLysGlyLysTyrThrLysGluValAenPheAspGlu 680
Db 1981 GAAATATGATTAGCGCCGCAAGAAAGGGAATATATACCAAGAGGTAAATTTCTTTGATGAA 2040
QY 681 LeuLysPheLysLeuAlaAlaLysSerSerHisValValLysTrpAenGluLysGluSer 700
Db 2041 TTAAAAATTCAAATTTGGCAGCCCAAAAGTTTCACATGTTGTCAAAATGCAACGAGAAAGAGAGC 2100
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QY 701 SerTyrThrLysAenLysSerLeuLysValValArgValGlyAspSerAspProSerGly 720
Db 2101 AGTTTATACAAAATAAATCAATCAATGAAAGTGGTTCGTGTCGGTGATCCGATCCGTCGGGT 2160
QY 721 TyrLeuLeuSerHisGluGluLeuLeuLysGlyIleGluLysSerGlnIleIleTyrSer 740
Db 2161 TATTTCCTAAGCCACAGAGGTTACTTAAAGGTATAGAAAAAGTCAAAATCATATATAGC 2220
QY 741 ArgLeuGluGluAenSerSerLeuSerGluLysSerLysThrAenLeuSerLeuGlySer 760
Db 2221 CGACTTTGAAGAAACACAGCTCCCTTTTCAGAAAAATCAAAAACGAATCTTTCTTTAGGATCT 2280
QY 761 GluIleSerGlyTyrMetAlaArgThrIleGlnAspThrIleSerGluTyrAlaGluGlu 780
Db 2281 GAAATATCGGTTATATGCGNAGAACCATACAGATACAGATATCAGAAATATGCCGAAGAG 2340
QY 781 HisLysTyrArgSerAenHisProAspPheTyrSerGluThrAspPheAlaLeuMet 800
Db 2341 CATAAATATAGAAGTAAATCACCCCTGATTTTATTTCAGAAAACCGATTTCTTTGCGTTAATG 2400
QY 801 AspLysSerGluLysAenAspTyrSerGlyGluArgLysIleTyrAlaIleMetGluVal 820
Db 2401 GATAAAGTCAAAAAATGATTTATCCCGTGAAGAAAAATTTATGCGGCAATGGAGGTT 2460
QY 821 LysValTyrHisAspLeuLysAenLysGlnSerGluLeuHisValAenTyrAlaLeuAla 840
Db 2461 AAGTTTATCATGATTTTAAAAATAAACAATCAGAATTACATGTCACATGATGCGCC 2520
QY 841 HisProTyrThrGlnLeuSerAenGluArgAlaLeuLeuGlnGluThrGluProAla 860
Db 2521 CATCCCTATACGCAATTGAGTAATGAAGAAAGAGCGCTGTTGCAAGAAAACAGAACCCGCT 2580
QY 861 IleAlaIleAspArgGluTyrAenPheLysGlyValGlyLysPheLeuThrMetLysAla 880
Db 2581 ATTGCAATAGATAGAGAATATAATTTCAAAGGTTGGCAAAATTCCTGACAAATGAAAGCA 2640
QY 881 IleLysLysSerLeuLysGlyHisLysIleAenArgIleSerThrGluAlaIleAenIle 900
Db 2641 ATTAAAAATCATTTGAAGGACATAAATTAATAGATATCAACAGAGGCTATTATATT 2700
QY 901 ArgSerAlaAlaIleAlaGluAenLeuGlyMetArgArgThrSer 915
Db 2701 CGCTCTCGCGCTATCGCTGAGAATTTAGGAATCGGAGAACTTCA 2745

RESULT 3
US-10-609-113-48
; Sequence 48, Application US/10609113
; Publication No. US20040110184A1
; GENERAL INFORMATION:
; APPLICANT: Bintrim, Scott
; APPLICANT: Bevan, Scott
; APPLICANT: Zhu, Baolong
; APPLICANT: Merlo, Donald J.
; TITLE OF INVENTION: Pesticidally Active Proteins and Polynucleotides Obtainable from
; FILE REFERENCE: DAS-101XC2
; CURRENT APPLICATION NUMBER: US/10/609,113
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US 60/392,633
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/441,647
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 48
; TYPE: DNA
; ORGANISM: Photorhabdus strain W14
US-10-609-113-48

Alignment Scores: 7.37e-243 Length: 2817
Pred. No.: 2960.00 Matches: 607
Score:
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Percent Similarity:	73.01%	Conservative:	91
Best Local Similarity:	63.49%	Mismatches:	186
Query Match:	62.45%	Indels:	72
DB:	7	Gaps:	13
US-10-647-956A-6 (1-915) x US-10-609-113-48 (1-2817)			
Qy	1	MetSerSerTyAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn	20
Db	1	ATGGAAAACATTGACCCAAACCTTATACCATACGCTACCGCTAGTGTCACGATAAC	60
Qy	21	ArgLysLeuAsnValArgThrLeuGluThrLeuArgThrGlnAlaAspGluAsnSerAsp	40
Db	61	CGTGGACTAGCTATCCGTAATATTAGTTTCCCGCACTACCGCAGAACCAATACCGAT	120
Qy	41	GluLeuIleThrPheTyrgLysPheAsnIleProGlyPheGlnValLysSerThrAspPro	60
Db	121	ACCGTATTACCGCCCATCAATATAATGCGGCGGATATTGACCAAGCATTGATCTCT	180
Qy	61	Arg-----LysAsnLysAsnGlnSerGlyProAsnPheIleArgValPhe	75
Db	181	CGCCTGTATGACGCCAAACAGACTAACACGCTGTACAAACCGAATTTTATCTGGCGACAT	240
Qy	76	AsnLeuAlaGlyClnValLeuArgGluGluSerValAspAlaGlyArgThrIleThrLeu	95
Db	241	AATTTGACCGGCAATATCTCGCAACAGAGAGCGTCCGTCGCGAGCATTTACCTTC	300
Qy	96	AsnAspIleGluSerArgProValLeuIleIleAsnAlaThrGlyValArgGlnAsnHis	115
Db	301	AACGATATTGAAGCGCCCGGTGTTGACCATCAATGACGCGGTGTCGCGCAAAACCAT	360
Qy	116	ArgTyrgLysAsnThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAla	135
Db	361	CGCTACGAAGATAACACCCCTGCGCGTTCGCTCGCTATCAGCGAAACAAGGACAGCA	420
Qy	136	GlyGluLysThrThrGluArgLeuIleThrAlaGlyAsnThrProGlnGluLysAspTyrg	155
Db	421	GAAGAGAAAACGACCGAGCGCTTATCTGGCGCGCAATACGCGCAAGAAAAGACCAC	480
Qy	156	AsnLeuAlaGlyClnCysValArgHisTyrgAspThrAlaGlyLeuThrGlnLeuAsnSer	175
Db	481	AACCTTGGCGGTGAGTGGTCCGCCATACGATACCGAGGACTCACTCAACTCAACAGC	540
Qy	176	LeuSerLeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAspAsnGlnAsp	195
Db	541	CTTGCCCTGACCGCGCGCTTCTATCAATCTCAACACTGCTTACCGATAACAGGAT	600
Qy	196	AlaAspTrpThrGlyGluAspGlnSerLeuTrpGlnGlnLysLeuSerSerAspValTyrg	215
Db	601	GCCGACTGGACAGGTGAAGACCAAGAGCCTCTGGCAACAAAACCTAGTAGTGTCTAT	660
Qy	216	IleThrGlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrClnThrAspAlaLysGly	235
Db	661	ATCACCAAGTAACACTGATGCCACCGGGGCTTTTACTGCCAGACCGATGCCAAAGGC	720
Qy	236	AsnIleGlnArgLeuAlaTyrgAspValAlaGlyClnLysGlySerTrpLeuThrLeu	255
Db	721	AACATTCAGCGGTGCGCTATGATGTGGCGGCGCAGCTAAAGGGAGTTGGTTAACTC	780
Qy	256	LysGlyClnAlaGluGlnValIleIleLysSerLeuThrTyrgSerAlaAlaGlyGlnLys	275
Db	781	AAAGGTGAGCGGACAGGTGATTATCAATCGTAACCTACTCTCCGCGCGCGGCAAAA	840
Qy	276	LeuArgGluClnHisGlyAsnGlyIleValThrGluTyrgSerTyrgLysProGluThrGln	295
Db	841	TTACGTGAAGAGACCGGTAAACGGGATTTGTCATGAATACAGCTACGAAACCGGAAAC	900
Qy	296	ArgLeuIleGlyIleThrThrArgArgProSerAspAlaLysValLeuGlnAspLeuArg	315
Db	901	CGGCTTATCGGCATTACCACTCGCGTCCATCAGACGCCAGGTGTTGCAAGACCTACGC	960
Qy	316	TyrgLntTyrgAspProValGlyAsnValIleAsnIleArgAsnAspAlaGluAlaThrArg	335

Db	961	TATCAATATGACCCAGTAGGCAATGTCTATTAGTATCCGTAAATGATCGGAAAGCCACTCGC	1020
Qy	336	PheTrpArgAsnGlnLysValAlaProGluAsnSerTyrgThrTyrgAspSerLeuTyrgLys	355
Db	1021	TTTTGGCGCAATCAGAAAGTAGCCCCGGAGATAGCTATACCTACGATTCCCTGTATCAG	1080
Qy	356	LeuIleSerAlaThrGlyArgGluMetAlaAsnIleGlyGlnAsnAsnGlnLeuPro	375
Db	1081	CTTATCAGCGCACCGGCGCGAGATGGCCAATATCGGTTCAGCAAAAGCAACCAACTTCCC	1140
Qy	376	SerProAlaLeuProSerSerAspAsnAsnThrTyrgThrAsnTyrgThrArgSerTyrgSerTyrg	395
Db	1141	TCCTCGCGCTACCTTCGTATAACAACTACCTACCACTATCTCGCATCTATCTAT	1200
Qy	396	AspHisSerGlyAsnLeuThrGlnIleArgHisSerSerProAlaThrGlnAsnAsnTyrg	415
Db	1201	GACCGTGGCGGCAATTTGACGAAATTCAGCATAGTTTACCAGCGCGCAAAATACTAC	1260
Qy	416	ThrValAlaIleThrLeuSerAsnArgSerAsnArgGlyValLeuSerThrLeuThrThr	435
Db	1261	ACGACGGATATTAACGGTTTCAAATCGCAGCAACCGCGCGTACTCAGCACTTGACCGCA	1320
Qy	436	AspProAsnGlnValAspThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuPro	455
Db	1321	GATCCAACTCAAGTCGATGCCCTTATTGATGCGGAGGCCATCAAAACCACTTGTTATCC	1380
Qy	456	GlyGlnThrLeuIleTrpThrProArgGlyGluLeuLysGlnValAsnAsnGlyProGly	475
Db	1381	GGCCAAAGTTCTAACTTGGACACCGCGAGCGGAATTGAAACAAGCCCAACAAATAGCGCAGGA	1440
Qy	476	AsnGluTrpTyrgArgTyrgAspSerAsnGlyMetArgGlnLeuLysValSerGluGlnPro	495
Db	1441	AATGAGTGATTCGCTACGATAGCAACGCATACGCAGCTAAAGAGTAAATGAACAACAA	1500
Qy	496	ThrGlnAsnThrThrClnGlnGlnArgValIleTyrgLeuProGlyLeuGluLeuArgThr	515
Db	1501	ACTCAGATATATCCGCAACAAAGGGTAACCTTATCTACCGGGGCTGGAAATACGTACA	1560
Qy	516	ThrGlnSerAsnAlaThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGly	535
Db	1561	ACCGAACAACGCCACACACAGAGAGTTTACAGTTTATCACACTCGGTAAAGCGCGC	1620
Qy	536	ArgAlaGlnValArgValLeuHisTrpGluSerGlyLysProGluAspValAsnAsnAsn	555
Db	1621	CGCGCGCAAGTCCGAGTATTGCAATTTGGAGAGCGGTAAACCCAGAGATATTAATAACAAT	1680
Qy	556	GlnLeuArgTyrgSerTyrgAspAsnLeuIleGlySerSerGlnLeuLysLeuLeuAspGln	575
Db	1681	CAGCTTCGTTACAGCTACGATTAATCTTATGGCTCCAGCCAACTTCAATTAGATAGCGAC	1740
Qy	576	GlyGlnIleIleSerGluGluGluTyrgTyrgProPheGlyGlyThrAlaLeuTrpAlaAla	595
Db	1741	GGACAAATTTTACGTGAAGAGAAATATTTATCCATTTGGTGGTACAGCGCTGTGGCGGCA	1800
Qy	596	AsnSerGlnThrGluAlaSerTyrgTyrgThrIleArgTyrgSerGlyLysGluArgAspAla	615
Db	1801	AGGAATCAACCGAAGCCAGCTATATAAACCAITTCGTTATTCGTTAAAGACCGGATGTT	1860
Qy	616	ThrGlyLeuTyrgTyrgTyrgTyrgTyrgTyrgTyrgTyrgTyrgTyrgTyrgTyrgTyrg	635
Db	1861	ACCGGCTGTATTTATGCTACCGTTATTTACCAACCGTGGCGGCGAGATGGTAAAGT	1920
Qy	636	AlaAspProAlaGlyThrIleAspGlyLeuAsnLeuTyrgArgMetValArgAsnAsnPro	655
Db	1921	GCAGACCGCGGAGGAACCACTTGATGACTGAATTTATATCGCATGCTGAGAAATAACCCG	1980
Qy	656	ValSerLeuGlnAspGluAsnGlyLeuAlaPro-----	666
Db	1981	GTGACGCAATTTGATGTTCCAGGGATTATCACCGGCCCAACAGAAAGAGCGGATAATA	2040
Qy	667	GluLysGlyLysTyrgTyrgTyrgTyrgTyrgTyrgTyrgTyrgTyrgTyrgTyrgTyrg	686
Db	2041	AAACAGGGTTCCTTTACGGGA-----ATCGAAGAGAGCTGTTTATAAAAAATG	2088

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QY 687 AlAlAs-----SerSerHisValValLysTrpAenGluLysGluSer 700
Db 2089 GCTAAACCTCAAACTTCAACAGCCAAAGAGCTATCGCTGCCCAACAGAGCAAGAGCC 2148
QY 701 -----SerTyrThrLysAenLysSerLeuLysValValArgValGlyAspSerAspPro 718
Db 2149 CATGAATCATGACCAACACCTAGTGTAGATATT-----AGCCCAATT 2193
QY 719 SerGlyTyrLeuLeuSerHisGluLulLeuLysGlyLeGluLysSerGlnIle 738
Db 2194 AAAAACTACACACAGATAGCTACAAATTAATGCCGCGATAGAGGAAATCGTATTACG 2253
QY 739 TyrSerArgLeuGluGluAenSerSerLeuLysSerLysThrAsnLeuSerLeu 758
Db 2254 CCAGCGTGGAAAGTTAGACGCCACATATCTCCCTCAACAGTAGACAATAGAGGGTA 2313
QY 759 GlySerGluIleSerGlyTyrMetAlaArgThr----- 769
Db 2314 ACTATCGGTGATGACCTATGTAGATAATTCCAGGCCATCGCTTGGCACTGCCACAG 2373
QY 770 -----IleGlnAspThrIleSerGluTyrAla-----Glu 779
Db 2374 GAAGGAAATAGTATTATGTTGGTGATATGTTTCGGATTAACGCTTATTTATCAACATCG 2433
QY 780 GluHisLysTyrArgSerAsn-----HisProAspPheTyrSerGluThrAspPhePhe 797
Db 2434 GCCCATCGTGGTTTCTGGAATTTTGTTCACAAAAAGAACCCAGTGAATCTCGATACGTC 2493
QY 798 AlAlAu-----MetAspLysSerGluLysAsnAspTyr 808
Db 2494 AAGATGSCATTTTAAAGAAATCGGGGTCAATGTCTCAGCAGCATCTATGATAATAAT 2553
QY 809 SerGlyGluArgLysIleTyrAlaAlaMetGluValLysValTyrHisAspLeuLysAsn 828
Db 2554 GCTGGCAGGAGCAAGATTATAAATG-----GATTAAACGAT 2592
QY 829 LysGlnSerGluLeuHisValAenTyrAlaLeuAlaHisProTyrThrGlnLeuSerAsn 848
Db 2593 TCAGAAAAACCCCTTGCTGAAAAATTAAACTAAGAGTCAGTGGACCAATCGGGACAA 2652
QY 849 GluGluArgAlaLeuGlnGluThrGluProAlaIleAlaIleAspArgGluTyrAsn 868
Db 2653 GCGGAATATTACTACCTAGGAAACACAGTTCGAAGTTGTT-----TCAATGAA 2703
QY 869 PheLysGlyValGlyLysPheLeuThrMetLysAlaIleLysLysSerLeuLysGlyHis 888
Db 2704 CATCAAGGCAGAGATACCTATGTATTATTGCAAGATATTAAACCAATCCGAGCCACTCAT 2763
QY 889 LysIleAsnArgIleSerThrGluAlaIleAsnIleArgSerAlaAla 904
Db 2764 AGA---AATGTACGTAACACTTACACCGGTAATTTCAATCATCCAGT 2808

RESULT 4
US-10-706-424-15
; Sequence 15, Application US/10706424
; Publication No. US20040103455A1
; GENERAL INFORMATION:
; APPLICANT: french-Constant, Richard
; APPLICANT: Waterfield, Nicholas
; TITLE OF INVENTION: DNA Sequences from tcd Genomic Region of Photorhabdus luminescens
; FILE REFERENCE: 62878
; CURRENT APPLICATION NUMBER: US/10706,424
; CURRENT FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2814)
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US-10-706-424-15

Alignment Scores:
Pred. No.: 1,62e-242 Length: 2817
Score: 2956.00 Matches: 608
Percent Similarity: 73.01% Conservative: 90
Best Local Similarity: 63.60% Mismatches: 186
Query Match: 62.36% Indels: 72
DB: 7 Gaps: 14

US-10-647-956A-6 (1-915) x US-10-706-424-15 (1-2817)

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QY 1 MetSerSerTyrAenSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn 20
Db 1 ATGGAACAACATTGACCCAAACCTTTATACCATACGCTACCTACCTAGTGTTCAGATAAC 60
QY 21 ArgLysLeuAenValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAenSerAsp 40
Db 61 CGTGGACTAGCTATCGGTAATATTAGTTTTCACCGCACTACCGCAGAAACAAATACCGAT 120
QY 41 GluLeuIleThrPheTyrGluPheAenIleProGlyPheGlnValLysSerThrAspPro 60
Db 121 ACCCGATTACCGCCATCAATATAATGCGGCGGATATTTGAACCAACGATTTGATCTCT 180
QY 61 Arg-----LysAenLysAsnGlnSerGlyProAsnPheIleArgValPhe 75
Db 181 CGCTGTATGACGCCAAACAGACTAACACGCTGTACACCGAATTTTATCTGGCGACAT 240
QY 76 AsnLeuAlaGlyGlnValLeuArgGluGluSerValAspAlaGlyArgThrIleThrLeu 95
Db 241 AATTTGACGGCAATATCTCTGCAACAGAGAGCGTGATGCGCGGTGCGGACGATTACCCCTC 300
QY 96 AsnAspIleGluSerArgProValLeuIleIleAenAlaThrGlyValArgGlnAenHis 115
Db 301 AACGATATTGAAGCCGCGCGGTGTGACCATCAATGACGCGCGGTGTCGCGAAAAACCAT 360
QY 116 ArgTyrGluAspAsnThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAla 135
Db 361 CGCTACGAGATAACACCTTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 136 GlyGluLysThrThrGluArgLeuIleTyrAlaGlyAsnThrProGlnGluLysAspTyr 155
Db 421 GAAGAGAAACAGACCGAGCGCTTATCTGCGCGCGCAATACGCGCGCAAGAAAAAGCAC 480
QY 156 AsnLeuAlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAenSer 175
Db 481 AACCTTTCGCGGTGAGTCCGCTGCGCCATACGATACCGCAGAGTCTACTCAACTCAACAGC 540
QY 176 LeuSerLeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAspAenGlnAsp 195
Db 541 CTTGCCCTGACCGCGCGCTTCTATCACAATCTCAACACTGCTTACCGATAACCGAGAT 600
QY 196 AlaAspTrpThrGlyGluAspGlnSerLeuTrpGlnLysLeuSerSerAspValTyr 215
Db 601 GCCGACTGGACAGGTGAAGACACAGAGCTCTGGCAACAAAACTAGTAGTAGTGTCTAT 660
QY 216 IleThrGlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGly 235
Db 661 ATCACCACAAAGTAACACTGATGACCGGGGCTTTACTGACCCAGACCGATGCCAAAGGC 720
QY 236 AsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLysGlySerTrpLeuThrLeu 255
Db 721 AACATTGACGGGTGCGCTATGATGCGCGGCGAGCTAAAGGGAGTTGTTTAACACTC 780
QY 256 LysGlyGlnAlaGluGlnValIleIleLysSerLeuThrTyrSerAlaAlaGlyGlnLys 275
Db 781 AAAGGTGAGCGGAAACAGGTGATTATCAAACTCGTAACCTACTCTCGCGCGCGGCAAAA 840
QY 276 LeuArgGluGluHisGlyAenGlyIleValThrGluTyrSerTyrGluProGluThrGln 295
Db 841 TTACGTGAAGAGCAGCGTACCGGGATTGTCTACCTACAGTACAGACCGGAAACCCAA 900
QY 296 ArgLeuIleGlyIleThrThrArgArgProSerAspAlaLysValLeuGlnAenLeuArg 315
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; APPLICANT: Meade, Thomas
; TITLE OF INVENTION: Mixing and Matching TC Proteins for Pest Control
; FILE REFERENCE: DAS-104XC1
; CURRENT APPLICATION NUMBER: US/10/754,115
; PRIOR FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US 60/441,723
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens strain W14
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1)..(2817)
US-10-754-115-57

Alignment Scores:
Pred. No.: 1,62e-242 Length: 2817
Score: 2956.00 Matches: 608
Percent Similarity: 73.01% Conservative: 90
Best Local Similarity: 63.60% Mismatches: 186
Query Match: 62.36% Indels: 72
DB: 8 Gaps: 14

US-10-647-956A-6 (1-915) x US-10-754-115-57 (1-2817)
Qy 1 MetSerTyrAnSerAlaileAaspGlnlysthrProSerIleLysValLeuAspAsn 20
Db 1 ATGGAACATTCAGCCCAAACTTTATCACCATACGCTACCGTCAGGTTCACGATAAC 60
Qy 21 ArgLysLeuAnValArgThrLeuGluTyrLeuArgThrGlnAlaAaspGluAnSerAsp 40
Db 61 CGTGACTAGTATCGTGAATATTAGTTTTCACCGCATACCGCAGAGCAATACCGAT 120
Qy 41 GluLeuIleThrPheTyrGluPheAnIleProGlyPheGlnValLysSerThrAspPro 60
Db 121 ACCGCTATTACCGCATCAATATAATGCCGGCGGATATTGAAACCAAGCATTTGATCCT 180
Qy 61 Arg-----LysAnLysAsnGlnSerGlyProAnPheIleArgValPhe 75
Db 181 CGCTGTATGACGCCAAACAGACAGTAAACACCTGTACAAACGAATTTTATCTGCGCAT 240
Qy 76 AnLeuAlaGlyGlnValLeuArgGluSerValAspAlaGlyArgThrIleThrLeu 95
Db 241 AATTGACCGGCAATATCTCGAAGACAGAGCGTTCGATGCGGTTCGACGATTTACCCCTC 300
Qy 96 AnAspIleGluSerArgProValLeuIleIleAnAlaThrGlyValArgGlnAnHis 115
Db 301 AACGATATTGAAGCCCGCGGTGTGACCATCAATGACGCGGTGTTCGGCAAAACCAT 360
Qy 116 ArgTyrGluAspAnThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAla 135
Db 361 CGCTAGGAAGATAACACCTCGCGGTGCTGCTGCTGCTATCAGCGAAACAGGACAGGCA 420
Qy 136 GlyGluLysThrThrGluArgLeuIleThrAlaGlyAnThrProGlnGluLysAspTyr 155
Db 421 GAAGAGAAACGACGAGCGCTTATCTGCGCGGCAATACGCGCGCAAGAAAAAGACCC 480
Qy 156 AnLeuAlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAnSer 175
Db 481 AACCTTCGCGTTCAGTGGCTCGCCATTTACGATACCGGAGGACTCACTCAACTCAACAGC 540
Qy 176 LeuSerLeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAspAnGlnAsp 195
Db 541 CTGCGCTCGACCGCGCGCTTCTATCAACTCTCAACAACTGCTTACCGATAACCGGAT 600
Qy 196 AlaAspThrThrGlyGluAspGlnSerLeuThrGlnGlnLysLeuSerSerAspValTyr 215
Db 601 GCCGACTGGACAGGTGAAGACAGAGCCTCTGGCAACAAACAACTGAGTAGTGTCTAT 660
Qy 216 IleThrGlnSerAnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGly 235
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Db 661 ATCACCCAAAGTAACACTGATGCCCGGGCTTTACTGACCAGACCGATGCCAAAGGC 720
Qy 236 AnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLeuLysGlySerTyrLeuThrLeu 255
Db 721 AACATTCAGCGCTGCGCTATGATGTGGCGGCGAGCTAAAGAGGAGTGTGTTAACTC 780
Qy 256 LysGlyGlnAlaGluGlnValIleIleLysSerLeuThrTyrSerAlaAlaGlyGlnLys 275
Db 781 AAAGGTGAGCGGGAACAGGTGATATCAAACTGCTAACCTACTCCGCGCGCGGCAAAA 840
Qy 276 LeuArgGluGluHisGlyAnGlyIleValThrGluTyrSerTyrGluProGluThrGln 295
Db 841 TTACGTGAAGAGACACGTAACGGATTGTCACTGAATACAGCTACGAACCGGAACCAA 900
Qy 296 ArgLeuIleGlyIleThrThrArgArgProSerAspAlaLysValLeuGlnAnAspLeuArg 315
Db 901 CGGCTTATCGGCATTTACCACTCGCCGTCATCAGACGCCAAGGTGTTCGAAGACCTACGC 960
Qy 316 TyrGlnTyrAspProValGlyAnValIleAnIleArgAnAspAlaGluAlaThrArg 335
Db 961 TATCAATATGACCCAGTAGGCAATGTCATTTAGTATCGGTAAATGATGCGGAAGCCACTCGC 1020
Qy 336 PheTyrArgAnGlnLysValAlaProGluAnSerTyrThrTyrAspSerLeuTyrGln 355
Db 1021 TTTTGGCGCAATCAGAAAGTAGCCCGGAGATAGCTATACCTACGATTCCCTGTATCAG 1080
Qy 356 LeuIleSerAlaThrGlyArgGluMetAlaAnIleGlyGlnGlnAnAnGlnLeuPro 375
Db 1081 CTTATCAGCCGCCACCGCGCGAGATGGCCAATATCGGTGAGCAACCAACCACTTTCCC 1140
Qy 376 SerProAlaLeuProSerAspAnAnThrTyrThrAnTyrThrArgSerTyrSerTyr 395
Db 1141 TCTCCGCGCTACTCTTGATAACAATACCTACCACTATATCTCGCACTTATCTACTTAT 1200
Qy 396 AspHisSerGlyAnLeuThrGlnIleArgHisSerSerProAlaThrGlnAnAnSerTyr 415
Db 1201 GACCGTGGCGCAATTTGACGAAATTCAGCATAGTTTCCACGCGCGCAAAATAACTAC 1260
Qy 416 ThrValAlaIleThrLeuSerAnArgSerAnArgGlyValLeuSerThrLeuThrThr 435
Db 1261 ACGACGGATATAACGGTTTCAAAATCGCAGCAACCGCGGTACTCAGCACATTGACCGCA 1320
Qy 436 AspProAnGlnValAspThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuPro 455
Db 1321 GATCCAACTCAAGTCGATGCTTATTTGATGCGGAGGCCATCAACACGAGCTGTATTCC 1380
Qy 456 GlyGlnThrLeuIleThrThrProArgGlyGluLeuLysGlnValAnAnGlyProGly 475
Db 1381 GGCCAAAGTCTTAAGTTCGACACCGCGAGCGCAATTTGAAACAAAGCAACAATAGCGCAGGA 1440
Qy 476 AnGluTyrTyrArgTyrAspSerAnGlyMetArgGlnLeuLysValSerGluGlnPro 495
Db 1441 AATGAGTGGTATCGCTACGATAGCACCGCATACCGCAGCTAAAGTGAATGAACAACAA 1500
Qy 496 ThrGlnAnThrThrGlnGlnAlaGlyValIleTyrLeuProGlyLeuLeuLeuArgThr 515
Db 1501 ACTCAGAAATATCCCGCAACCAACAAAGGTAACCTTATCTACCGGGCTGTGAATACGTACA 1560
Qy 516 ThrGlnSerAnAlaThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGly 535
Db 1561 ACCCAGAAACACGCCCAACACAGAGAGTTACACGTATTACACTTCGCTAAAGCGCGC 1620
Qy 536 ArgAlaGlnValArgValLeuHisTyrGluSerGlyLysProGluAnAspValAnAsn 555
Db 1621 CGCGCGAAGTCCGAGTATTGCAATTTGGAGCGCGTAAACAGAGAGATATTAATTAACAAT 1680
Qy 556 GlnLeuArgTyrSerTyrAspAnLeuIleGlySerSerGlnLeuGluLeuAspAnGln 575
Db 1681 CAGCTTCTGATACAGTACGATATCTTATTGGCTCCAGCCCACTTCAATTAGATAGCGAC 1740
Qy 576 GlyGlnIleLeuSerGluGluTyrTyrProPheGlyGlyThrAlaLeuThrAlaAla 595
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1741	Db	GGACAAATATTCAGTGAAGAAGAAATATATTCATTTGGTGGTACAGCGCTGTGGCGCGCA	1801
596	Qy	AsnSerGlnThrGluAlaSerTyrLysThrIleArgTyrSerGlyLysGluArgAspAla	615
1801	Db	AGGAATCAAAACCGAAGCCAGCTATAAACCATTCGTTATTCTGGTAAAGAGCGGATGTT	1860
616	Qy	ThrGlyLeuTyrTyrTyrGlyTyrArgTyrTyrGlnProThrAlaGlyArgTrpLeuSer	635
1861	Db	ACCGGGCTGTATTATTATGGCTACCGTATTATACCAACCGTGGCGGCGACAGTGGTAGGT	1920
636	Qy	AlaAspProAlaGlyThrIleAspGlyLeuAsnLeuTyrArgMetValArgAsnAsnPro	655
1921	Db	GCAGCCCGCAGCAACCATTTGATGGACTGAATTTATCGATGGTGAGAAATAACCCG	1980
656	Qy	ValSerLeuGlnAspGluAsnGlyLeuAlaPro	666
1981	Db	GTGACGCAATTTGATGTTTCAGGGATTATCACCGCCCAACAGACAGAAGCGATAATA	2040
667	Qy	GluLysGlyLysTyrThrLysGluValAsnPheAspGluLeuLysPheLysLeuAla	686
2041	Db	AAACAGGGTTCCTTTTACGGGA-----ATGGAAGAAGCTGTTTATAAAAAAATG	2088
687	Qy	AlaLys-----SerSerHisValValLysTrpAsnGluLysGluSer	700
2089	Db	GCTAAACCTCAAACTTCAACAGCCAAAGAGCTATCGTCCCAACAGAGCAAGAAGCC	2148
701	Qy	-----SerTyrThrLysAsnLysSerLeuLysValValArgValGlyAspSerAspPro	718
2149	Db	CATGAATCATTGACCAACACCCCTAGTGTAGATATT-----AGCCCAATT	2193
719	Qy	SerGlyTyrLeuLeuSerHisGluGluLeuLysGlyIleGluLysSerGlnIleIle	738
2194	Db	AAAACTACACCACAGATAGCTCACAAATAATGCCGCGATAAGGGAATAATCGTATTACG	2253
739	Qy	TyrSerArgLeuGluGluAsnSerSerLeuSerGluLysSerLysThrAsnLeuSerLeu	758
2254	Db	CCAGCAGTGGAAAGTTTGACGCGCACATATTCTTCCCTACAAGATAGCAAAATGAGGGTA	2313
759	Qy	GlySerGluIleSerGlyTyrMetAlaArgThr-----	769
2314	Db	ACTTATCGGTGATGACCTATGTAGATAATTCCAGCGCATCGCTTGGCACTGCCACAG	2373
770	Qy	-----IleGlnAspThrIleSerGluTyrAla-----Glu	779
2374	Db	GAAGGAAATAGTATTAAATGTTGGTGATATCGTTTCGGATAACGCTTATTTTCAACATCG	2433
780	Qy	GluHisLysTyrArgSerAsn-----HisProAspPheTyrSerGluThrAspPhe---	796
2434	Db	GCCCATCGTGGTTTTCTGGAATTTTGTTCACAAAAAGAAACCAAGTGAACCTCGATCGTC	2493
797	Qy	--PheAlaLeuMetAspLysSerGluLysAsn-----AspTyr	808
2494	Db	AAGATGCAATTTTAAACGATGCGGGTGTCATGTCCAGCAGCATCTATGTATAATAAT	2553
809	Qy	SerGlyGluArgLysIleTyrAlaAlaMetGluValLysValTyrHisAspLeuLysAsn	828
2554	Db	GCTGCGCAGGACCAAGTATTAAAAATG-----GATTTAAACGAT	2592
829	Qy	LysGlnSerGluLeuHisValAsnTyrAlaLeuAlaHisProTyrThrGlnLeuSerAsn	848
2593	Db	TCAGAAAAAGCCTTGCTGAAAAATTTAAACTACGTACGTGACCAACATCGGAGCAA	2652
849	Qy	GluGluArgAlaLeuLeuGlnThrGluProAlaIleAlaIleAspArgGluTyrAsn	868
2653	Db	GCGGAATATTACTCTAGGGAACACAGTTTCAAGTTGTT-----TCAATGAAA	2703
869	Qy	PheLysGlyValGlyLysPheLeuThrMetLysAlaIleLysLysSerLeuLysGlyHis	888
2704	Db	CATCAAGCAGAGATACCTATGTATTATTGCAAGATATTAAACCAATCCGAGCCACTCAT	2763
889	Qy	LysIleAsnArgIleSerThrGluAlaIleAsnIleArgSerAlaAla	904
2764	Db	AGA---AATGTACGTAACTACTACACCGGTAAATTTCAATCATCTCCACT	2808

RESULT 6

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US-10-706-424-11
; Sequence 11, Application US/10706424
; Publication No. US20040103455A1
;
; GENERAL INFORMATION:
; APPLICANT: ffrench-Constant, Richard
; APPLICANT: WATERFIELD, Nicholas
; TITLE OF INVENTION: DNA Sequences from tC
; FILE REFERENCE: 62878
; CURRENT APPLICATION NUMBER: US/10/706,424
; CURRENT FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 2883
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2880)
US-10-706-424-11

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Alignment Scores:		
Pred. No.:	1.12e-206	Length:
Score:	2537.50	Matches:
Percent Similarity:	74.12%	Conservative:
Best Local Similarity:	62.94%	Mismatches:
Query Match:	53.53%	Indels:
DB:	7	Gaps:
		12
		2883

US-10-647-956A-6 (1-915) X US-10-706-424-11 (1-2883)

Qy	1	MetSerSerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn	20
Db	1	ATCAAAAACATTGATCCCAAACTTTATCAAAAAACCCCTACTGTGCAGCGTTTACGATAAC	60
Qy	21	ArgLysLeuAsnValArgThrLeuGluLysLeuArgThrGlnAlaAspGluAsnSerAsp	40
Db	61	CGTGGTCTGATAATCCGTAACATCGATTTTCATCGTACTACCGCAATAGTGTATCCCGAT	120
Qy	41	GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro	60
Db	121	ACCCGTATTACCCGCCCATCAATACGATATTACCGACACCTAAATCAAAAGCATCGATCCG	180
Qy	61	Arg-----LysAsnLysAsnGlnSerGlyProAsnPheIleArgValPhe	75
Db	181	CGCCTATATGAAGCCACGACCAACCAATACGATCAAAACCCCAATTTCTTTGGCAGTAT	240
Qy	76	AsnLeuAlaGlyGlnValLeuArgGluLysSerValAspAlaGlyArgThrIleThrLeu	95
Db	241	GATTTTGACCGGTAATCCCTCTATGTACAGAGAGCAATTGATGCAGGTCCGACTGTACACCTTG	300
Qy	96	AsnAspIleGluSerArgProValLeuIleIleAsnAlaThrGlyValArgGlnAsnHis	115
Db	301	AATGATATTGAAGGCGGTCCGCTACTAAACGGTGACTGCACACGGGGTTATACAAACTCGA	360
Qy	116	ArgTyrGluAspAsnThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAla	135
Db	361	CAATATGAACACTTCTTCGCTGCCGGTGGTCTGTATTCTGTGTGCCGAACAAACACCCGAG	420
Qy	136	GlyGluLysThr-----ThrGluArgGluIleTrpAlaGlyAsnThrProGlnGlu	155
Db	421	---GAAAAAAACATCCCGTATACCCGAACGCTGATTTGGGCTGGCAATACCGAAGCAGAG	477
Qy	153	LysAspTyrAsnLeuAlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGln	172
Db	478	AAAGACCATAACCTTGCCGGCCAGTGGCGTGCCTACTACTATGCACGCGGGGAGTTACCCGG	537
Qy	173	LeuAsnSerLeuSerLeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAsp	192
Db	538	TTAGAGAGTTTATCACTGACCGGTACTGTTTATCTCAATCCAGCCCAACTATTGATCGAC	597


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; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
; LENGTH: 2883
; TYPE: DNA
; ORGANISM: Photorhabdus strain W14
US-10-609-113-46

Alignment Scores:
Pred. No.:      1.12e-206      Length:      2883
Score:          2537.50      Matches:     518
Percent Similarity: 74.12%      Conservative: 92
Best Local Similarity: 62.94%      Mismatches: 159
Query Match:      53.53%      Indels:      55
DB:                7          Gaps:         12

US-10-647-956A-6 (1-915) x US-10-609-113-46 (1-2883)

QY      1 MetSerSerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn 20
DB      1 ATGAAAAACATTGATCCCAACTTTATCAAAAACCCCTACTGTACGCGTTTACGATAAC 60

QY      21 ArgLysLeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAsnSerAsp 40
DB      61 CGTGGTCTGATATCCGTAACATCGATTTTCATCGTACTACCGCAATGGTGTATCCGAT 120

QY      41 GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro 60
DB      121 ACCCGTATTACCCGCCATCAATACGATATTTCACGGACACCTAAATCAAAGCATCGATCCG 180

QY      61 Arg-----LysAsnLysAsnGlnSerGlyProAsnPhelleArgValPhe 75
DB      181 CGCCTATATGAAGCCCAAGCAACCAACAATACGATCAAAACCCCAATTTCTTTGGCAGTAT 240

QY      76 AsnLeuAlaGlyGlnValLeuArgGluGluSerValAspAlaGlyArgThrIleThrLeu 95
DB      241 GATTTGACCGGTAAATCCCTCTATGTACAGAGCATTTGATCGAGTGCACATGTCACCTTG 300

QY      96 AsnAspIleGluSerArgProValLeuIleAsnAlaThrGlyValArgGlnAsnHis 115
DB      301 AATGATATTGAAGCCGTCGCTACTAAACGGTGACTGCAACAGGGGTATACAAACTCGA 360

QY      116 ArgTyrGluAspAsnThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAla 135
DB      361 CAATATGAACATTCTTCCCTGCGCGTCTGCTGTATCTGTTGCCGAACAAACACCCGAG 420

QY      136 GlyGluLysThr-----ThrGluArgLeuIleThrAlaGlyAsnThrProGlnGlu 152
DB      421 ---GAAAAACATCCCGTATFCACCGAACCGCTGATTTGGGCTGGCAATACCGAAGCAGAG 477

QY      153 LysAspTyrAsnLeuAlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGln 172
DB      478 AAAGACCAATACCTTTCGCGCCAGTGGTGGTCTACTATGACACGCGGGGAGTTACCCGG 537

QY      173 LeuAsnSerLeuSerLeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAsp 192
DB      538 TTAGAGAGTTTATCACTGACCGGTACTGTTTATCTCAATCCAGCCAACTATTGATCGAC 597

QY      193 AsnGlnAspAlaAspThrPheTyrGlyLysAspGlnSerLeuTrpGlnGlnLysLeuSerSer 212
DB      598 ACTCAAGAGGCAAACTGGACAGGTGATTAACGAAACCGCTCTGGCAAAACATGCTGGCTGAT 657

QY      213 AspValTyrIleThrGlnSerAsnThrAspAlaThrGlyValAlaLeuLeuThrAsp 232
DB      658 GACATCTACACACCTTGACACCTTCGATGCCACCGGTGCTTTACTGACTCAGACCGAT 717

QY      233 AlaLysGlyAsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLeuLysGlySerTrp 252
DB      718 GCGAAAGGGAACATTACAGACTGGCTTATGATGTGGCGGGCAGCTAAACGGGAGCTGG 777

QY      253 LeuThrLeuLysGlyGlnAlaGluGlnValIleIleLysSerLeuThrTyrSerAlaAla 272
DB      778 CTAAACACTCAAGGCCAGACGGAACAGTGATTTATCAAAATCCCTGACCTACTCCCGCGCC 837
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QY      273 GlyGlnLysLeuArgGluGluHisGlyAsnGlyIleValThrGluTyrSerTyrGluPro 292
DB      838 GGACAAAAATTACGTGAGGAACACGCAATATGATGTTATCACCGAATACAGTTATGAACCG 897

QY      293 GluThrGlnArgLeuIleGlyIleThrArgArgProSerAspAlaLysValLeuGln 312
DB      898 GAAACCCAAACGGCTGATCGTATCAAAACCCGCGTCGTCAGACACTAAAGTGCTACAA 957

QY      313 AspLeuArgTyrGlnTyrAspProValGlyAsnValIleAsnIleArgAsnAspAlaGlu 332
DB      958 GACCTGGCTATGAATATGACCGGTAGGCAATGTCTATCAGCATCCGTAATGACGCGGA 1017

QY      333 AlaThrArgPheTrpArgAsnGlnLysValAlaProGluAsnSerTyrThrTyrAspSer 352
DB      1018 GCCACCCGCTTTTGGCACAATCAGAAAGTGATGCGGAAACACTTATACCTACGATTC 1077

QY      353 LeuTyrGlnLeuIleSerAlaThrGlyArgGluMetAlaAsnIleGlyGlnGlnAsnAsn 372
DB      1078 CTGTATCAGCTTATCAGCCGCCCGGCGGCAATGGCAATATAGGTCAACAAAGTCAC 1137

QY      373 GlnLeuProSerProAlaLeuProSerAspAsnAsnThrTyrThrAsnTyrThrArgSer 392
DB      1138 CAATTTCCTCACCCTCTACTCTCTGATTAACAACACCTATACCACTATATACCCGTACT 1197

QY      393 TyrSerTyrAspHisSerGlyAsnLeuThrGlnIleArgHisSerSerProAlaThrGln 412
DB      1198 TATACTTATGACCGTGGCGCAATCTGACCAAAATCCAGCACAGTTCCACGGGAGCGCA 1257

QY      413 AsnAsnTyrThrValAlaIleThrLeuSerAsnArgSerAsnArgGlyValLeuSerThr 432
DB      1258 AACAACTACACCAACCAATATCAGGTTTCAAAATCGCAGAACCGCGCAGTACTCAGCAC 1317

QY      433 LeuThrThrAspProAsnGlnValAspThrLeuPheAspAlaGlyHisGlnThrSer 452
DB      1318 TTGACCGAAGATCCCGCGCAGTAGTGTCTTGTGTTGATGCGCGCGGACATCAGAACC 1377

QY      453 LeuLeuProGlyGlnThrLeuIleThrProArgGlyGlyLeuLysGlnVal----- 470
DB      1378 TTGATATCAGGACAAACCTGAACTACTCGTGGTGAACCTGCAACAAAGTAACACTG 1437

QY      471 -----AsnAsnGlyProGlyAsn-----GluTyrTyrArgTyrAspSerAsnGly 495
DB      1438 GTTAAACGGGACAAAGCGCGCCAAATGATGATCGGGAATGTTATCGTTATAGCGTACGGA 1497

QY      486 MetArgGlnLeuLysValSerGluGlnProThrGlnAsnThrThrGlnGlnArgVal 505
DB      1498 AGAAGGATGTTAAATCAATGAACAGCAGGCGCAGCAACAGCTCAACACAACTGTGTG 1557

QY      506 IleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAlaThrThrThrGluGlu 525
DB      1558 ACTTATTTCCGGAACCTTAGAATCTGCTCTAACACAAACAGCAGCAGCCCAACCGAAGAT 1617

QY      526 LeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArgValLeuHisTrpGlu 545
DB      1618 TTGCAAGTTATCACCCTGAGCGAAGCGGCGCGGACAGGTACGAGTATTACATTGGGAG 1677

QY      546 SerGlyLysProGluAspValAsnAsnAsnGlnLeuArgTyrSerTyrAspAsnLeuIle 565
DB      1678 AGCGGTAAACCCGGAAGATATCGCAATAATAGTTGCGTTATAGTTACGATTAATCTTATC 1737

QY      566 GlySerSerGlnLeuLeuAspAsnGlnGlyGlnIleIleSerGluGluGluTyrTyr 585
DB      1738 GGTTCAGTCACTTGAATTAGTAGCGAAGGACAAATTTATCAGTGAAGAGAATATTAT 1797

QY      586 ProPheGlyGlyThrAlaLeuTrpAlaAlaAsnSerGlnThrGluAlaSerTyrLysThr 605
DB      1798 CCTATGTTGGAACAGCATTTATGGCGCGCGCAGGAATCAGACAGAGCCAGTTATAAACT 1857

QY      606 IleArgTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyrTyrGlyTyrArgTyr 625
DB      1858 ATCCGTTATTCAGGCAAGAGCGGATGCCCGGCTATATTACTACGGCTATTCGGTAT 1917
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Qy 626 TyrGlnProTrpAlaGlyArgTrpLeuSerAlaAspProAlaGlyThrIleAspGlyLeu 645
Db 1918 TACCAACCGTGGATAGACCGGTGGTAAAGCTCCGATCCGGCAGGAAACAATGATGGGCTG 1977
Qy 646 AsnLeuTyrArgMetValArgAsnAsnProValSerLeuGlnAspGluAsnGlyLeuAla 665
Db 1978 AATTTATATCGGATGGTGGAGGAATAATCCAGTACCCTCCTTGATCCTCGATGATTAATG 2037
Qy 666 Pro-----GluLysGlyLysTyrThr----- 672
Db 2038 CCAACAATTGAGAACGCATAGCAGCACTAAATAAATAAAGTAACAGACTCAGCGCCT 2097
Qy 673 -----LysGluValAsnPheAspGluLeuLysPheLysLeuAlaAlaLysSer 689
Db 2098 TCGCCAGCAATGCCAACAACGCTAGCAGTAACATCCGCCGCTGTAGCACCAAACT 2157
Qy 690 SerHisValVallystPheAsnGluLysGluSerTyrThrTyrAsnLysSerLeuLys 709
Db 2158 AGCTT-ACCGAAAGCATCAAGAGTAGCAACCAACACACACCTTATCGAGCTGCAAA 2216
Qy 710 -----ValValArg-ValGlyAspSerAspProSerGlyTyrLe 722
Db 2217 CATAAAAACCAACGAGCTGGGTCTATCTATTGTTGCTCCATTGAGTCCAGTAGGAATAA 2276
Qy 722 uLeuSerHisGluGluLeuLysGlyIleGluLysSerGlnIleIleTyrSerArgLe 742
Db 2277 ATCTACTTCTGAAATCTCTCTGCCA-----GAAAGCGCTCA----- 2313
Qy 742 uGluGluAsnSerSerLeuSerGluLysSerLysThrAsnLeuSerLeuGlySerGluI 762
Db 2314 -----AGCAGTTCTTCAACGACACTACCTCGACAAATCTACAGAAAAATCA---TT 2360
Qy 762 eSerGlyTyrMetAla-----ArgThrIleGluAspThrIleSerGluTyrAlaGlu 780
Db 2361 TACTTTATAGACGATACAGATCCTTTTGAAGAAATGCAAAAGTAAATTCCTCGAAGG 2420
Qy 780 uHisLys 782
Db 2421 ATTTAAA 2427

RESULT 8
US-10-754-115-46
; Sequence 46, Application US/10754115
; Publication No. US20040208907A1
; GENERAL INFORMATION:
; APPLICANT: Hey, Timothy
; APPLICANT: Schleper, Amanda
; APPLICANT: Bevan, Scott
; APPLICANT: Bintrim, Scott
; APPLICANT: Mitchell, Jon
; APPLICANT: Li, Ze Sheng
; APPLICANT: Ni, Weiting
; APPLICANT: Zhu, Baolong
; APPLICANT: Merlo, Don
; APPLICANT: Apel-Birkhold, Patricia
; APPLICANT: Meade, Thomas
; TITLE OF INVENTION: Mixing and Matching TC Proteins for Pest Control
; FILE REFERENCE: DAS-104XC1
; CURRENT APPLICATION NUMBER: US/10/754,115
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US 60/441,723
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
; LENGTH: 2883
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2880)
US-10-754-115-46
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Alignment Scores:
Pred. No.: 1-12e-206 Length: 2883
Score: 2537.50 Matches: 518
Percent Similarity: 74.12% Conservative: 92
Best Local Similarity: 62.94% Mismatches: 159
Query Match: 53.53% Indels: 55
DB: 8 Gaps: 12

US-10-647-956A-6 (1-915) x US-10-754-115-46 (1-2883)

Qy 1 MetSerSerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn 20
Db 1 ATGAAAAACATTGATCCCAAACTTTATCAAAAACCCCTACTGTCCAGCGTTTACGATAAC 60
Qy 21 ArgLysLeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAsnSerAsp 40
Db 61 CGTGGTCTGATAATCCGTAACATCATGATTTCATCGTACTACCCGAATAGTGATCCCGAT 120
Qy 41 GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro 60
Db 121 ACCCGTATTACCGCCCATCAATACGATATTACGGGACACCTAAATCAAGCATCGATCCG 180
Qy 61 Arg-----LysAsnLysAsnGlnSerGlyProAsnPheIleArgValPhe 75
Db 181 CGCCTATATGAGCCCAAGCAACCAACAATACGATCAAAACCCCAATTTCTTTGGCAGTAT 240
Qy 76 AsnLeuAlaGlyGlnValLeuArgGluSerValAspAlaGlyArgThrIleThrLeu 95
Db 241 GATTTCACCGGTAATCCCTCATGTACAGAGAGCATTTGATGCGAGTGCACCTGTCCACTTG 300
Qy 96 AsnAspIleGluSerArgProValLeuIleIleAsnAlaThrGlyValArgGlnAsnHis 115
Db 301 AATGATATTGAGCGCGCTCGCTACTTAACGGTGACTGCAACAGGGGTATACAACTCGA 360
Qy 116 ArgTyrGluAspAsnThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAla 135
Db 361 CAATATGAAACTTCTTCCCTGCCGCTCGTCTGTTATCTGTCGCCGAAACAACCCCGAG 420
Qy 136 GlyLysLysThr-----ThrGluArgLeuIleTrpAlaGlyAsnThrProGlnGlu 152
Db 421 ---GAAAAAACATCCCGTATCACCGAACCGCTGATTTGGGCTGGCAATACCGAAGCAGAG 477
Qy 153 LysAspTyrAsnLeuAlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGln 172
Db 478 AAGAGCATTAACCTTGGCGCCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 537
Qy 173 LeuAsnSerLeuSerLeuAlaGlyValValLeuSerGlnSerGlnLeuLeuLeuThrAsp 192
Db 538 TTAGAGAGTTTATCACTGACCGGTACTGTTTATCTCAATCCAGCCAACTATTGATCGAC 597
Qy 193 AsnGlnAspAlaAspTrpThrGlyGluAspGlnSerLeuTrpGlnLysLeuSerSer 212
Db 598 ACTCAAGAGGCAAACTGGACAGGTGATACGAAACCGCTCTGGCAAAACATGCTGGCTGAT 657
Qy 213 AspValTyrIleThrGlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAsp 232
Db 658 GATCTACCAACACCTCGACACCTTCGATGCCACCGGTGCTTTACTGACTCAGACCGAT 717
Qy 233 AlaLysGlyAsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLeuLysGlySerTrp 252
Db 718 GCGAAAGGGAACATTCAGAGACTGGCTTATGATGTGGCGCGGAGCTAAACGGGAGCTGG 777
Qy 253 LeuThrLeuLysGlyGlnAlaGluGlnValIleIleLysSerLeuThrThrSerAlaAla 272
Db 778 CTAACTCAAGGCCACAGCGGAACAGTATTATCAAAATCCCTGACTACTCTCCGCCGCC 837
Qy 273 GlyGlnLysLeuArgGluGluHisGlyAsnGlyIleValThrGluTyrSerTyrGluPro 292
Db 838 GGACAAAAAATTACGTGGGAAACACGCGAATGATGTTATCACCAGATACAGTTATGAACCG 897
Qy 293 GluThrGlnArgLeuIleGlyIleThrThrArgProSerAspAlaLysValLeuGln 312
Db 898 GAAACCCCAACGGCTGATCGGTATCAAAAACCCCGCGTCCGTCCAGACACTAAAGTCTACAA 957
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RESULT 10

US-10-609-113-47
; Sequence 47, Application US/10609113
; Publication No. US20040110184A1
; GENERAL INFORMATION:
; APPLICANT: Bintrim, Scott
; APPLICANT: Bevan, Scott
; APPLICANT: Zhu, Baolong
; APPLICANT: Merlo, Donald J.
; TITLE OF INVENTION: Pesticidally Active Proteins and Polynucleotides Obtainable from
; FILE REFERENCE: DAS-101XC2
; CURRENT APPLICATION NUMBER: US/10/609,113
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US 60/392,633
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/441,647
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47
; LENGTH: 2850
; TYPE: DNA
; ORGANISM: Photorhabdus strain W14
US-10-609-113-47

Alignment Scores:

Pred. No.: 1,68e-204 Length: 2850
Score: 2512.00 Matches: 497
Percent Similarity: 76.17% Conservatives: 88
Best Local Similarity: 64.71% Mismatches: 143
Query Match: 53.00% Indels: 40
DB: 7 Gaps: 10

US-10-647-956A-6 (1-915) x US-10-609-113-47 (1-2850)

QY 1 MetSerSerTyrAsnSerAlaIleApsGlnLysThrProSerIleLysValLeuAspAsn 20
||| : : : : :
DB 1 ATGAAAAACATTGACCCCAAACTTTATCAATACAGCCCAACCGTAAACGCTACGATAAC 60
QY 21 ArgLysLeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAsnSerAsp 40
||| : : : : :
DB 61 CGTGGCCCTGACCAATCGTAACATCGACTTTCCAGCCGACGTCGCGGAGCGATACAGAT 120
QY 41 GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro 60
||| : : : : :
DB 121 ACTCGTATTACCGCCCAACCAATATGATACCCGAGGACACTTGAGCCAAAGCATTGATCCA 180
QY 61 Arg-----LysAsnLysAsnGlnSerGlyProAsnPhelIleArgValPhe 75
||| : : : : :
DB 181 CGGCTGTATGACGCCAAACAAACCAATAACTCGACAAACCCCAACTTCCTCTGGCAATAC 240
QY 76 AsnLeuAlaGlyGlnValLeuArgGluSerValAspAlaGlyArgThrIleThrLeu 95
||| : : : : :
DB 241 AATCTCACCGCGGACACTTTGCGGACAGAAAGTGTGATGCGCGCGGTACCGTAGCCCTC 300
QY 96 AsnAspIleGluSerArgProValLeuIleAsnAlaThrGlyValArgGlnAsnHis 115
||| : : : : :
DB 301 AATGATATTGAGCGCGTCAAGTGTGATTTGATTAACCGCAACCGCGCCATTACAGCCGA 360
QY 116 ArgTyrGluAspAsnThrLeuProGlyArgLeuLeuAlaIleThrGlnValGlnAla 135
||| : : : : :
DB 361 CAATATGAAGCAATACCTGCGCGTCTGCTATTATCCGTAAGTGAACAAGCC---CCC 417
QY 136 GlyGluLysThr-----ThrGluArgLeuIleThrAlaGlyAsnThrProGlnGlu 152
||| : : : : :
DB 418 GGAGAACAGACTCCCGCGCTTACTGAGCATTTTATTTGGCTGGTAAATACACAGCGCGAG 477
QY 153 LysAspTyrAsnLeuAlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGln 172
||| : : : : :
DB 478 AAAGATCATTAATCTTGCGCGCCAGTATGTGCGCCACTTACGACACAGCAGGAGTGAACGCA 537

QY 173 LeuAsnSerLeuSerLeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAsp 192
||| : : : : :
DB 538 CTGGAAGAGCTGTCAATTGACAGAAAACATCTTATCTCAATCCCGTCACTTATTATGCGGAC 597
QY 193 AsnGlnAspAlaAspTyrThrGlyGluAspGlnSerLeuTyrGlnGlnLysLeuSerSer 212
||| : : : : :
DB 598 GGTGAGAGAGAGACTGGACAGGTACGATGAACCCCTCTGGCAGACCAAACTCAATAGC 657
QY 213 AspValTyrIleThrGlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAsp 232
||| : : : : :
DB 658 GAAACTTACAGACACAAAGCACCTTTGATGCTACCGCGCTTTGCTGACCCAAACCGAT 717
QY 233 AlaLysGlyAsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLysLeuSerTyr 252
||| : : : : :
DB 718 GCAAAAGGCAACATGCAACGCTCTGGCTTACAACTGGCAGGACCAATTTACAAGTAGCTGG 777
QY 253 LeuThrLeuLysGlyGlnAlaGlnValIleLysSerLeuThrTyrSerAlaAla 272
||| : : : : :
DB 778 CTGACATTTGAAAACCAAGAGTGAGCAAGTCATTTGTCAATCCCTGACCTATTTCGCGCGCA 837
QY 273 GlyGlnLysLeuArgGluGluHisGlyAsnGlyIleValThrGluTyrSerTyrGluPro 292
||| : : : : :
DB 838 GGCAGAAATTCGCTGAAGAACACGCTAATGGCGTTATCACTGAATACAGCTATGAACCG 897
QY 293 GluThrGlnArgLeuIleGlyIleThrThrArgArgProSerAspAlaLysValLeuGln 312
||| : : : : :
DB 898 GAAACTCTACGATTGATCGGTACCACTACTCGCGCTCAATTCAGATAGCAAGGTGTACAA 957
QY 313 AspLeuArgTyrGlnTyrAspProValGlyAsnValIleAsnIleArgAsnAspAlaGlu 332
||| : : : : :
DB 958 GATCTACGCTATGAACATGATCTGTAGGGAATATTATTAGTCTCGTATGATGAGAA 1017
QY 333 AlaThrArgPheTyrArgAsnGlnLysValAlaProGluAsnSerTyrThrTyrAspSer 352
||| : : : : :
DB 1018 GCCACCGCTTCTGGCGCAATCAGAAATAGTCCCTGAAATACCTTACCTACGATTCC 1077
QY 353 LeuTyrGlnLeuIleSerAlaThrGlyArgGluMetAlaAsnIleGlyGlnGlnAsnAsn 372
||| : : : : :
DB 1078 CTGTATCAGCTTATCAGTCAACAGACGCTGAGATGGCTTAACATCGGCCCAAGCAAC 1137
QY 373 GlnLeuProSerPro-----AlaLeuProSerAspAsnAsnThrTyrThrAsnTyrThr 390
||| : : : : :
DB 1138 CAACTTCTTTCGCAATCATCTCTCTCTCTGATGAAACCTCATATACCAATATACT 1197
QY 391 ArgSerTyrSerTyrAspHisSerGlyAsnLeuThrGlnIleArgHisSerSerProAla 410
||| : : : : :
DB 1198 CGCAGCTAATATTACGATCGCGCGCAATTTGGTTCAATCCGCGACAGTTCCCGCGCC 1257
QY 411 ThrGlnAsnAsnTyrThrValAlaIleThrLeuSerAsnAsnArgSerAsnArgGlyValLeu 430
||| : : : : :
DB 1258 GCCAAAATAAATACACACAGATATCACCGTTTCGAATCGCAGTAACCGGCGAGTCTG 1317
QY 431 SerThrLeuThrThrAspProAsnGlnValAspThrLeuPheAspAlaGlyGlyHisGln 450
||| : : : : :
DB 1318 AGTTCCTTAACCTCAGACCCAAACAGGTGGAGGCACTGTTTGTATCGCGCGACATCAA 1377
QY 451 ThrSerLeuLeuProGlyGlnThrLeuIleTyrThrProArgGlyGluLeuLysGlnVal 470
||| : : : : :
DB 1378 ACMAAATTTGTACCGGGCAAGAGCTGAGTTGGAATACAGAGGTGACACTAAAACAGGTA 1437
QY 471 -----AsnAsnGlyProGlyAsnGluTyrTyrArgTyrAspSerAsnGly 485
||| : : : : :
DB 1438 AGCCAGTCAGTCGCGAGAGCGCCAGCATCGGAATGGTATCGTTACGCAACAGCGGC 1497
QY 486 MetArgGlnLeuLysValSerGluGlnProThrGlnAsnThrThrGlnGlnArgVal 505
||| : : : : :
DB 1498 ATGCGAGCGTTAAAGTCAAGTGAACACAGACTGGCAACAGCAGCGCAGCAACAGGTA 1557
QY 506 IleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAlaThrThrThrGluGlu 525
||| : : : : :
DB 1558 ACTTATCTCCCGATCTGGAGCTACGTACACAAATAATGGGACTACTATCATCAGAAGAC 1617
QY 526 LeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArgValLeuHisTyrGlu 545

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Db 1618 CTGCATGCTATTACCGTGGAGCAGCAGCGCCACGACCAAGTGCAGATTCTACACTGGAA 1677
Qy 546 SerGlyLysProGluAspValAsnAsnGlnLeuArgTyrSerTyrAspAsnLeuLe 565
Db 1678 ACTAGCCACACCGCGGTATCAATAACAATCAGCTTCGCTATAGTATGATAATTTGATT 1737
Qy 566 GlySerGlnLeuGluLeuAspAsnGlnGlyGlnLeuLeuLeuLeuLeuLeuLeu 585
Db 1738 GGTTCAGTCACTTGAATCGGATACGAGGACAAATTTATCAGTCAGGAGAGATTAT 1797
Qy 586 ProPheGlyGlyThrAlaLeuTrpAlaAlaAsnSerGlnThrGluAlaSerTyrLysThr 605
Db 1798 CCATTGGCGCAGCAGCATTATGGCAGCAAGAAACCAATAGAACCCAGCTACAAATC 1857
Qy 606 IleArgTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyrGlyTyrArgTyr 625
Db 1858 CTCGGTTACTCAGTAAGAACCGGATGCTACCGGGCTTATTATTACGGCTACCGCTAT 1917
Qy 626 TyrGlnProTrpAlaGlyArgTyrLeuSerAlaAspProAlaGlyThrIleAspGlyLeu 645
Db 1918 TATCAGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1977
Qy 646 AsnLeuTyrArgMetValArgAsnAsnProValSerLeuGlnAspGluAsnGlyLeuAla 665
Db 1978 AATCTATACCGGATGGTGAGAAATAATCCGTCACACACTGGTGTGATATTCTCGGGCTTGCA 2037
Qy 666 ProGluLysGlyLysTyrThrLysGluValAsnPheAspGluLeuLysPheLysLeu 685
Db 2038 CCTACG-----AAATACAATATTTCCCGGATTTTGACTTTTGAT----- 2073
Qy 686 AlaAlaLysSerSerHisValValLysTrpAsnGluLysGluSerTyrThrLysAsn 705
Db 2074 -----GTAGAATAGATGAGCAAAAGATCTAAATTTAAACCA 2112
Qy 706 LysSerLeuLysValValArgValGlyAspSer-----AspProSerGlyTyr 721
Db 2113 -----ACGTTGATAAGAAATCAAGATGAATTTTACATTATGTCCTGTAGATAAG 2163
Qy 722 LeuLeuSerHisGluGluLeuLysGlyGlyLeuLysGlyGlyLeuLysGlyGlyLeuLys 741
Db 2164 CTGTTA-----GAAGAAAAAAACCCCGGCTCAATGTACCAGAGAGCTATTGTGATAGA 2217
Qy 742 LeuGluGluAsnSerSerLeuSer 749
Db 2218 GGTCCATCCGGAATGGAGTGTC 2241
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RESULT 11

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US-10-262-794A-60
; Sequence 60, Application US/10262794A
; Publication No. US20030207806A1
; GENERAL INFORMATION:
; APPLICANT: Ensign, Jerald C
; APPLICANT: Bowen, David J
; APPLICANT: Petell, James
; APPLICANT: Fatig, Raymond
; APPLICANT: Schoonover, Sue
; APPLICANT: French-Constant, Richard
; APPLICANT: Rocheleau, Thomas A.
; APPLICANT: Blackburn, Michael B.
; APPLICANT: Hey, Timothy D.
; APPLICANT: Merlo, Donald J.
; APPLICANT: Orr, Gregory L.
; APPLICANT: Roberts, Jean L.
; APPLICANT: Strickland, James A.
; APPLICANT: Guo, Lining
; APPLICANT: Ciche, Todd A.
; APPLICANT: Sukhupinda, Kitisri
; TITLE OF INVENTION: Insecticidal Protein Toxins From Photorhabdus
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dow Agrosciences Patent Department
; STREET: 9330 Zionsville Road
```

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; CITY: Indianapolis
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/262,794A
; FILING DATE: 02-OCT-2002
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: US 08/851,567
; FILING DATE: 05-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/063,615
; FILING DATE: 18-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/395,497
; FILING DATE: 28-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/007,255
; FILING DATE: 06-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/608,423
; FILING DATE: 28-FEB-1996
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/705,484
; FILING DATE: 28-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.93804
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3132 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-10-262-794A-60
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Alignment Scores:

Pred. No.:	1.35e-200	Length:	3132
Score:	2467.00	Matches:	470
Percent Similarity:	81.25%	Conservative:	89
Best Local Similarity:	68.31%	Mismatches:	111
Query Match:	52.05%	Indels:	18
DB:	6	Gaps:	5

US-10-647-956A-6 (1-915) x US-10-262-794A-60 (1-3132)

Qy	1	MetSerSerTyrAsnSerAlaLleAppGlnLysThrProSerIleLysValLeuAspAsn	20
Db	1	ATGAGTCCGTCGTGAGACTACTCTTTATCTACAAACCCCAACAGCTGCGTGTAGATAAT	60
Qy	21	ArgLysLeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAsnSerAsp	40
Db	61	CGCGGCTCTGCCAATTCGTGATATTGGTTTTCACCGTATTGTAATTCGGGGGGGATCTGAC	120
Qy	41	GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro	60
Db	121	ACCGCGCTACCCGTCACAGTATGATGCCCGTGGACACCTGACACTAGATTATGACCCA	180
Qy	61	Arg-----LysAsnLysAsnGlnSerGlyProAsnPheIleArgValPhe	75
Db	181	CGCTTGTATGATGCAAAAGCAGGCTGATACTAGTAAGCCTAATTTTGTCTGCGACGAT	240

QY 76 AsnLeuAlaGlyGlnValLeuArgGluSerValAspAlaGlyArgThrLeu 95
DB 241 GATCTGCGCGGTATGCTGCGGACAGAGAGTGTGCTGCTACTGTTGCAATTG 300
QY 96 AsnAspIleGluSerArgProValLeuIleAsnAlaThrGlyValArgGlnAsnHis 115
DB 301 ATGATATTGAAGGTCTGTCGGTAATAGCAATGAATGCGACCGGTCTGTCAGACCCGT 360
QY 116 ArgTyrGluAspAsnThrLeuProGlyArgLeuAlaIleThrGluGlnVal----- 133
DB 361 CGCTATGAAGGCAACACCTTGCCCGTCTGTTATCTGTGAGCGAGCAAGTTTCAAC 420
QY 134 GlnAlaGlyGluLysThrThrGluArgLeuIleTTPAlaGlyAsnThrProGlnGluLys 153
DB 421 CAAGAGAGTCTAAAGTGACAGAGCGCTTTATCTGGCTGGGAATACAACTCGGAGAAA 480
QY 154 AspTyrAsnLeuAlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeu 173
DB 481 GAGTATAACCTCTCCCGTCTGTGTATACGCCACTACGACACAGCGGAGTGACCCGGTTG 540
QY 174 AsnSerLeuSerLeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAspAsn 193
DB 541 ATCAGTCACTGCGGCGGCCATGCTATCCCAATCTCACCAATGCTGCGGGAAGGG 600
QY 194 GlnAspAlaAspTTPThrGlyGluAspGlnSerLeuTTPGlnGlnLysLeuSerSerAsp 213
DB 601 CAGAGGCTAACTGGAGCGGTGACGACGAACTGTCTGCGAGGAATGCTGGCAAGTGAG 660
QY 214 ValTyrIleThrGlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAla 233
DB 661 GTCTATACGACACAAAGTAGTACCAATAATGCCATCGGGGCTTTACTGACCCAAACCGATGG 720
QY 234 LysGlyAsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLysLysGlySerTTPLeu 253
DB 721 AAGGCAATATTGAGGCTCTGGCTTATGACATTCGCCGTGAGTTAAAGGAGTGTGGTTG 780
QY 254 ThrLeuLysGlyGlnAlaGluGlnValIleIleLysSerLeuThrTyrSerAlaAlaGly 273
DB 781 ACGGTGAAGGCCAGAGTGAACAGGTGATTTAAAGTCCCTGAGCTGGTCAGCGCAGGT 840
QY 274 GlnLysLeuArgGluGluHisGlyAsnGlyIleValThrGluTyrSerTyrGluProGlu 293
DB 841 CATAAATTCGTGAGAGCAGCGTAACGCGCTGTTACGAGTACACAGTTATGAGCGCGAA 900
QY 294 ThrGlnArgLeuIleGlyIleThrThrArgArg-----ProSerAspAlaLys 309
DB 901 ACTCAACGTCTGATAGGTATCACCCCGCGCGTCCGGAAGGAGTCAATCAGGAGCCAGA 960
QY 310 ValLeuGlnAspLeuArgTyrGlnTyrAspProValGlyAsnValIleAsnIleArgAsn 329
DB 961 GTATTGCGAGATCTACGCTATAAGTATGATCCGTGCGGAAATGTTATCAGTATCCATAT 1020
QY 330 AspAlaGluAlaThrArgPheTTPArgAsnGlnLysValAlaProGluAsnSerTyrThr 349
DB 1021 GATCCGGAAGCTACCCGCTTTTGGCGTAATCAGAAAGTGCAGCGCGAGAATCGCTATGTT 1080
QY 350 TyrAspSerLeuTyrGlnLeuIleSerAlaThrGlyArgGluMetAlaAsnIleGlyGln 369
DB 1081 TATGATTTCTGTATCAGCTTATGAGTGCACAGGCGGTGAATGGCTAATATCGGTCTAG 1140
QY 370 GlnAsnAsnGlnLeuProSerProAlaLeu-----ProSerAspAsnAsnThrTyrThr 387
DB 1141 CAAGCAACCAACTTCCTCCCGTTATACCTGTTCTTACTGACGACGACCTTATACC 1200
QY 388 AsnTyrThrArgSerTyrSerTyrAspHisSerGlyAsnLeuThrGlnIleArgHisSer 407
DB 1201 AATTACCTTCGTACCTATATCTATACCGTGGCGTAATTTGGTTCAAATCCGACACAGT 1260
QY 408 SerProAlaThrGlnAsnAsnTyrThrValAlaIleThrLeuSerAsnArgSerAsnArg 427
DB 1261 TCACCCGCGACTCAAAATAGTTACACACAGATATACCGGTTTCAAGCGCGAGTAACCGG 1320

QY 428 GlyValLeuSerSerThrIleuThrThrAspProAsnGlnValAspThrLeuPheAspAlaGly 447
DB 1321 GCGGTATTGAGTACATTAACGACAGATCCAAACCCGAGTGCATGCTATTGATTCGGC 1380
QY 448 GlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIleIleTTPThrProArgGlyGluLeu 467
DB 1381 GGTCAATCAGAAGATGTTAATACCGGGGCAAAATCTGGATTGGAATATTGCGGGTGAATTG 1440
QY 468 LysGlnVal-----AsnAsnGlyProGlyAsnGluTTPThrTyrArgTyrAsp 482
DB 1441 CAACGAGTCACACCGGTGAGCCGTGAAAATAGCAGTGACAGTGAATGGTATCGCTATAGC 1500
QY 483 SerAsnGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAsnThrThrGlnGln 502
DB 1501 AGTGATGGCATCGGCTGCTAAAGTGAGTGAACAGCAGACGCGGCAACAGTACTCAAGTA 1560
QY 503 GlnArgValIleTyrLeuProGlyLeuGluLeuArgTTPThrGlnSerAsnAlaThrThr 522
DB 1561 CAACGGGTGACTTATCTCCGGGATTAGAGCTACGGACAACCTGGGTTGCGAGNTAAACA 1620
QY 523 ThrGluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArgValLeu 542
DB 1621 ACCGAAGATTTGCAGGTGATTACGTAGGTGAAGCGGTCCGCGACACAGTAAAGGTATTG 1680
QY 543 HisTTPGluSerGlyLysProGluAspValAsnAsnGlnLeuArgTyrSerTyrAsp 562
DB 1681 CACTGGGAAGTGTAAAGCCGACAGATATTGACAAATCAGTGCCTACAGTACGAT 1740
QY 563 AsnLeuIleGlySerSerGlnLeuGluLeuAspAsnGlnGlyGlnIleIleSerGluGlu 582
DB 1741 AATCTGTTGGCTTCAGCCAGCTTGAACCTGGATAGCGAAGGCGAGATTCTCAGTCAGGA 1800
QY 583 GluTyrTyrProPheGlyGlyThrAlaLeuTTPAlaAlaAsnSerGlnThrGluAlaSer 602
DB 1801 GAGTATTATCCGTATGCGGTACGCGATATGCGCGCGAGAAATCAGACAGAGCCAGC 1860
QY 603 TyrLysThrIleArgTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyrGly 622
DB 1861 TACAAATTTATTCTTACTCCGTAAAGAGCGGATGCCACTGGATTGATTATTACCGC 1920
QY 623 TyrArgTyrTyrGlnProTTPAlaGlyArgTTPLeuSerAlaAspProAlaGlyThrIle 642
DB 1921 TACCGTTATTATCAACCTTGGGTGGGTGATGGTTGAGTGCTGATCCGCGGGAACCGTG 1980
QY 643 AspGlyLeuAsnLeuTyrArgMetValArgAsnAsnProValSerLeuGlnAspGluAsn 662
DB 1981 GATGGCTGAATTTGTACCGAATGGTGAGAAATACCCCATCACATTGATGACCATGAC 2040
QY 663 GlyLeuAlaProGluLysGlyLys 670
DB 2041 GGATTAGCACCGTCTCCAAATAGA 2064

RESULT 12

US-10-609-113-44
; Sequence 44, Application US/10609113
; Publication No. US20040110184A1
; GENERAL INFORMATION:
; APPLICANT: Bintraxim, Scott
; APPLICANT: Bevan, Scott
; APPLICANT: Zhu, Baolong
; APPLICANT: Merlo, Donald J.
; TITLE OF INVENTION: Pesticidally Active Proteins and Polynucleotides Obtainable from
; FILE REFERENCE: DAS-101XC2
; CURRENT APPLICATION NUMBER: US/10/609,113
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US 60/392,633
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/441,647
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44

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/ LENGTH: 3132
; TYPE: DNA
; ORGANISM: Photorhabdus strain W14
US-10-609-113-44

Alignment Scores:
Pred. No.: 1.35e-200 Length: 3132
Score: 2467.00 Matches: 470
Percent Similarity: 81.25% Conservative: 89
Best Local Similarity: 68.31% Mismatches: 111
Query Match: 52.05% Indels: 18
DB: 7 Gaps: 5

US-10-647-956A-6 (1-915) x US-10-609-113-44 (1-3132)

QY 1 MetSerSerTyrAnSerAlaIleAAspGlnLysThrProSerIleLysValLeuAAsn 20
Db 1 ATGAGCCCGTCTGAGACTACTCTTATATACTCAAAACCCCAACAGTCAGCGTGTAGATAAT 60
QY 21 ArgLysLeuAenValArgThrLeuGluTyrLeuArgThrGlnAlaAAspGluAAsnSerAsp 40
Db 61 CGCGTCTGTCATCTCGTATATGGTTTTCACCGTATTGTAATCGGGGGGGATCTGAC 120
QY 41 GluLeuIleThrPheTyrGluPheAAsnIleProGlyPheGlnValLysSerThrAspPro 60
Db 121 ACCCGCTCACCCGTACACAGTATGATGCCCGTGCACACCTGAACACTACAGTATTGACCCA 180
QY 61 Arg-----LysAsnLysAsnGlnSerGlyProAnPheIleArgValPhe 75
Db 181 CGCTTGATGATCAAAAGCAGCGGTGATAAATCACTGAAGCGCTAATTTTGTGCGCAGCAT 240
QY 76 AsnLeuAlaGlyGlnValLeuArgGluGluSerValAAspAlaGlyArgThrIleThrLeu 95
Db 241 GATTCGCCCGGTATGCCCCGCGGACAGAGAGTGCATGCTGCTGCTACTGTGTGCAATTG 300
QY 96 AsnAspIleGluSerArgProValLeuIleLeuAsnAlaThrGlyValArgGlnAsnHis 115
Db 301 AATGATATTGAAGTCTCGGTAAATGACAAATGAATGGACCGGTGTTCTGCAGACCCGT 360
QY 116 ArgTyrGluAAspAenThrLeuProGlyArgLeuLeuAlaIleThrGluGlnVal----- 133
Db 361 CGCTATGAGGCAACACCTTGCCCGTTCGTTGTTATCTGTGAGCGAGCAAGTTTTTCAAC 420
QY 134 GluAlaGlyGluLysThrThrGluArgLeuIleThrAlaGlyAenThrProGlnGluLys 153
Db 421 CAAGAGAGTGTAAAGTGCACAGACGCTTTATCTGGGCTGGGAATACAACTCGGAGAAA 480
QY 154 AspTyrAsnLeuAlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeu 173
Db 481 GAGTATAACCTCTCCGGTCTGTGTATACGCCACTACACACAGCGGAGTGACCCGGTTG 540
QY 174 AsnSerLeuSerLeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAspAsn 193
Db 541 ATGAGTCAGTCACCTGGCGGGCGCCATGATATCCCAATCTCACCAATTTGCTGGCGGAAGG 600
QY 194 GlnAspAlaAspTyrThrGlyGluAAspGlnSerLeuThrGlnGlnLysSerSerAsp 213
Db 601 CAGGAGGCTAACTGGAGCGGTGACGAGAACTGTCTGGCAGGGAATGCTGGCGGAAGTGAG 660
QY 214 ValTyrIleThrGlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAla 233
Db 661 GTCTATACGACACAAAGTACCACTAATGCCATCGGGCTTTACTGACCCAAACCGATGCG 720
QY 234 LysGlyAsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLeuLysGlySerThrLeu 253
Db 721 AAAGGCAATATTCAGCGTCTGGCTTATGACATTGCGGTTCAGTTAAAAAGGGAGTTGGTTG 780
QY 254 ThrLeuLysGlyGlnAlaGluGlnValIleIleLysSerLeuThrTyrSerAlaAlaGly 273
Db 781 ACGGTGAAGGCCAGAGTGAACAGGTGATTGTTAAGTCCCTGAGCTGCTGACGCCAGGT 840
QY 274 GlnLysLeuArgGluGluHisGlyAsnGlyIleValThrGluTyrSerTyrGluProGlu 293
Db 293
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841 CATAAATTCGCTGAAGAGCACCGTAAACGCGGTGTTTACGAGGTACAGTTATGAGCCGGAA 900
294 ThrGlnArgLeuIleGlyIleThrThrArgArg-----ProSerAspAlaLys 309
901 ACTCAACGTCCTGATAGGTATCACCCCGCGGTGCCGAAGGGAGTCAATCAGGAGCCAGA 960
310 ValLeuGlnAAspLeuArgTyrGlnTyrAspProValGlyAsnValIleAenIleAAsn 329
961 GTATTTCAGGAGTCTACGCTATAAGTATGATCGGTGGGGAATGTTATCAGTATCCATAAT 1020
330 AspAlaGluAlaThrArgPheThrArgAsnGlnLysValAlaProGluAAsnSerTyrThr 349
1021 GATGCCGAAGCTACCCGCTTTTGGCGTAATCAGAAAGTGGAGCCGGAGAAATCGCTATGT 1080
350 TyrAspSerLeuTyrGlnLeuIleSerAlaThrGlyArgGluMetAlaAenIleGlyGln 369
1081 TATGATTTCTGTATCAGCTTATGAGTGCACAGGGCGTGAATGGCTAATATATCGTCAAG 1140
370 GlnAsnAAsnGlnLeuProSerProAlaLeu-----ProSerAspAenAenThrTyrThr 387
1141 CAAAGCAACCAACTTCCCTCACCCGTTATACCTGTTCTTACTGACGACGACCTTATACC 1200
388 AsnTyrThrArgSerTyrSerTyrAspHisSerGlyAsnLeuThrGlnIleArgHisSer 407
1201 AATTACCTTCGTACCTATATCTATGACCGTGGCGGTAATTTGGTTCAAAATCCGACACAGT 1260
408 SerProAlaThrGlnAAsnAsnTyrThrValAlaIleThrLeuSerAsnArgSerAsnArg 427
1261 TCACCCGCGACTCNAATAGTTACACACAGATATCACCGTTTCAAGCCGCGCAGTAAACCGG 1320
428 GlyValLeuSerThrLeuThrThrAspProAAsnGlnValAAspThrLeuPheAAspAlaGly 447
1321 GCGGTATTGAGTACATTAAACGACAGATCCAAACCGAGTGGATCGCTATTTGATTCGGCG 1380
448 GlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIleThrProArgGlyGluLeu 467
1381 GGTCAATCAGAAGATGTAAATACCGGGGCAAAATCTGGATTGGGAATATTCGGGGTGAATTG 1440
468 LysGlnVal-----AsnAAsnGlyProGlyAAsnGluTyrTyrArgTyrAsp 482
1441 CAACGAGTACACCGGTGAGCCGTGAAATATAGCAGTGACAGTGAATGGTATCCCTATAGC 1500
483 SerAsnGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAenThrThrGlnGln 502
1501 AGTGATGGCATCGCGTCTAAAGTGAGTGAACACAGACGACGCGGCAACAGTACTCAAGTA 1560
503 GlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAlaThrThr 522
1561 CAACGGGTGACTTATCTCGCGGATTAGAGCTACGGACAACTCGGGTTGCAGATAAAACA 1620
523 ThrGluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArgValLeu 542
1621 ACCGAAGATTTGCGGTGATTACGGTAGGTGAAGCGGTCCGCGACAGGTAAAGGTATTG 1680
543 HisThrGluSerGlyLysProGluAAspValAAsnAAsnGlnLeuArgTyrSerTyrAsp 562
1681 CATGGGAAGTGTGAAGCCGACAGATATTGACAACTACAGTCCGCTACAGCTACGAT 1740
563 AsnLeuIleGlySerSerGlnLeuGluLeuAAspAAsnGlnGlyGlnIleIleSerGluGlu 582
1741 AATCTGCTTGGCTCCAGCCAGCTTGAACGTGATAGCGAAGGAGGAGGATTTCTCAGTCAGAA 1800
583 GluTyrTyrProPheGlyThrAlaLeuTyrAlaAAsnSerGlnThrGluAlaSer 602
1801 GAGTATTATCCGTATGCGGTATGCGCGATATGGCGCGGAGTCCCAATCAGACAAAGCCAGC 1860
603 TyrLysThrIleArgTyrSerGlyLysGluArgAAspAlaThrGlyLeuTyrTyrTyrGly 622
1861 TACAATTTATTCGTTACTCCGTAAGACGCGGATGCCACTGGATTGTATTATTACCGC 1920
623 TyrArgTyrTyrGlnProThrAlaGlyArgThrLeuSerAlaAspProAlaGlyThrIle 642
1921 TACCGTTATTATCAACCTTGGGTGGGTCCGATGTTGATGCTGATCCGCGGGGAACCGTG 1980
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QY 643 AspGlyLeuAsnLeuTyrArgMetValArgAsnAsnProValSerLeuGlnAspGluAsn 662
Db 1981 GATGGGTGAATTTGTACCGAATGGTGAGGAATAAACCCCATCATTGACTGACCATGAC 2040
QY 663 GlyLeuAlaProGluLysGlyLys 670
Db 2041 GGATTAGCACCGTCTCCAAATAGA 2064

RESULT 13
US-10-754-115-25
; Sequence 25, Application US/10754115
; Publication No. US20040208907A1
; GENERAL INFORMATION:
; APPLICANT: Hey, Timothy
; APPLICANT: Schleper, Amanda
; APPLICANT: Bevan, Scott
; APPLICANT: Bintrim, Scott
; APPLICANT: Mitchell, Jon
; APPLICANT: Li, Ze Sheng
; APPLICANT: Ni, Weiting
; APPLICANT: Zhu, Baolong
; APPLICANT: Merlo, Don
; APPLICANT: Apel-Birkhold, Patricia
; APPLICANT: Meade, Thomas
; TITLE OF INVENTION: Mixing and Matching TC Proteins for Pest Control
; FILE REFERENCE: DAS-104XC1
; CURRENT APPLICATION NUMBER: US/10/754,115
; CURRENT FILING DATE: 2004-01-07
; PRIOR FILING DATE: 2004-01-21
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 3132
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1)..(3132)
US-10-754-115-25

Alignment Scores:
Pred. No.: 1.35e-200 Length: 3132
Score: 2467.00 Matches: 470
Percent Similarity: 81.25% Conservative: 89
Best Local Similarity: 68.31% Mismatches: 111
Query Match: 52.05% Indels: 18
DB: 8 Gaps: 5

US-10-647-956A-6 (1-915) x US-10-754-115-25 (1-3132)

QY 1 MetSerSerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn 20
Db 1 ATGAGTCCGCTCAGACTACTCTTTATTACTCAAAACCCCAACAGTCAGCGTGTAGATAAT 60
QY 21 ArgLysLeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAsnSerAsp 40
Db 61 CGCGGTCTGTCATTCGTGATTTGGTTTCCACCGTATTGTAATCGGGGGGATCTGAC 120
QY 41 GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro 60
Db 121 ACCCGCTCACCCGTACACAGTATGATGCCGTGGACACCTGAACACTAGATTGACCCA 180
QY 61 Arg-----LysAsnLysAsnGlnSerGlyProAsnPheIleArgValPhe 75
Db 181 CGCTTGATGATGCAAGCAGCGGTGATAACTCAGTAAAGCCTAATTTGTCTGCGCAT 240
QY 76 AsnLeuAlaGlyGlnValLeuArgGluSerValAspAlaGlyArgThrIleThrLeu 95
Db 241 GATCGCCCGGTATGCGCCCTGCGACAGAGTGTCGATGCTGCTGCTGCTGCTGCTGCTG 300
QY 96 AsnAspIleGluSerArgProValLeuIleAsnAlaThrGlyValArgGlnAsnHis 115
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Db 301 AATGATATTGAAGGTCTGTCGGTAATGACAAATGAAATGCGACCGGTGTTCTGTCAGACCCGT 360
QY 116 ArgTyrGluAspAsnThrLeuProGlyArgLeuLeuAlaIleThrGluGlnVal----- 133
Db 361 CGCTATGAAGGCAACACCTTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 134 GlnAlaGlyGluLysThrThrGluArgLeuIleThrAlaGlyAsnThrProGlnGluLys 153
Db 421 CAAGAGAGTGTAAAGTGAACAGAGCGCTTTATCTGGGCTGGGAATACACCTCGGAGAAA 480
QY 154 AspTyrAsnLeuAlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeu 173
Db 481 GAGTATAACCTCTCCCGTCTGTGTATACGCCCTACACACCGGAGTGAACCGGTG 540
QY 174 AsnSerLeuSerLeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAspAsn 193
Db 541 ATGAGTCAGTCAGTGGGGGGCCATGCTATCCCAATCTCACCAATTGCTGGCGGAAGGG 600
QY 194 GlnAspAlaAspThrThrGluAspGlnSerLeuThrGlnGlnLysLeuSerSerAsp 213
Db 601 CAGGAGGCTAACTGGAGCGGTGACGACGAACTGCTCTGGCAGGAAATGCTGGCAAGTGAG 660
QY 214 ValTyrIleThrGlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAla 233
Db 661 GTCATATACGACACAAAGTACCATAATGCCATCGCGGCTTTACTGACCCCAACCGATGCG 720
QY 234 LysGlyAsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLeuLysGlySerThrLeu 253
Db 721 AAAGGCAATATTCAGCGCTGCGCTTATGACATTCGCGGTGAGTTAAAGGAGGTGGTTG 780
QY 254 ThrLeuLysGlyGlnAlaGluGlnValIleIleLysSerLeuThrTyrSerAlaAlaGly 273
Db 781 ACGGTGAAAGGCCAGAGTGAACAGGTGATTGTTAGTCCCTGAGCTGGTCAGCGCAGGT 840
QY 274 GlnLysLeuArgGluGluHisGlyAsnGlyIleValThrGluTyrSerTyrGluProGlu 293
Db 841 CATAAATTCGTTGAAGACGACGCGTAACGCGGTGTTACGGAGTACAGTTATAGACCGGAA 900
QY 294 ThrGlnArgLeuIleGlyIleThrThrArgArg-----ProSerAspAlaLys 309
Db 901 ACTCAACGCTGATAGGTATCACCCCGCGTGGCGAAGGGAGTCAATCAGAGCCAGA 960
QY 310 ValLeuGlnAspLeuArgTyrGlnTyrAspProValGlyAsnValIleAsnIleArgAsn 329
Db 961 GTATTGCGAGATCTACGCTATAAGTATGATCCGCGTGGGAATGTTATCAGTATCCATAAT 1020
QY 330 AspAlaGluAlaThrArgPheThrArgAsnGlnLysValAlaProGluAsnSerTyrThr 349
Db 1021 GATCGCAAGCTACCGCTTTTGGCGTAAATCAGAAAGTGGAGCGGAGAAATCGCTATGTT 1080
QY 350 TyrAspSerLeuTyrGlnLeuIleSerAlaThrGlyArgGluMetAlaAsnIleGlyGln 369
Db 1081 TATGATTCCTGTCATCAGCTTATGAGTGCACAGGCGTGAAATGGCTAATATCGGTGAC 1140
QY 370 GlnAsnAsnGlnLeuProSerProAlaLeu-----ProSerAspAsnAsnThrTyrThr 387
Db 1141 CAAAGCAACCACTTCCCTCACCGTTATACCTGTTCTTACTGACGACAGCAGCTTATACC 1200
QY 388 AsnTyrThrArgSerTyrSerTyrAspHisSerGlyAsnLeuThrGlnIleArgHisSer 407
Db 1201 AATTACCTCGTACCTATCTTATGACCGTGGCGTAAATTTGGTTCAAATCCGACACAGT 1260
QY 408 SerProAlaThrGlnAsnAsnTyrThrValAlaIleThrLeuSerAsnArgSerAsnArg 427
Db 1261 TCACCGCGGACTCAAATAGTTACACACAGATATCACCGTATCACCGCTTTCAGCCGAGTAACCG 1320
QY 428 GlyValLeuSerThrLeuThrAspProAsnGlnValAspThrLeuPheAspAlaGly 447
Db 1321 GCGGTATTGATACATTACACAGATCCAAACCGGAGTGGATCGGCTATTGATTCGCGC 1380
QY 448 GlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIleThrProArgGlyGluLeu 467
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Db 1381 GGTCAATCAGAAAGATGTTAATACCGGGGCAAAATCTGGATGGGAATATTCGGGGTGAATTG 1440
Qy 468 LysGlnVal-----AsnAsnGlyProGlyAsnGluTrpTyrArgTyrAsp 482
Db 1441 CAACGAGTCAACACCGGTGAGCCGTGAAATAAGCAGTACAGTGAATGGTATCGCTATAGC 1500
Qy 483 SerAsnGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAsnThrThrGlnGln 502
Db 1501 AGTGATGGCATCGCGTCTAAAGTGAAGTGAACAGCAGCGGCGCAACAGTACTCAAGTA 1560
Qy 503 GlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAlaThrThr 522
Db 1561 CAACGGGTGACTTATCTCCCGGATTAGAGTACCGGCAAACTGGGGTTCAGATAAAACA 1620
Qy 523 ThrGluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArgValLeu 542
Db 1621 ACCGAAGATTGGCAGGTGATTCGGGTAGGTGAACGGGTGCGGCACAGGTAAAGGGTATTG 1680
Qy 543 HisTrpGluSerGlyLysProGluAspValAsnAsnAsnGlnLeuArgTyrSerTyrAsp 562
Db 1681 CACTGGGAAGTGGTAGCCGACAGATATTGACAAACAATCAGGTGCGCTACAGTACGAT 1740
Qy 563 AsnLeuIleGlySerSerGlnLeuGluLeuAspAsnGlnGlyIleIleSerGluGlu 582
Db 1741 AATCTGCTTGGCTCCAGCAGCTTGAACCTGGATAGCGAAGGGCAGATTCTCAGTCAGGAA 1800
Qy 583 GluTyrTrpProPheGlyGlyThrAlaLeuTrpAlaAlaAsnSerGlnThrGluAlaSer 602
Db 1801 GAGTATTATCCGTATGCGGTACCGCATATGGCGCGCGAGAATCAGACAGAAAGCCAGC 1860
Qy 603 TyrLysThrIleAspTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyrGly 622
Db 1861 TACAAATTTATCTGTTACTCCGGTAAGAGCGCGGATGCCACTGGATTGTATTATTCGGC 1920
Qy 623 TyrArgTyrTrpGlnProTrpAlaGlyArgTrpLeuSerAlaAspProAlaGlyThrIle 642
Db 1921 TACCGTTATTATCAACCTTGGGTGGTTCGATGGTTGATGCTGATCCGGCGGAACCGTG 1980
Qy 643 AspGlyLeuAsnLeuTyrArgMetValArgAsnAsnProValSerLeuGlnAspGluAsn 662
Db 1981 GATCGGCTGAATTTGTACCGGAATGGTGAGGAATAACCCCATCACATTGACTGACCATTGAC 2040
Qy 663 GlyLeuAlaProGluLysGlyLys 670
Db 2041 GGATTAGCACCCGCTCTCCAAATAGA 2064

RESULT 14
US-10-754-115-50
; Sequence 50, Application US/10754115
; Publication No. US20040208907A1
; GENERAL INFORMATION:
; APPLICANT: Hey, Timothy
; APPLICANT: Schleper, Amanda
; APPLICANT: Bevan, Scott
; APPLICANT: Bintrim, Scott
; APPLICANT: Mitchell, Jon
; APPLICANT: Li, Ze Sheng
; APPLICANT: Ni, Weiting
; APPLICANT: Zhu, Baolong
; APPLICANT: Merlo, Don
; APPLICANT: Apel-Birkhold, Patricia
; APPLICANT: Meade, Thomas
; TITLE OF INVENTION: Mixing and Matching TC Proteins for Pest Control
; FILE REFERENCE: DAS-104XC1
; CURRENT APPLICATION NUMBER: US/10/754.115
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US 60/441,723
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50
; LENGTH: 2889
; TYPE: DNA
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; ORGANISM: Xenorhabdus bovienii
US-10-754-115-50

Alignment Scores:      1,03e-176      Length:      2889
Pred. No.:            2187.50         Matches:     463
Score:                67.30%          Conservative: 140
Percent Similarity:   51.67%          Mismatches:  213
Best Local Similarity: 46.15%          Indels:      81
Query Match:          8               Gaps:        17
DB:

US-10-647-956A-6 (1-915) x US-10-754-115-50 (1-2889)

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Qy 21 ArgLysLeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAsnSerAsp 40
Db 61 CGAGGGCTGTGCTGCGGGATATTGCTTATCACCGTACAACAGCAGGAGAGCGGCTGAC 120
Qy 41 GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro 60
Db 121 ACTCGCATCATCCCGCATCAATACAGTCCCAATAAATTTTAACTCAGAGCATTTGATCCA 180
Qy 61 Arg-----LysAsnLysAsnGlnSerGlyProAsnPheIleArgValPheAsn 76
Db 181 CGCTTTTTCATTTGCAATCTCAGACGACCACTAAACCTAATTTTCACCTACTGCTCGGCC 240
Qy 77 LeuAlaGlyGlnValLeuArgGluGluSerValAspAlaGlyArgThrIleThrLeuAsn 96
Db 241 TTCAAGGGTGATGCTCTACGGACAGAGAGTGTGGATGCCGACCAAACTGTCAATTTTGAT 300
Qy 97 AspIleGluSerArgProValLeuIleAsnAlaThrGlyValArgGlnAsnHisArg 116
Db 301 GACATCGAAGGTGCTCGTTACTGAATATCAGTGGCATGGTGTGTCGTCGTCAGTCAAACTG 360
Qy 117 TyrGluAspAsnThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGly 136
Db 361 TATGAGAGAGTACATATGCGGGCGCGTGTCTCGTGTCTAGTGAA-----CGGAAGAAT 414
Qy 137 GluLysThrThr-----GluArgLeuIleTrpAlaGlyAsnThrProGlnGlu 152
Db 415 GAGGCTTCAACACCCCAAAATTTATTGAACGGTTTTATTGGTCGGGAAATAGCCCATCAGAA 474
Qy 153 LysAspTyrAsnLeuAlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGln 172
Db 475 AAAGATCACAATTTGGCGGGAATAATCTCTCGTCATTATGATACCGCCGGATTAAACAG 534
Qy 173 LeuAsnSerLeuSerLeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAsp 192
Db 535 CTTAATGCTGTGCTCTGACACCGGTGGATCTCTCAACATCCCGTCAGTTATTTCGAGAT 594
Qy 193 AsnGlnAspAlaAspTrpThrGlyGluAspGlnSerLeuTrpGlnGlnLysLeuSerSer 212
Db 595 GATGTACACAGCATTTGGAGCGGAAGTGACGAATCCCAAGTGAAGACGCGACTGAGTAAC 654
Qy 213 AspValTyrIleThrGlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAsp 232
Db 655 GACATATTCAAAACCCGAAATCACCGCTGATGCGGTTGGCAATTTCTTTCGACTCGAATGAT 714
Qy 233 AlaLysGlyAsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLeuLysGlySerTrp 252
Db 715 GCCAAAAGCAACCAACAGCAACGATTGTCTTATGATGTGGCAGGGCAGTTAAAGGCAGTGG 774
Qy 253 LeuThrLeuLysGlyGlnAlaGluGlnValIleIleLysSerLeuThrTyrSerAlaAla 272
Db 775 CTGACGATAAAGCCAGCAATGACGAGTGTATGATTAACCTCCCTGACTTACTCCGCGCA 834
Qy 273 GlyGlnLysLeuArgGluGluHisGlyAsnGlyIleValThrGluTyrSerTyrGluPro 292
Db 835 GGGCAGAAACTGGCTGGAAGAGCAGGGGTAAACGGCGTTGTCCTCACTGAATACTCCTTGAAGCA 894
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! ORGANISM: Xenorhabdus bovienii
US-11-020-848-3

Alignment Scores:

Pred. No.: 1,03e-176 Length: 2889
Score: 2187.50 Matches: 463
Percent Similarity: 67.30% Conservative: 140
Best Local Similarity: 51.67% Mismatches: 213
Query Match: 46.15% Indels: 81
Dbs: 10 Gaps: 17

US-10-647-956A-6 (1-915) x US-11-020-848-3 (1-2889)

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QY 1 MetSerTyrAenSerAlaIleAaspGlnLysThrProSerIleLysValLeuAaspAsn 20
DB 1 ATGNATGTTTAAATCAACTTATATGCGGGTACACCGACTGTCCCGTCATGGACAAT 60
QY 21 ArgLysLeuAenValArgThrLeuGluTyrLeuArgThrGlnAlaAaspGluAenSerAsp 40
DB 61 CGAGGGTGTGAGTGGCGGATATTGCTTATCACCGTACAAACAGCAGGAGAGAGCGCTGAC 120
QY 41 GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro 60
DB 121 ACTCGCATCACCCGCCATCAATACAGTCCCATTAATTTTAAATCGAGAGCATTTGATCCA 180
QY 61 Arg-----LysAenLysAenGlnSerGlyProAenPheIleArgValPheAsn 76
DB 181 CGCCTTTTGTGTAATCTCAGAGCAGCACCATAAACTTAATTTACACTACTGTCTGCC 240
QY 77 LeuAlaGlyGlnValLeuArgGluSerValAaspAlaGlyArgThrIleThrLeuAen 96
DB 241 TTGAAGGTGATGCTTACGACAGAGAGTGTGATGCGGCAAACTGTCAATTTTGAGT 300
QY 97 AspIleGluSerArgProValLeuIleAenAlaThrGlyValArgGlnAenHisArg 116
DB 301 GACATCAAGGTGCTCGCTTACTCAATATCATGTCGATGGTGTGCTCAAAACACTGGCAA 360
QY 117 TyrGluAaspAenThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGly 136
DB 361 TATGAGAGAGTACATTTGCCGGGCGCTTGTCTGCTGTGAGTGA-----CGGAAGAAT 414
QY 137 GluLysThrThr-----GluArgLeuIleTrpAlaGlyAenThrProGlnGlu 152
DB 415 GAGGCTTCAACACACCCCAATTTATTGAACGGTTTATTGTCGGGAATAGCCCATCAGAA 474
QY 153 LysAspTyrAenLeuAlaGlyClnCysValArgHisTyrAspThrAlaGlyLeuThrGln 172
DB 475 AAAGATCACAAATTTGGCGGGAATAATCTTCGTCATTATGATACCGCGGATTAACCCAG 534
QY 173 LeuAenSerLeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAsp 192
DB 535 CTTAATGCTGTGCTCTGACACCGGTGATCTCTCAATCCCGTCAGTTATTCAGCAT 594
QY 193 AsnGlnAaspAlaAaspTrpThrGlyAaspGlnSerLeuTrpGlnLysLeuSerSer 212
DB 595 GATGTCACAGCAGATGGAGCGGAAGTGACGAATCCCAAGTGAAGACGCGACTGAGTAAC 654
QY 213 AspValTyrIleThrGlnSerAenThrAaspAlaThrGlyAlaLeuLeuThrGlnThrAsp 232
DB 655 GACATATTCAACACCGGAATCACCGCTGATCGGTTGGCAATTTCTTGACTCAGATGAT 714
QY 233 AlaLysGlyAenIleGlnArgLeuAlaTyrAaspValAlaGlyGlnLeuLysGlySerTrp 252
DB 715 GCCAAAAGCAACACAGCAACGATGTCCTATGATGGCGGGCGAGTTAAAGCGAAGCTGG 774
QY 253 LeuThrLeuLysGlyGlnAlaGlnValIleIleLysSerLeuThrTyrSerAlaAla 272
DB 775 CTGACGATAAAGCCAGAAATGACAGGTGATAGTTAACTCCCTGACTTACTCCCGCGCA 834
QY 273 GlyGlnLysLeuArgGluGluHi6LysAenGlyIleValThrGluTyrSerTyrGluPro 292
DB 835 GGGCAGAAATGCGGTGAAGAGCAGCGGTAAACGGCGTGTGCTCACTGAATACTCTTATGAAGCA 894
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QY 293 GluThrGlnArgLeuIleGlyIleThrThrArgArgProSerAaspAlaLysValLeuGln 312
DB 895 CAAACCTGGCGTTTGATAGGTGTAACGGCTTACCGCTCAGTCAGTAAAAAAGATTGCGAG 954
QY 313 AspLeuArgTyrGlnTyrAaspProValGlyAenValIleAenIleArgAenAepAlaGlu 332
DB 955 GATCTTGTCTATAACTATGATCGGTCGGTATCTCCTGAATATTCCGAATATGAGCAGAG 1014
QY 333 AlaThrArgPheTyrArgAenGlnLysValAlaProGluAenSerTyrThrTyrAaspSer 352
DB 1015 GCNAACCGGTTCTGGCGTAAATCAGATAGTAGAACACAGACACCATATGCTTATGACTCG 1074
QY 353 LeuTyrGlnLeuIleSerAlaThrGlyArgGluMetAlaAenIleGlyGlnGlnAenAen 372
DB 1075 CTTTATCAACTCATCAGTGTAGTGTGAGAAATCGCCAGTATCGGTATCGTCAGCGGAGC 1134
QY 373 GlnLeuProSerPro-----AlaLeuProSerAaspAenAenThrTyrThrAenTyrThr 390
DB 1135 CGGCTGCTGTACCGAATATTCTCTCTCTGCAATGACGATGTTTATCTCGCTACACC 1194
QY 391 ArgSerTyrSerTyrAspHisSerGlyAenLeuThrGlnIleArgHisSerSerProAla 410
DB 1195 CGCACATATCACTATGATCGCGTGAATCTCTGCAGATCGGCAATCGCGCTCTGCT 1254
QY 411 ThrGlnAenAenTyrThrValAlaIleThrLeuSerAenArgSerAenArgGlyValLeu 430
DB 1255 ACAGATAAATAAGTACACCAACAAAGATCACCGTATCGAATCGTAGTAATCGTCGAGTAGG 1314
QY 431 SerThrLeuThrThrAspProAenGlnValAaspThrLeuPheAaspAlaGlyGlyHisGln 450
DB 1315 GATACCTTGACCAACATCCGCAAGTGAATCACCTGTTGATCATGAGGGGATCAAA 1374
QY 451 ThrSerLeuLeuProGlyGlnThrLeuIleTrpThrProArgGlyGluLeuLysGlnVal 470
DB 1375 CTTCAACTCAGTCAGCCAGACTTATGTTGGAATCTATCGGGTGAATCTACAGCAATA 1434
QY 471 -----AenAenGlyProGlyAen---GluTrpTyrArgTyrAaspSerAen 484
DB 1435 ACAAGATACAGCGTACGCAAAAACCCGAGATAAAGAGCGGTATCGCTATGTTGGG 1494
QY 485 GlyMetArgGlnLeuLysValSerGluGlnProThrGlnAenThrThrGlnGlnArg 504
DB 1495 GCTGCGCGGTGCTGAAATTCAGCACACAGCAGCGGGGGAAGACGCCATGTGCGACGT 1554
QY 505 ValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAenAlaThrThrThrGlu 524
DB 1555 GTTGTATTATCGCGGGTTGGAACTACGCACAACTCAGCATGATGCGACATTAATCGAA 1614
QY 525 GluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArgValLeuHisTrp 544
DB 1615 GACTTACAGGTGATTATCATGGGTGAAGCAGGACGTGCTCAGGTACGCTACTTCATTGG 1674
QY 545 GluSerGlyLysProGluAaspValAenAenAenGlnLeuArgTyrSerTyrAaspAenLeu 564
DB 1675 GAAATACCAACACCGGATATCTTAACATGACTCACTGCGTTACAGCTACGATAGTTG 1734
QY 565 IleGlySerSerGlnLeuGluLeuAaspAenGlnGlyGlnIleIleSerGluGluGluTyr 584
DB 1735 ATGGGTTCCAGTCAGCTTGAATTTGGATGGAGCGGCGAGATATTACCGAGGAAGATAC 1794
QY 585 TyrProPheGlyGlyThrAlaLeuTrpAlaAenSerGlnThrGluAlaSerTyrLys 604
DB 1795 TACCCCTATGAGGTACAGCAATATGGCGGCAAGAAACCCAGACCGAAGCAATTACAA 1854
QY 605 ThrIleArgTyrSerGlyLysGluArgAaspAlaThrGlyLeuTyrTyrGlyTyrArg 624
DB 1855 ACCATTGCTACTCCGCAAGAGCGTGTGCGACGGGGCTTTTATTACTACGGGACCGT 1914
QY 625 TyrTyrGlnProTrpAlaGlyArgTyrLeuSerAlaAaspProAlaGlyThrIleAaspGly 644
DB 1915 TATTATCAGCGGTGCTAGGGCGCTGTTGAGCGAGATCCCCCGGCAACCGTGGACGGA 1974
QY 645 LeuAenLeuTyrArgMetValArgAenAenProValSerLeuGlnAaspGluAenGlyLeu 664
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D	b	1975	CTGAATCTTATTCGAATGGTGAGAAATAACCCCGATTACTTACC	GGGATGCAGATGGCGTT	2034
Q	y	665	AlaProGluLysGlyIleThrLysAsnValAsnPhePheaspGluLeuLysPheLys	684	
D	b	2035	GCGCGCATAGCAGTAGATCAGCAAGGANT--TATGAGCCTGAGTTCCGAGTTGGT	2091	
Q	y	685	LeualaalaLysSerSerHisValValuYtRpAsnGluLysGlusSerSeryrThrLys	704	
D	b	2092	CTTGAACGAGATGACCCAAATGTTCAGAGATTATGACCGGTTTTATCTGATACGCCAAG	2151	
Q	y	705	AsnLysSerLeuLysValArgValGlyAspSerAspproSerGlyTyrrLeuLeuSer	724	
D	b	2152	ACAGATGATCGAAGCAACTGCGCACCAATTGCT---CCCAGTCAAATGTTATCGCGC	2208	
Q	y	725	HisGlu-----GluLeuLysGlyIleGluLysSerGlnIleIleTyrrSer	740	
D	b	2209	CATGCTTTTGCATCTGTACCTATATTCACAGATTGTTTAATCCTCAA-----	2256	
Q	y	741	ArgLeuGluGluAsnSerSerLeuSerGluLysSerLysThrAsnLeuSerLeu----	758	
D	b	2257	-----ACAGCAAGGCTTTCTCAAAAGACA--ACGGATATTGTATTAAACACA	2301	
Q	y	759	-----GlySerGluIleSerGly-----Tyr	765	
D	b	2302	CAAGGTGGAGCGGATTTAAATCTTTACGTGGCATGAATATTAAAGGTAAAGGAAAAGAATTT	2361	
Q	y	766	MetAlaArgThrlieGlnAspThrIleSerGluTyrrAlaGluGluHisLysTyrrArgSer	785	
D	b	2362	AATGCATTAATAAATCGTTGATACT-----TATGGCGGA	2394	
Q	y	786	AsnHisProAspPheTyrrSerGluThrAspPhePheAlaLeuMetAspLys-----	802	
D	b	2395	GAATGCTGTAT-----AGCAAAACCGC-TATTTACGATATTGGCTTCGCAAGGTGG	2447	
Q	y	803	-----SerGluLysAsnAspTyrrSerGlyGluArgLysIleTyrrAla-Alame	818	
D	b	2448	GTATACTGATATTCGGATACATCCGACTGGAATACAAAGATTTTGTTTACGCGCTCGGTT	2507	
Q	y	818	tGlu-----ValllysValTyrrHisAs	825	
D	b	2508	TAGTGGTTGCATCTCGGCAGTAGATAAGCTTACGAAAAATACATTACGGCGGTATCACT	2567	
Q	y	825	pLeuLysAsnLysGlnSerGluLeuHisValAsnTyrrAlaLeuala	840	
D	b	2568	CGAAGGAAGTAAGCAAGATGCTCAATATAATAATTTAGCAGTTGCA	2613	

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Job time : 1535 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 14, 2005, 23:16:20 ; Search time 281 Seconds
(without alignments)
1596.057 Million cell updates/sec

Title: US-10-647-956A-6
Perfect score: 4740
Sequence: 1 MSYNSAIDQKTPSIKVLN.....EAINRSAIAENLGMRTS 915

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4161359 seqs, 245077644 residues

Total number of hits satisfying chosen parameters: 8322718

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=Published Applications NA.New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINLEN=0
-LOOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blom62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10647956.CGN 1 184 @runat 12122005 091822 29856
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA.New:
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2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:
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10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4740	100.0	2745	6	US-10-647-956A-5
2	169	3.6	3840	6	US-10-793-626-3187
3	166.5	3.5	3543	6	US-10-793-626-4149
4	166	3.5	3285	6	US-10-793-626-3153
5	166	3.5	3730	6	US-10-793-626-3499
6	163.5	3.4	3626	6	US-10-821-234-245
7	163.5	3.4	7786	9	US-11-096-051-3
8	163.5	3.4	8362	9	US-11-096-051-1

9	163.5	3.4	8645	9	US-11-096-051-9	Sequence 9, Appli	
10	163.5	3.4	8657	9	US-11-096-051-7	Sequence 7, Appli	
C	11	144	3.0	3068	6	US-10-793-626-3824	Sequence 3824, Ap
12	144	3.0	15071	6	US-10-793-626-2963	Sequence 2963, Ap	
13	143.5	3.0	8354	7	US-11-113-424-13	Sequence 13, Appli	
14	136.5	2.9	3055	6	US-10-793-626-4075	Sequence 4075, Ap	
15	135.5	2.9	6921	6	US-10-623-155-117	Sequence 117, App	
16	132	2.8	3204	6	US-10-793-626-3940	Sequence 3940, Ap	
C	17	131.5	2.8	2307	7	US-11-055-557-17	Sequence 17, Appli
18	130.5	2.8	2796	6	US-10-793-626-4335	Sequence 4335, Ap	
19	130.5	2.8	3520	6	US-10-793-626-4160	Sequence 4160, Ap	
20	130.5	2.8	7551	6	US-10-647-956A-1	Sequence 1, Appli	
C	21	130	2.7	2305	6	US-10-485-517-389	Sequence 389, App
22	130	2.7	16792	6	US-10-995-561-262	Sequence 262, App	
23	130	2.7	17292	6	US-10-995-561-260	Sequence 260, App	
24	130	2.7	17507	6	US-10-995-561-254	Sequence 254, App	
25	130	2.7	17610	6	US-10-995-561-258	Sequence 258, App	
26	130	2.7	17642	6	US-10-995-561-256	Sequence 256, App	
27	130	2.7	19023	6	US-10-995-561-259	Sequence 259, App	
28	129.5	2.7	2947	6	US-10-793-626-3805	Sequence 3805, Ap	
29	129.5	2.7	3867	6	US-10-793-626-3769	Sequence 3769, Ap	
30	129.5	2.7	6159	7	US-11-013-759-8	Sequence 8, Appli	
31	129	2.7	2580	7	US-11-189-521-1	Sequence 1, Appli	
32	129	2.7	3016	7	US-11-189-521-3	Sequence 3, Appli	
33	129	2.7	4167	6	US-10-467-657-333	Sequence 333, App	
34	129	2.7	11447	7	US-11-186-284-25	Sequence 25, Appli	
35	128.5	2.7	2307	7	US-11-055-557-5	Sequence 5, Appli	
36	127.5	2.7	6942	7	US-11-013-759-10	Sequence 10, Appli	
37	127	2.7	1752	6	US-10-793-626-1357	Sequence 1357, Ap	
38	127	2.7	2304	7	US-11-055-557-9	Sequence 9, Appli	
39	127	2.7	17436	6	US-10-995-561-257	Sequence 257, App	
40	126.5	2.7	2307	7	US-11-055-557-3	Sequence 3, Appli	
41	125.5	2.6	2307	7	US-11-055-557-7	Sequence 7, Appli	
42	125.5	2.6	2820	6	US-10-510-386-9	Sequence 9, Appli	
43	125.5	2.6	4181	6	US-10-909-125-1738	Sequence 1738, Ap	
44	125	2.6	2304	7	US-11-055-557-1	Sequence 1, Appli	
45	125	2.6	2304	7	US-11-055-557-13	Sequence 13, Appli	

ALIGNMENTS

RESULT 1
US-10-647-956A-5
; Sequence 5, Application US/10647956A
; Publication No. US20050251878A1
; GENERAL INFORMATION:
; APPLICANT: french-Constant, Richard
; APPLICANT: Bowen, David
; APPLICANT: Rocheleau, Thomas
; APPLICANT: Waterfield, Nicholas
; TITLE OF INVENTION: DNA SEQUENCES FROM PHOTORHABDUS LUMINESCENS
; FILE REFERENCE: 61645
; CURRENT APPLICATION NUMBER: US/10/647, 956A
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/817, 514
; PRIOR FILING DATE: CURRENT FILING DATE: 2000-03-26
; PRIOR APPLICATION NUMBER: US 60/191806
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 2745
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2745)
US-10-647-956A-5
Alignment Scores:
Pred. No.: 0 Length: 2745
Score: 4740.00 Matches: 915
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0
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Qy	1	MetSerSerTyrAenSerAlaIleAaspGlnLysThrProSerIleLysValLeuAaspAsn	20
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Qy	21	ArgLysLeuAenValArgThrLeuGluTyrLeuArgThrGlnAlaAaspGluAenSerAsp	40
Db	61	AGGAAATTAATGTACGTACTTTAGATAATCTACGCACCTCAAGCTGACGAAACAGTGAT	120
Qy	41	GluLeuIleThrPheTyrGluPheAenIleProGlyPheGlnValLysSerThrAaspPro	60
Db	121	GAATTAATACGTTCTATGATTCAATATTTCCGGGATTTCCAGGTAAAGACCCGATCCT	180
Qy	61	ArgLysAenLysAenGlnSerGlyProAenPheIleArgValPheAenLeuAlaGlyGln	80
Db	181	CGTAAATATAAACACAGAGCGGCCCAATTTCAATTCGTGTCTTTAATCTTTGCCGGTCAA	240
Qy	81	ValLeuArgGluGluSerValAaspAlaGlyArgThrIleThrLeuAenAaspIleGluSer	100
Db	241	GTTTTACGTGAAGAAAGTTGATGCGCGTCCGACTATTACCCTCAATGATATTGAAAGT	300
Qy	101	ArgProValLeuIleIleAenAlaThrGlyValArgGlnAenHisArgTyrGluAaspAsn	120
Db	301	CGCCCGGTGTGATCATCAATCGCAACCGGTGTCGCCCAAAACCATCGTTATGAAGATAAC	360
Qy	121	ThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGlyGluLysThrThr	140
Db	361	ACCTCTCCGGTGTGCTGCTCGCTATCACCAGAACAGTACAGGAGGAGAGAAACGACC	420
Qy	141	GluArgLeuIleTrpAlaGlyAaspThrProGlnLysAaspTyrAenLeuAlaGlyGln	160
Db	421	GAACGTCTTCTCGGCCGGCAATACGCCGCAAGAAAGATTACAACTCTCGCGGTGAG	480
Qy	161	CysValArgHisTyrAaspThrAlaGlyLeuThrGlnLeuAenSerLeuSerLeuAlaGly	180
Db	481	TGTCGCGCATTACGATACCGCGGACTTACTCAACTCAATAGCCTTTCTCTGCGTGGC	540
Qy	181	ValValLeuSerGlnSerGlnGlnLeuLeuThrAaspAenGlnAaspTrpThrGly	200
Db	541	GTCGTGTCTATCACAACTCTCAACAACTGCTTACCATTAACAGGATGCCGCTGACACAGT	600
Qy	201	GluAaspGlnSerLeuTrpGlnLysLeuSerSerAaspValTyrIleThrGlnSerAsn	220
Db	601	GAAGCCAGAGCCTCTGGCAACAAAACCTGAGTAGTGTATATATATATATATATATATAT	660
Qy	221	ThrAaspAlaThrGlyAlaLeuLeuThrGlnThrAaspAlaLysGlyAenIleGlnArgLeu	240
Db	661	ACTGATGCCACCGGGCTTTACTGACCCAGACCGATGCCAAAGGCAACATTCAGCGCTG	720
Qy	241	AlaTyrAaspValAlaGlyGlnLeuLysGlySerTrpLeuThrLeuLysGlyGlnAlaGlu	260
Db	721	GCCTATGATGGCGGGCGAGCTAAAGGGAGTTGGTTAACTCAAGAGGTCAAGCGGAA	780
Qy	261	GlnValIleIleLysSerLeuThrTyrSerAlaAlaGlyGlnLysLeuAtrGluGluHis	280
Db	781	CAGGTGATTATCAATCGTAACTTACTCTCCCGCGGGCAAAAATTAACGTGAAGAGCAC	840
Qy	281	GlyAenGlyIleValThrGluTyrSerTyrGluProGluThrGlnArgLeuIleGlyIle	300
Db	841	GGTAACGGGATGTCACTGAATACAGCTTACGAAACCGGAAACCCCAACGCGCTTATCGGCAT	900
Qy	301	ThrThrArgArgProSerAaspAlaLysValLeuGlnAaspLeuArgTyrGlnTyrAaspPro	320
Db	901	ACCACTGCCCTCCATCAGACCGCAAGGTGTGAAGACCTTACGCTATCAATATGACCCCA	960
Qy	321	ValGlyAenValIleAenIleArgAaspAlaGluAlaThrArgPheTrpArgAenGln	340
Db	961	GTAGGCAATGTCTAATATCCGTAAATGATGCGGAAGCCACTCGCTTTTGGCGCAATCAG	1020
Qy	341	LysValAlaProGluAenSerTyrThrTyrAaspSerLeuTyrGlnLeuIleSerAlaThr	360
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Qy	361	GlyArgGluMetAlaAaspIleGlyGlnGlnAenAaspGlnLeuProSerProAlaLeuPro	380
Db	1081	GGCGCGGAATGGCCAATATCGGTGAGCAAAACAACAACCTTCCCTCCCTCGGTACCT	1140
Qy	381	SerAaspAenAenThrTyrThrAenTyrThrArgSerTyrSerTyrAaspHisSerGlyAen	400
Db	1141	TCTGACAACAATACCTACCTAACTATCTCGCAGCTACAGCTATGATCAGAGTGTGTAAT	1200
Qy	401	LeuThrGlnIleArgHisSerSerProAlaThrGlnAenAenTyrThrValAlaIleThr	420
Db	1201	CTGACCAAAATTCGGCACAGCTCGCCAGCTACCCAGAACAACTACACCGTGGGTATCACC	1260
Qy	421	LeuSerAenArgSerAenArgGlyValLeuSerThrLeuThrThrAaspProAenGlnVal	440
Db	1261	CTCTCAACCGCAGCAATCGGGGTGTTCTCAGTACGCTAACCCACCGATCCAAATCAAGTG	1320
Qy	441	AspThrLeuPheAaspAlaGlyGlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIle	460
Db	1321	GATACGTTGTTTGTGTCGGTGTGTCACCAAAACCAAGTTTATACCCGGACAGACACTTATC	1380
Qy	461	TrpThrProArgGlyGluLeuLysGlnValAenAenGlyProGlyAenGluTyrTyrArg	480
Db	1381	TGACACACCGAGAGAGTTAAAGCAGGTTAATAATGGCCCGGAAATGATGTTACCGC	1440
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Qy	501	GlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAenAla	520
Db	1501	CAGCAACAACCGGTAATCTATTTGCCGGGACTGAGCTACGCAACAACCCAGAGCAACGCC	1560
Qy	521	ThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArg	540
Db	1561	ACAACAACGGAAGAGTTACACGTTATCACACTCGGTGAAGCCGTCGCGCACAGGTACGG	1620
Qy	541	ValLeuHisTrpGluSerGlyLysProGluAaspValAasnAasnGlnLeuArgTyrSer	560
Db	1621	GTGTTGCACCTGGGAGAGCGGTAAAGCAGAGATGTCAACAATAATCAACTACGTTACAG	1680
Qy	561	TyrAaspAenLeuIleGlySerSerGlnLeuGluLeuAaspAenGlnGlyGlnIleIleSer	580
Db	1681	TACGATAATCTGATCGGCTCCAGCCAGCTTGAACCTGACAAACCAAGGACAAATTTATCAG	1740
Qy	581	GluGluGluTyrTyrProPheGlyGlyThrAlaLeuTrpAlaAlaAenSerGlnThrGlu	600
Db	1741	GAGGAAGAGTATTATTCATTTGGCGGACAGCCCTGTGGCAGCAAAACACCAACAGAA	1800
Qy	601	AlaSerTyrLysThrIleArgTyrSerGlyLysGluArgAaspAlaThrGlyLeuTyrTyr	620
Db	1801	GCCAGCTATAAACGATTCCGTATTCCGCAAAAGACGAGATGCCACCGGTTGTAATTAT	1860
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Db	1861	TACGGTTATCGTTATTACCAACCGTGGCGGCGAGATGGTTAAGCGCGGACCCCGGACGGA	1920
Qy	641	ThrIleAaspGlyLeuAenLeuTyrArgMetValArgAasnAenProValSerLeuGlnAasp	660
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Qy	661	GluAenGlyLeuAlaProGluLysGlyLysTyrThrLysGluValAasnPheAaspGlu	680
Db	1981	GAATAATGGATTAGCGGCAGAAAAGGAATAATACCAAGAGGTAAATTTCTTTTGATGAA	2040
Qy	681	LeuLysPheLysLeuAlaLysSerSerHisValValLysTrpAenGluLysGluSer	700
Db	2041	TTAAATTTCAATTTGGCAGCAAAAAGTTTCACTGTTGTCAATGGAACGAGAAAGAGAGC	2100

QY 701 SerTyrThrLysAsnLysSerLeuLysValValArgValGlyAspSerAspProSerGly 720
Db 2101 AGTTATACAAAATAAATCAITGAAAGGTGTCGTGCGTGAATCCGATCCGTCGGGT 2160
QY 721 TyrLeuLeuSerHisGluGluLeuLeuLysGlyIleGluLysSerGlnIleIleTyrSer 740
Db 2161 TAITTGCTAAGCCACGAGAGTACTAAAGGTATAGAAAAAGTCAATCATATATAGC 2220
QY 741 ArgLeuGluGluAsnSerSerLeuSerGluLysSerLysThrAsnLeuSerLeuGlySer 760
Db 2221 CGACTTGAAGAAAAACAGCTCCCTTTTCAGAAAAATCAAAACGAATCTTTCTTAGGATCT 2280
QY 761 GluIleSerGlyTyrMetAlaArgThrIleGlnAspThrIleSerGluTyrAlaGluGlu 780
Db 2281 GAAATATCCGGTTATATGGCAAGAACCATACAGATACGATATCAAGATATGCCGAGAG 2340
QY 781 HisLysTyrArgSerAsnHisProAspPheTyrSerGluThrAspPheAlaLeuMet 800
Db 2341 CATAAATATAGAGTAAATCACCTCGATTTTATTCAGAAACCGATTTCTTGGGTTAATG 2400
QY 801 AspLysSerGluLysAsnAspTyrSerGlyGluArgLysIleTyrAlaLeuMetGluVal 820
Db 2401 GATAAAGTCAAAAAAATGATTATCCGGTGAAGAAAAAATTTATCGCGCAATGGAGGTT 2460
QY 821 LysValTyrHisAspLeuLysAsnLysGlnSerGluLeuHisValAsnTyrAlaLeuAla 840
Db 2461 AAGGTTTATCATGATTATTAATAAATAACCAATCAAGATTAATCATGCAATGGGCC 2520
QY 841 HisProTyrThrGlnLeuSerAsnGluGluArgAlaLeuLeuGlnGluThrGluProAla 860
Db 2521 CATCCCTATACGCAATTTAGTATAGAAAGAGCGCTGTTGCAGAAACAGAACCCGCT 2580
QY 861 IleAlaIleAspArgGluTyrAsnPheLysGlyValGlyLysPheLeuThrMetLysAla 880
Db 2581 ATTGCAATAGATAGAGATATAATTTCAAAGGTGTTGGCAATTCCTGACAATGAAAGCA 2640
QY 881 IleLysLysSerLeuLysGlyHisLysIleAsnArgIleSerThrGluAlaIleAsnIle 900
Db 2641 ATTAAAAAATCATTTGAAGAGACATAAAATTAATAGGATATCAACAGAGGCTATTATATT 2700
QY 901 ArgSerAlaAlaIleAlaGluAsnLeuGlyMetArgArgThrSer 915
Db 2701 CGCTCTGGCGTATCGCTGAGAAATTTAGGAATCGGAGAACTTCA 2745

RESULT 2
US-10-793-626-3187
; Sequence 3187, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3187
; LENGTH: 3840
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3187

Alignment Scores:
Pred. No.: 0.000275 Length: 3840
Score: 169.00 Matches: 175
Percent Similarity: 36.34% Conservative: 175
Best Local Similarity: 18.17% Mismatches: 369
Query Match: 3.57% Indels: 244

DB: 6 Gaps: 42
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QY 9 AspGlnLysThrProSerIleLysValLeuAspAsnArgLysLeuAenValArgThrLeu 28
Db 871 GATGCAAAACCTGAGCTATAGATACGATACTATATTCACGCAATGTTGCAAAAAA 930
QY 29 GluTyrLeuArgThrGlnAlaAspGluAsnSerAspGluLeuIleThrPheTyrGluPhe 48
Db 931 CCATCGCTCGAGTGAATTAGATTCAAAGTTTGAGGATTTAAAGCGT----- 978
QY 49 AsnIleProGlyPheGlnValLysSerThrAspProArgLysAsnLysAsnGlnSerGly 68
Db 979 -----CAAATCAATGCAACG-----CCCAATGCTACACAAGAAAGAAACAA 1020
QY 69 ProAsnPheIleArg-----ValPheAsnLeuAlaGlyGlnVal 81
Db 1021 GATGCAATTCAAAGATTGAATGTAAGAGAGATGAAGTTAAGNATCTAATAATCAAGAT 1080
QY 82 LeuArgGluGluSerValAspAlaGlyArgThrIleThrLeuAsnAspIleGluSerArg 101
Db 1081 AGACGTGCAACATGAGTTGCAACAGCACAAAAATATTGGACTTCAAGAAATTAGAAACG--- 1137
QY 102 ProValLeuIleAsnAlaThrGlyValArgGlnAsnHisArgTyrGluAspAsnThr 121
Db 1138 -----ATTCAATGCTAATCCAACTAGAAAATCTGATCGCTCCAAGAG----- 1179
QY 122 LeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGlyGluLysThrGlu 141
Db 1180 TTACAACCTAAATTTATTTTCACAACAGAGTTAATTAATAAACAAGATGCACTAAT 1239
QY 142 ArgLeuIleTrpAlaGlyAsnThrProGlnGluLysAspTyrAsnLeuAlaGlyGlnCys 161
Db 1240 -----GAAGAAAAAGATGAA-----GCCAAACGACTT 1266
QY 162 ValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAsnSerLeuSerLeuAlaGlyVal 181
Db 1267 CTTGAGATTAGTAAAAATAAACTATATAACAATATCAAT----- 1305
QY 182 ValLeuSerGlnSerGlnGlnLeuLeuThrAspAsnGlnAspAlaAspTrpThrGlyGlu 201
Db 1306 -----CHAGCGCAAACTAATAATCAAA---GTTGAT---AATGCTAA 1341
QY 202 AspGlnSerLeuTrpGlnGlnLysLeuSerSerAspValTyrIleThrGlnSerAsnThr 221
Db 1342 GATAACGGCATG-----AATGAGATTGCTACCAATAATACCAGCAACAACAATTAAACA 1395
QY 222 AspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGlyAsnIleGlnArgLeuAla 241
Db 1396 GATGCAAAACCGCTATTGATAAAAAAGCTGACCAACAAGTTACATCATCAATGGTAAC 1455
QY 242 TyrAspValAlaGlyGlnLeuLysGlySerTrpLeuThrLeuLysGlyGlnAlaGluGln 261
Db 1456 AACGATGCAACAGATGAAGAAAAAGCAGAGCTAGAAAGCTGTTGAAAAGCGAAAT 1515
QY 262 ValIleIleLysSerLeuTyrSerAlaAlaGlyGlnLysLeuArgGluGluHisGly 281
Db 1516 GAAGCCAAATCTAATATTAACAATAGTATCTGAAGGGAAGTCAATGGTGTAAACC 1575
QY 282 AsnGlyIleValThrGluTyrSerTyrGluProGluThrGlnArgLeuIleThr 301
Db 1576 AATGGGTTAGAAAAAATAAACAATATTCACCTCAACTCAA----- 1617
QY 302 ThrArgArgProSerAspAlaLysValLeuGlnAspLeuArgTyrGlnTyrAspProVal 321
Db 1618 ACTAAACCAAAATGCTAAGCAAGAAATAATGACAAAGCTCAAGAACAA----- 1665
QY 322 GlyAsnValIleAsnIleArgAsnAspAlaGluAlaThrArgPheTrpArgAsnGlnLys 341
Db 1666 -----TTAATCCAAATTAATTAACCGCTGATGCACCCGAGAGAAAGCAAGAG--- 1716
QY 342 ValAlaProGluAsnSerTyrThrTyrAspSerLeuTyrGlnLeuIleSerAlaThrGly 361

Db 1717 -----GCAACAAT 1725
Qy 362 ArgGluMetAlaAenIleGlyGlnGlnAsnAsnGlnLeuProSerProAlaLeuProSer 381
Db 1726 AGGTCATGCTGATTTAGCACAA-----GCAATACAAAT 1761
Qy 382 AspAsnAsnThrThrAsnThrThrArgSerThrArgSerThrAspHisSerGlyAsnLeu 401
Db 1762 ATTAATATGACATAGT-----ACTCAAGAATAATGAATCTAAACAATAATAGTATT 1815
Qy 402 ThrGlnIleArgHisSerSerProAlaThrGlnAsnAsnThrThrValAlaIleThrLeu 421
Db 1816 GCTACATCAAGAGTGATACACCCCAATGTGATCAAAAACCGACT----- 1860
Qy 422 SerAsnArgSerAsnArgGlyValLeuSerThrLeuThrThrAspProAsnGlnValAsp 441
Db 1861 -----GCTATAAATAGTTTGACTCAAGAAGCTAATAATCAAAAG 1899
Qy 442 ThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIleTrp 461
Db 1900 ACGTTAATAGTAATGATGTAATGCTACTGAT----- 1932
Qy 462 ThrProArgGlyGluLeuLeuGlnValAsnAsnGlyProGlyAsnGluTrpTyrArgTyr 481
Db 1933 GATCAAAAAGAGGCTGCAGACCAATAGTACCACCAAAATTAATGAACAATTCAA--- 1989
Qy 482 AspSerAsnGlyMetArgGlnLeuLeuValSerGluGlnProThrGlnAsnThrThrGln 501
Db 1990 -----AAAATTCAATGAAGTACACAAGATCAATCAAGTTGAT 2025
Qy 502 GlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAlaThr 521
Db 2026 AACGTAAAGACACAAGTATCACTGCAATTAATG-----ATTAATGCAATGACAT 2079
Qy 522 ThrThrGluGlu-----LeuHisValIleThr---LeuGlyGluAlaGlyArgAlaGlnVal 539
Db 2080 AAAAGACAAGATGCCATTATATTTGCTACTGCTGAAAGTAAATAATCAGATATA 2139
Qy 540 ArgValLeuHisTrpGluSerGlyLeuProGluAspValAsn----- 553
Db 2140 AGAGCCAAAT-----CAAGATGCAACTACTGAAGAGAAAATACGGCAATCAATCTATA 2193
Qy 554 AsnAsnGlnLeuArgTyrSerTyrAspAsnLeuIleGlySerSerGlnLeuLeuAsp 573
Db 2194 GATGATACGTTAGCACAGCAGTAAACAATTAATGCTGCA----- 2235
Qy 574 AsnGlnGlyGlnIleIleSerGlu-----GluGluTyrTyrProPheGlyGlyThrAla 591
Db 2236 AATACAAATGCTTAGTGATGAGAAATTTAGAAGATGGTAAGCAAAAGTTACAAGTATT 2295
Qy 592 LeuTrpAlaAlaAsnSerGlnThrGluAlaSerTyrIleThrIleArgTyrSerGlyIle 611
Db 2296 GTGTTGTCAACTCAAACTAAAAACAAGCTAAAGCAGACATTGCTCAAGCAATAGGTCAA 2355
Qy 612 GluArgAspAlaThrGlyLeuTyrTyrGlyTyrArgTyrTyrGlnProTrpAlaGly 631
Db 2356 CAAAGG----- 2361
Qy 632 ArgTrpLeuSerAlaAspProAlaGlyThrIleAspGlyLeuAsnLeuTyrArgMetVal 651
Db 2362 -----TCGACATAGAC----- 2373
Qy 652 ArgAsnAsnProValSerLeuGlnAspGluAsnGlyLeuAlaProGluLeuGlyIleTyr 671
Db 2374 -----CAGAATCAAAATGCTACACAGAGAAGAAAAACAAGAGCC 2412
Qy 672 ThrIleGluValAsn-----PhePheAspGluLeuLeuPheLeuAla 686
Db 2413 CTTGAGAGACTTAATCAAGAAACAAATGGAGTCAATGATAGATACAGCAGCTTTAGCA 2472
Qy 687 AlalysSerSerHisValValIleTrpAsnGluLeuGluSer----- 700

Db 2473 AATCAAAAATGTTACACGCAAAAAAATAATATATTAGAAACAATAAGAAATGTTGAACCT 2532
Qy 701 ---SerTyrThrIleAsnIleValValArgValGlyAspSerAspProSer 719
Db 2533 ATTGTAAATTGTAAACCAAGGCTAATGAATAATATTAGAAAAAAGCTGGGAAACACG 2592
Qy 720 GlyTyrLeuLeuSerHisGluGluLeuLeuGlyIleGluLeuSerGlnIleIleTyr 739
Db 2593 ACTTTAATAATCAAAATCAAGATGCGACA-----CTAGAAGAAAAACAATAGCATT 2646
Qy 740 SerArgLeuGluGlu-----AsnSerSerLeuSerGluLeuSerIleThrAsnLeuSer 757
Db 2647 GGCATAATTAGAGAGTAAAGATGAAGCGTTAAATCAAGTATCACAGGCACAC- 2700
Qy 758 LeuGlySerGluIleSerGlyTyrMetAlaArgThrIleGlnAspThr 773
Db 2701 -----TCAATAATGATGAAAAATTGTGAAAAAATAATGGAATGCTAAA 2745
Qy 774 IleSerGluTyrAlaGluGluHisIleTyrArgSerAsn-----HisPro 788
Db 2746 ATTCTGAGGTCCATCTGAGACTATAATTAACGTAATGCTAAACAAGAAATGAACAA 2805
Qy 789 AspPheTyrSerGluThrAspPheAlaLeuMetAspIleSerGluLeuAsnAspTyr 808
Db 2806 GATCGCGAAGTCAAATTGATCTACTATCAATGCAATAATAATAATCAACTAATGAAGAAAA 2865
Qy 809 SerGlyGlu-----ArgIleIleTyrAla 816
Db 2866 TCAGCGCTATAGATAGATTAAATGAGCTAAATGATGCTATTAAACAATATTACTAAT 2925
Qy 817 AlaMetGluValIleTyrHisAspLeuLeuAsnIle----- 829
Db 2926 GCTACAACACTACACAATTAGTTAATGATGCTAAAAAATAGTGGTAACAGAGTATTAGCCAA 2985
Qy 830 -----GlnSerGluLeuHisValAsnTyrAlaLeuAlaHisProTyrThrGlnLeu 846
Db 2986 ATATTACCAAGTACAGCAGTCAAACTAAT---GCATTAGCAGCTCTAGCTAGCGAAGCT 3042
Qy 847 SerAsnGluGluArgAlaLeuLeuGlnGluThrGluProAlaIleAlaIleAspAspGlu 866
Db 3043 AAAAAT---AAAAACGCTAATAGATCAAAACACCAATCGCAGACGAGAGAAAAAGAA 3099
Qy 867 TyrAsnPheIleGlyValGlyIlePheLeuThrMetIleAlaIleIleLeuLeuLeu 886
Db 3100 GAAGCAATAATAAAGTTGATGCT---CTTCAAGAGAGACGAGTGTCTAATATCTTAAAA 3156
Qy 887 GlyHis-----LysIleAsnArgIleSerThrGluAlaIle---AsnIleArgSer 902
Db 3157 GCACACACTACTGATGAAGTTAATAATATTTAAAAATCAAGCTGTTCAAAATATTAAACGCT 3216
Qy 903 AlaAlaIle 905
Db 3217 GTTCAAGTT 3225
RESULT 3
US-10-793-626-4149/c
; Sequence 4149, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4149
; LENGTH: 3543
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: nucleic acid sequence
 US-10-793-626-4149

Alignment Scores:

Argument Scores:				
Pred. No.:	0.000408	Length:	3543	
Score:	166.50	Matches:	173	
Percent Similarity:	36.23%	Conservative:	173	
Best Local Similarity:	18.11%	Mismatches:	366	
Query Match:	3.51%	Indels:	243	
DB:	6	Gaps:	41	

US-10-647-956A-6 (1-915) X US-10-793-626-4149 (1-3543)

Qy	9	AspGlnIysThrProSerIleIysValLeuAspAsnArgIysLeuAsnValArgThrLeu	28
Db	2344	GATGCAAAAACTGAGCGTATAGATACAACTAAATAATTCACCAAAATGTTGCACAAAAA	2285
Qy	29	GluTyrLeuArgThrGlnAlaAspGluAsnSerAspGluLeuIleThrPheTyrGluPhe	48
Db	2284	CCATCCGCTCGAGTGGGAATTAGATTCAAAGTTTGAGGATTTAAAGCGT-----	2237
Qy	49	AsnIleProGlyPheGlnValIysSerThrAspProArgIysAsnIysAsnGlnSerGly	68
Db	2236	-----CAAATCAATGCACAG-CCCAATGCTCAGCAAGCAAGAAAAACAA	2195
Qy	69	ProAsnPheIleArg-----ValPheAsnLeuAlaGlyGlnVal	81
Db	2194	GATGCAATTCAAAGATTGAATGGTTAAAGAGATGAAGTTAAGATCTATATAATCAAGAT	2135
Qy	82	LeuArgGluSerValAspAlaGlyArgThrIleThrLeuAsnAspIleGluSerArg	101
Db	2134	AGACGTGACAATGAAGTTGAACAGACACAAAAATATTGGACTTCAAGAATATTAGAAACG--	2078
Qy	102	ProValLeuIleAsnAlaThrGlyValArgGlnAsnHisArgTyrGluAspAsnThr	121
Db	2077	-----ATTCAATGCTAATCCAACTAGAAAAATCTGATCGGCTCCAAAGAG-----	2036
Qy	122	LeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGlyGluIysThrThrGlu	141
Db	2035	TTCAAACTAAATTTATTTCCAAACACAGAGCTTAATTAATAATAACAAGATGCAACTAAT	1976
Qy	142	ArgLeuIleTrpAlaGlyAsnThrProGlnGluIysAspTyrAsnLeuAlaGlyGlnCys	161
Db	1975	-----GAAAGAAAAAGATGAA-----GCCAAACGCACTT	1949
Qy	162	ValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAsnSerLeuSerLeuAlaGlyVal	181
Db	1948	CTTGAGATTAGTAAAAATAAACTATTAACAAATATCAAT-----	1910
Qy	182	ValLeuSerGlnSerGlnLeuLeuThrAspAsnGlnAspAlaAspTyrThrGlyGlu	201
Db	1909	-----CAAGCGCAAACTAAATAATCAA--GTTGAT--AATGCTAAA	1874
Qy	202	AspGlnSerLeuTrpGlnGlnIysLeuSerSerAspValTyrIleThrGlnSerAsnThr	221
Db	1873	GATAACGCGCATG-----AATGAGATTGCTACCATAATAACAGCAACAACAAATTAACAA	1820
Qy	222	AspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaIysGlyAsnIleGlnArgLeuAla	241
Db	1819	GATGCAAAAACGGCTATTGTATAAAAAGCTGAGCAACAAGTTACATCATCAATGGTAAAC	1760
Qy	242	TyrAspValAlaGlyGlnLeuIysGlySerTrpLeuThrIleThrIysGlyGlnAlaGluGln	261
Db	1759	AACGATGCAACAGATGAAGAAAAAGCAGAGCGCTAGAAAGCTGGTTGAAAAAGCGCAAAATT	1700
Qy	262	ValIleIleIysSerLeuThrTyrSerAlaAlaGlyGlnIysLeuArgGluGluHisGly	281
Db	1699	GAAGCCAAATCTATATATACAAATAGTAGATCTAGAAAGGGAAGTCAATGGTGTCTAAACACC	1640
Qy	282	AsnGlyIleValThrGluTyrSerTyrGluProGluThrGlnArgLeuIleGlyIleThr	301
Db	1639	AATGGGTTAGAAAAATAAACAATATTCAACCATCAACTCAA-----	1598

Qy	302	ThrArgArgProSerAspAlaLysValLeuGlnAspLeuArgTyrGlnTyrAspProVal	321
Db	1597	ACTAAACAAATCTTAAGCAAGAAATAAATGACAAAGCTCAAGACAA	1550
Qy	322	GlyAsnValIleAsnIleArgAsnAspAlaGluAlaThrArgPheIrpArgAsnGlnLys	341
Db	1549	-----TTAATCCAAATTAAATACAGCCCTGATGCACCCGAGAGAAAGACGAGG---	1499
Qy	342	ValAlaProGluAsnSerTyrThrTyrAspSerLeuTyrGlnLeuIleSerAlaThrGly	361
Db	1498	-----GCAACAAAT	1490
Qy	362	ArgGluMetAlaAsnIleGlyGlnAsnAsnGlnLeuProSerProAlaLeuProSer	381
Db	1489	AGAGTCAATCTGGATTAGCACAA-----GCATACAAAT	1454
Qy	382	AspAsnAsnThrTyrThrAsnTyrThrArgSerTyrSerTyrAspHisSerGlyAsnLeu	401
Db	1453	ATTAATAATGCCATAGT-----ACTCAAGAGTAATGAATCTAAAACAAATAGTATT	1400
Qy	402	ThrGlnIleArgHisSerProAlaThrGlnAsnAsnTyrThrValAlaIleThrLeu	421
Db	1399	GCTACATCAAGAGTGTCACACCAATGTGATCAAAAACCGACT-----	1355
Qy	422	SerAsnArgSerAsnArgGlyValLeuSerThrLeuThrThrAspProAsnGlnValAsp	441
Db	1354	-----GCTATAAATAGTTTGACTCAAGAAAGTAATAATCAAAAG	1316
Qy	442	ThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuLeuProGlyGlnThrLeuIleTrp	461
Db	1315	ACGTTAATAGTAATGATGTGTAATGCTACTGAT-----	1283
Qy	462	ThrProArgGlyGluLeuLysGlnValAsnAsnGlyProGlyAsnGluTrpTyrArgTyr	481
Db	1282	GATGAAAACAGCGCTGCAGAAAGCAATTAGTCAGCCCAAAATTAATGNACAAATTCAA---	1226
Qy	482	AspSerAsnGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAsnThrThrGln	501
Db	1225	-----AAAATTCATGAAAGTACACAAAGATAATCAAGTTGAT	1190
Qy	502	GlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAlaThr	521
Db	1189	AACGTAAAGCAACAGCTATCACTGCAATTAATG-----ATTAATGCAAAATGCACAT	1136
Qy	522	ThrThrGluGlu--LeuHisValIleThr--LeuGlyGluAlaGlyArgAlaGlnVal	539
Db	1135	AAAAGACAGATGCTTAATATTTTGACTTAATCTAGCTGAAAGTAAAAATTCAGATATA	1076
Qy	540	ArgValLeuHisIrpGluSerGlyLysProGluAspValAsn-----	553
Db	1075	AGACCAAT-----CAAGATGCAACTACTGAGAGAAAAATACGGCAATACAATCTATA	1022
Qy	554	AsnAsnGlnLeuArgTyrTyrAspAsnLeuIleGlySerSerGlnLeuGluLeuAsp	573
Db	1021	GATGATACGTTAGCACAAAGCAGCTAACATATTAATGGTGCA-----	980
Qy	574	AsnGlnGlyGlnIleIleSerGlu-----GluGluTyrTyrProPheGlyGlyThrAla	591
Db	979	AAATACAAATCGGTTAGTGATAGAAATTTAGAGATGGTAGCAAAAGTTACACGTATT	920
Qy	592	LeuTrpAlaAlaAsnSerGlnThrGluAlaSerTyrIlysthrIleArgTyrSerGlyLys	611
Db	919	GTGTTGTCACTCAACTAAACACAAAGCTTAAGCAGACATTCCTCAAGCAATAGGTCAA	860
Qy	612	GluArgAspAlaThrGlyLeuTyrTyrTyrGlyTyrArgTyrTyrGlnProTrpAlaGly	631
Db	859	CAAAAG-----	854
Qy	632	ArgTrpLeuSerAlaAspProAlaGlyThrIleAspGlyLeuAsnLeuTyrArgMetVal	651
Db	853	-----TCGACATAGAC-----	842

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Qy 652 ArgAsnAsnProValSerLeuGlnAspGluAsnGlyLeuAlaProGluLysGlyLysTyr 671
Db 841 -----CAGAATCAAAATGCTACACAGAGAGAAAACAGAGGCC 803
Qy 672 ThrLysGluValAsn-----PhePheAspGluLeuLysPheLysLeuAla 686
Db 802 CTTGAGAGACTTAATCAAGAAACAAATGGAGTCAATGATAGATAACAAGCAGCTTTAGCA 743
Qy 687 AlalysSerSerHisValValLysTyrAsnGluLysGluSer----- 700
Db 742 AATCAAAATGTTACAGACGAAATAAATAATATATTAGAAAACAATAAGAAATGTTGAACCT 693
Qy 701 ---SerTyrThrLysAsnLysSerLeuLysValValArgValGlyAspSerAspProSer 719
Db 682 ATTGTAATTGTAAACCAAGGCTTAATGAATAATATTAGAAAAGAGCTGGGAAACAACG 623
Qy 720 GlyTyrLeuLeuSerHisGluGluLeuLysGlyLeuLysGlyLeuLysSerGlnLeuLys 739
Db 622 ACTTTAATAAATAAATCAAGATGCGACA-----CTAGAAGAAACAAATAATAGCACTT 569
Qy 740 SerArgLeuGluGlu-----AsnSerSerLeuSerGluLysSerLysThrAsnLeuSer 757
Db 568 GGCAAAATTAGAGAAGTAAGAATGAAGCGTTAAATCAAGTATACAGGCACAC----- 515
Qy 758 LeuGlySerGluLysSerGlyTyrMetAlaArgThrIleGlnAspThr----- 773
Db 514 -----TCAATAATGATGTGAAATTTGTTGAAATAATATGAATTTGCTAAA 470
Qy 774 IleSerGluTyrAlaGluGluHisLysTyrArgSerAsn-----HisPro 788
Db 469 ATTCTGAGGTCCTATCCTGAGACTATAATTAAACGCTAATGCTAAACAAAGAAATTTGAACAA 410
Qy 789 AspPheTyrSerGluThrAspPhePheAlaLeuMetAspLysSerGluLysAsnAspTyr 808
Db 409 GATCGCAAGTCAAAATTTGATCTATCAATGCAAAATAATAATACTAATAATGAAGAAAAA 350
Qy 809 SerGlyGlu-----ArgLysIleTyrAla 816
Db 349 TCAGCCGCTATAGATAGATTAAATGCTAGCTAAATTTGATGCTATTAACTAATTTACTAAT 290
Qy 817 AlaMetGluValLysValTyrHisAspLeuLysAsnLys----- 829
Db 289 GCTCAACTACACAAATAGTTAATGATGCTAAAAATAAGTGGTAAACACGAGTATTAGCCAA 230
Qy 830 -----GlnSerGluLeuHisValAsnTyrAlaLeuAlaHisProTyrThrGlnLeu 846
Db 229 ATATTACCAAGTACAGCAGCTCAAACTAAT---GCATTAGCAGCTCTAGCTAGCGAAGCT 173
Qy 847 SerAsnGluGluArgAlaLeuLeuGlnGluThrGluProAlaIleAlaIleAspArgGlu 866
Db 172 AAAAAAT---AAAAACGCTTATATAGTCAACACCAAAATGCGACAGAGAAGAAAAGAA 116
Qy 867 TyrAsnPheLysGlyValGlyLysPheLeuThrMetLysAlaIleLysLysSerLeuLys 886
Db 115 GAAGCAAAATAATAAAGTTGATCGT---CTTCAAGAAGAAGCAGATGCTAATATCTTAAA 59
Qy 887 GlyHis-----LysIleAsnArgIleSerThrGluAlaIle 898
Db 58 GCACACACTACTGATGAAGTTAATAATATTAAAAAATCAAGCTGTT 14
RESULT 4
US-10-793-626-3153
; Sequence 3153, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3153
; LENGTH: 3285
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3153
Alignment Scores:
Pred. No.: 0.000407 Length: 3285
Score: 166.00 Matches: 204
Percent Similarity: 35.50% Conservative: 151
Best Local Similarity: 20.40% Mismatches: 413
Query Match: 3.50% Indels: 232
DB: 6 Gaps: 45
US-10-647-956A-6 (1-915) x US-10-793-626-3153 (1-3285)
Qy 8 IleAspGlnLysThrProSerIleLysValLeuAspAsnArgLysLeuAsnValArgThr 27
Db 331 TTTAAAGAGCAAAATCCAAGTGTAGCTGATGTCAACAATGCACATAAATAAAGTAAGAGAA 390
Qy 28 LeuGluTyrLeuArgThrGlnAla-----AspGluAsnSerAsp 40
Db 391 GTACACAAAAATAAACAAGCCAGACACTTTTACAAAAATAAAGAGATAATAGTGCA 450
Qy 41 GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro 60
Db 451 CTAGTTTCGAGCCCAAGAACAACTTCAACAGGCGAGTTGACCAAGTCCCTTCCACAGAAAGT 510
Qy 61 ArgLysAsnLysAsnGlnSerGlyProAsnPheIleArgValPheAsnLeuAlaGlyGln 80
Db 511 ATGACGCAACAACTAAAGATGAT-----TACAAATCCAAAACAACAA 552
Qy 81 ValLeuArgGluGluSerValAspAlaGlyArgThrIleThrLeuAsnAspIleGluSer 100
Db 553 GCTGCTCAACAGAAATATCAAAAGCACAACAGTTATCGATAATGGCGATGCGACTACA 612
Qy 101 ArgProValLeuIleIleAsnAla---ThrGlyValArgGlnAsnHisArgTyrGluAsp 119
Db 613 CAACAA-----ATTCTAACGCCCAAAACAAATGTTGAACGCGCTTTTAGAAGCATTAAT 666
Qy 120 AsnThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGln---AlaGlyGluLys 138
Db 667 AATGCAAAACTGGT---TTAAGACGAGATAAAGAGAACTTCAAAATGCTATATAATCAA 723
Qy 139 ThrThrGluArgLeuIleTyrAlaGlyAsnThrProGlnGlu---LysAspTyrAsnLeu 157
Db 724 TTAACCTCAAAATATTGATACGCGGTAAAAACGCTGCAAGTATCAGAAAAATACAATGAA 783
Qy 158 AlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAsnSerLeuSer 177
Db 784 GCTAAGTCAGCTATTCAA-----ACTCAAATTTGATTTCAGCTAAA 822
Qy 178 LeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThr---AspAsn---GlnAsp 195
Db 823 -----AATAAAGCAACACAGTATTTTAAACAATGAACAATCTCCAAGTA 864
Qy 196 AlaAspTrpThrGlyGluAspGlnSerLeuTrpGlnGlnLysLeuSerSerAspValTyr 215
Db 865 TCACAGTGACTGCTGGTTAAACAAAAATAAAGCTGTTCAACCTGAATTAGATAAAAGCG 924
Qy 216 IleThrGln---SerAsnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLys 234
Db 925 ATAGCAATGCTTAAAAATAAAGAGATAATAATATGCTATTGGTT-----CAAGCGAAA 975
Qy 235 GlyAsnIleGlnArgLeuAlaTyrAspVal-----AlaGlyGlnLeu 248
Db 976 CAACAACCTTCAACAATTTGTAATGATAGTAGATCCACAAAGCATGACACACAGATACT 1035
Qy 249 LysGlySerTrpLeuThrLeuLysGlyGlnAlaGluGlnValIleLysSerLeuThr 268
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Db 1036 GCTAAATACTATAAATCAAAAAACGCTGAAGCTGAAGATGAATAA 1080
QY 269 TyrSerAlaAlaGlyGlnLysLeuArgGluHisGlyAsnGlyIleValThrGluTyr 288
Db 1081 -----CAAAAGCTCAACAATCAATTAACATGCGCATGCGACAA 1125
QY 289 SerTyrGluProGluThrGlnArgLeuIleGlyIleThrThrArgArgProSerAspAla 308
Db 1126 CAAATTAATAACGAAAACAATAGA----- 1149
QY 309 LysValLeuGlnAspLeuArgTyrGlnTyrAspProValGlyAsnValIleAsnIleArg 328
Db 1150 -----GTAATCAAGCGATTAATGCAATA 1173
QY 329 AsnAspAlaGluAlaThrArgPheTyrArgAsnGlnLysValAlaProGluAsnSerTyr 348
Db 1174 AAC-----AAGCCAAAACGATTACGCTGCTGATAAGTCTCAATTTGGAAATGCT--- 1224
QY 349 ThrTyrAspSerLeuTyrGlnLeuIleSerAlaThrGlyArgGluMetAlaAsnIleGly 368
Db 1225 ---TATAACCAATTAATACAAATGTTGATACAAATGGTAAAAACCTGCTAGTATT--- 1278
QY 369 GlnGlnAsnAsnGlnLeuProSerProAlaLeuProSerAspAsnAsnThrTyrThrAsn 388
Db 1279 ---CAACAATACCAGCTGCTGCACAGCTATTGAG-----ACGCAA 1317
QY 389 TyrThrArgSerTyrSerTyrAspHisSerGlyAsnLeuThrGlnIleArgHisSerSer 408
Db 1318 TACAATAACGCTAATACAGAGCACAT-----CAAAATCTTGAATAATAGT 1362
QY 409 ProAlaThrGlnAsnAsnTyrThrValAlaIle----- 419
Db 1363 AACCCCTTCAGTTAATGAAGTAGCACAGCATTTACAAAAAGTTGAAGCTGTACAACTTAA 1422
QY 420 -----ThrLeuSerAsnAsnSerAsnArgGlyValLeuSerThrLeu 433
Db 1423 GTTAATGACCGCATTCATATGCTTCAAAATAAAGAGAAATAT-----ACTGCACATT 1473
QY 434 ThrThrAspProAsnGlnVal-----AspThrLeuPheAspAlaGlyGly 448
Db 1474 GTCACAGCTAAAATCACTTCAGCAGCAGTAAATGATCAACCATTAACACAGGTATG 1533
QY 449 HisGlnThrSerLeu-----LeuProGlyGlnThrLeuIleTyr 461
Db 1534 ACTCAAGATTCTATTAATACTATGCTAGCTAAGAGAAATGAGCTCAAGTCTATC--- 1590
QY 462 ThrProArgGlyGluLeuLysGlnValAsnAsnGlyProGlyAsnGluTyrTyrArgTyr 481
Db 1591 -----AGAAATGCAGAAGCTGTCATCAACAATGGCGATGCAACTGCCAAAAACAATTTCA 1644
QY 482 AspSerAsnGlyMetArgGlnLeuLysValSer-----GluGlnPro 495
Db 1645 GACAGAAATCTAAGTTGAACAGCNCCTAGCACATTTGAATGATGCTAAACAGCAATTA 1704
QY 496 ThrGlnAsnThrThrGlnGlnArgValIleTyr----- 507
Db 1705 ACTGCAGATACTACTGAAATTACAAACAGCAGTTCACAAATTAACAGAGCGGATACA 1764
QY 508 -----LeuProGlyLeuGluLeu 513
Db 1765 AATAATAAAAAAGCAAGTATCAATGTCATATAATAAAGCAATTTCAATCATTAGAACA 1824
QY 514 ArgThrThr-----GlnSerAsnAlaThrThrThrGluGluLeuHisValIleThrLeu 531
Db 1825 CAAATTAATCTCTGTAAGATGATGATGCAACGCTGTGATACAAAAACCTTACGTACTGTT 1884
QY 532 GlyGluAlaGlyArgAlaGlnValArgValLeuHisTyrGluSerGlyLysProGluAsp 551
Db 1885 CAAGAGGTAAATATGATTACAAACAGTA----- 1914
QY 552 ValAsnAsnAsnGlnLeuArgTyrSerTyrAspAsnLeuIleGlySerSerGlnLeu--- 570
Db 1915 -----AATCAGTTG-----AATCAACAATTAAC 1938
QY 571 GluLeuAspAsnGlnGlyGlnIleIleSerGluGluGluTyrTyrProPheGlyGlyThr 590
Db 1939 GAAGCAATTAATCAACTTCAACCGCTATCAAAATATGAT----- 1977
QY 591 AlaLeuTyrAlaAlaAsnSerGlnThrGluAlaSerTyr---LysThrIleArgTyrSer 609
Db 1978 GCATTAAGAGCTGCAAGATTAATTTAGAAAAATAAAATTAATCAAACTGTACAAACTGAT 2037
QY 610 GlyLysGluArgAspAlaThrGlyLeuTyrTyrTyrGlyTyrArgTyrTyrGlnProTyr 629
Db 2038 GGTATGACACAAATCTATAGAGCTTATCAAAAGCTTAACGCGTAAACGCGTCCCAAAATGAA 2097
QY 630 AlaGlyArgTyrLeuSerAlaAspProAlaGlyThrIleAspGlyLeuAsnLeuTyr--- 648
Db 2098 TCTAACACTGCTTTAGCATTAATTAATAACGCGGATGCGCATGAACAACAATAATTAACA 2157
QY 649 -----ArgMetValArgAsnAsnProValSerLeuGlnAspGluAsnGlyLeuAla 665
Db 2158 GAAACAGACCGGATCAATCAGCAAACTTAACCTCAAGCAATTAACGCGTTAAACA 2217
QY 666 -----ProGluLysGlyLysTyrThrLysGluValAsnPhePheAspGluLeu 681
Db 2218 GTTAATAAAGAACCATTTAGAACCGCTAAACAGCGTTACAAATTAACATCGACCAAGTA 2277
QY 682 LysPheLysLeuAlaLysSerSerHisValValLysTyrAsnGluLysGluSerSer 701
Db 2278 CCTAGTACAGATGTTATGACTCAGCAATCTGTTGCAAAATTAATTAATAA----- 2328
QY 702 TyrThrLysAsnLysSerLeuLysValValArgValGlyAspSerAspProSerGlyTyr 721
Db 2329 -----CTACAAATAGCTAAA---AACGAAATTAACACAATTAATAAAC 2367
QY 722 LeuLeuSerHisGluGluLeuLysGlyIleGluLysSerGlnIleIleTyrSerArg 741
Db 2368 GTTTTAGAACCAACAATCTAGATGTTAATGCAATCAAAACGAAATTAACAGACGCGAACGA 2427
QY 742 LeuGluGluAsnSerSerLeuSerGluLysSerLysThrAsnLeuSerLeuGlySerGlu 761
Db 2428 ATCAGTAAACGATTTAACA-----CAAGCTAACAATAACTTACAGTTGATCTCAA 2478
QY 762 IleSerGlyTyrMetAlaArgThrIleGlnAspThrIleSerGluTyrAlaGluGluHis 781
Db 2479 CCTTTAGAAAAATAAAGACACAACTTCAAGATGAAATTCATCAAGGTACTAACACAGAT 2538
QY 782 LysTyrArgSerAsnHisProAspPheTyrSerGluThrAspPhePheAlaLeuMetAsp 801
Db 2539 GGAATGACTCAAGATTCAGTGGATTAATTAATGATAGCTTAAGTCGACCAATTTATAGAA 2598
QY 802 LysSer-----GluLysAsnAspTyrSerGlyGluArgLysIleTyr 815
Db 2599 AAAGGCANAGTAAATAAATTAATAACGTAATCCGACAGTAGAACAAGTTAAAGAGAC 2658
QY 816 AlaAlaMetGluValLysValTyrHisAspLeuLysAsnLysGlnSerGluLeuHisVal 835
Db 2659 GTTGTCTAATGTCACAAACAGTCATACAAGATTTACAAATGCTCGAACT----- 2706
QY 836 AsnTyrAlaLeuAlaHisProTyrThrGlnLeuSerAsnGlu-----GluArg 851
Db 2707 -----TCACCTTTCCAGACAAAACTCACTTCAAGAGCTTAAATAATAGATTAGAAAAC 2760
QY 852 AlaLeuLeuGlnGluThrGlu---ProAlaIleAlaIleAsp-----ArgGluTyrAsn 868
Db 2761 AGTATTAAACCAACAACAGATACTGACGCGATGACTCAAGATTCGCTTAAACAATTAAT 2820
QY 869 PheLysGlyValGlyLysPheLeuThrMetLysAlaIleLysLysSerLeuLysGlyHis 888
Db 2821 GATAAATTAGCAAAAGCTAGACAAAACCTTGAAAAATATCTAAAGCTTTTAGTGTGCTCAA 2880
QY 889 LysIle-----AsnArgIleSerThrGluAlaIleAsnIleArgSerAlaAlaIle 905
Db 2881 CCTACTGTAGTGAATTAAGACAAAATAACAGATGAAGCAAAATGCACATAAACCAAGCATTA 2940

Db 1915 -----AATCAGTTG-----AATCAACAATTAAC 1938
QY 571 GluLeuAspAsnGlnGlyGlnIleIleSerGluGluGluTyrTyrProPheGlyGlyThr 590
Db 1939 GAAGCAATTAATCAACTTCAACCGCTATCAAAATATGAT----- 1977
QY 591 AlaLeuTyrAlaAlaAsnSerGlnThrGluAlaSerTyr---LysThrIleArgTyrSer 609
Db 1978 GCATTAAGAGCTGCAAGATTAATTTAGAAAAATAAAATTAATCAAACTGTACAAACTGAT 2037
QY 610 GlyLysGluArgAspAlaThrGlyLeuTyrTyrTyrGlyTyrArgTyrTyrGlnProTyr 629
Db 2038 GGTATGACACAAATCTATAGAGCTTATCAAAAGCTTAACGCGTAAACGCGTCCCAAAATGAA 2097
QY 630 AlaGlyArgTyrLeuSerAlaAspProAlaGlyThrIleAspGlyLeuAsnLeuTyr--- 648
Db 2098 TCTAACACTGCTTTAGCATTAATTAATAACGCGGATGCGCATGAACAACAATAATTAACA 2157
QY 649 -----ArgMetValArgAsnAsnProValSerLeuGlnAspGluAsnGlyLeuAla 665
Db 2158 GAAACAGACCGGATCAATCAGCAAACTTAACCTCAAGCAATTAACGCGTTAAACA 2217
QY 666 -----ProGluLysGlyLysTyrThrLysGluValAsnPhePheAspGluLeu 681
Db 2218 GTTAATAAAGAACCATTTAGAACCGCTAAACAGCGTTACAAATTAACATCGACCAAGTA 2277
QY 682 LysPheLysLeuAlaLysSerSerHisValValLysTyrAsnGluLysGluSerSer 701
Db 2278 CCTAGTACAGATGTTATGACTCAGCAATCTGTTGCAAAATTAATTAATAA----- 2328
QY 702 TyrThrLysAsnLysSerLeuLysValValArgValGlyAspSerAspProSerGlyTyr 721
Db 2329 -----CTACAAATAGCTAAA---AACGAAATTAACACAATTAATAAAC 2367
QY 722 LeuLeuSerHisGluGluLeuLysGlyIleGluLysSerGlnIleIleTyrSerArg 741
Db 2368 GTTTTAGAACCAACAATCTAGATGTTAATGCAATCAAAACGAAATTAACAGACGCGAACGA 2427
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QY 762 IleSerGlyTyrMetAlaArgThrIleGlnAspThrIleSerGluTyrAlaGluGluHis 781
Db 2479 CCTTTAGAAAAATAAAGACACAACTTCAAGATGAAATTCATCAAGGTACTAACACAGAT 2538
QY 782 LysTyrArgSerAsnHisProAspPheTyrSerGluThrAspPhePheAlaLeuMetAsp 801
Db 2539 GGAATGACTCAAGATTCAGTGGATTAATTAATGATAGCTTAAGTCGACCAATTTATAGAA 2598
QY 802 LysSer-----GluLysAsnAspTyrSerGlyGluArgLysIleTyr 815
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QY 816 AlaAlaMetGluValLysValTyrHisAspLeuLysAsnLysGlnSerGluLeuHisVal 835
Db 2659 GTTGTCTAATGTCACAAACAGTCATACAAGATTTACAAATGCTCGAACT----- 2706
QY 836 AsnTyrAlaLeuAlaHisProTyrThrGlnLeuSerAsnGlu-----GluArg 851
Db 2707 -----TCACCTTTCCAGACAAAACTCACTTCAAGAGCTTAAATAATAGATTAGAAAAC 2760
QY 852 AlaLeuLeuGlnGluThrGlu---ProAlaIleAlaIleAsp-----ArgGluTyrAsn 868
Db 2761 AGTATTAAACCAACAACAGATACTGACGCGATGACTCAAGATTCGCTTAAACAATTAAT 2820
QY 869 PheLysGlyValGlyLysPheLeuThrMetLysAlaIleLysLysSerLeuLysGlyHis 888
Db 2821 GATAAATTAGCAAAAGCTAGACAAAACCTTGAAAAATATCTAAAGCTTTTAGTGTGCTCAA 2880
QY 889 LysIle-----AsnArgIleSerThrGluAlaIleAsnIleArgSerAlaAlaIle 905
Db 2881 CCTACTGTAGTGAATTAAGACAAAATAACAGATGAAGCAAAATGCACATAAACCAAGCATTA 2940


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QY 508 -----LeuProGlyLeuGluLeu 513
Db 2210 AATAATAAAGCAAGAGTATCAATGATATATAATAAAGCAATTCATCAATAGAAACA 2269
QY 514 ArgThrThr-----GlnSerAsnAlaThrThrGluGluLeuHisValIleThrLeu 531
Db 2270 CAATTAATCTCTGCTAAAGATATGCAACGCTGTGATACAAAACCTATACCTACTGTT 2329
QY 532 GlyGluAlaGlyArgAlaGlnValArgValLeuHisTrpGluSerGlyLysProGluAsp 551
Db 2330 CAAGAGGTAAATAATGCTATCAACAAGTA----- 2359
QY 552 ValAsnAsnGlnLeuArgTyrSerTyrAspAsnLeuIleGlySerSerGlnLeu--- 570
Db 2360 -----AATCAGTTG-----AATCAACAATTAAC 2383
QY 571 GluLeuAspAsnGlnGlyGlnIleIleSerGluGluGluTyrTyrProPheGlyGlyThr 590
Db 2384 GAAGCAATTAATCACTTCACCGCTATCAATAATGAT----- 2422
QY 591 AlaLeuTrpAlaAlaAsnSerGlnThrGluAlaSerTyr---LysThrIleArgTyrSer 609
Db 2423 GCATTAAGACCTCGAAGATAATTTAGAAATAAATAATTAATCAAACTGTACAACTGAT 2482
QY 610 GlyLysGluArgAspAlaThrGlyLeuTyrTyrGlyTyrArgTyrTyrGlnProTrp 629
Db 2483 GGTATGACACAACAATCTATAGAGGCTTATCAAAACGCTAAACGCTAGGCCCAAAATGAA 2542
QY 630 AlaGlyArgTrpLeuSerAlaAspProAlaGlyThrIleAspGlyLeuAsnLeuTyr--- 648
Db 2543 TCTAACACTGCTTTAGCATTAATTAATAACGGCGATGCCGATGAACAACAATAATTAACA 2602
QY 649 -----ArgMetValArgAsnAsnProValSerLeuGlnAspGluAsnGlyLeuAla 665
Db 2603 GAAACAGACCGAGTCAATCAGCAAACTACAACTTAACCAACCAATTAACGGTTAACA 2662
QY 666 -----ProGluLysGlyLysTyrThrLysGluValAsnPhePheAspGluLeu 681
Db 2663 GTTAATAAAGAACCAATTAGAACCGCTAAACCGCTTACAAATAAATCAACATCGACAGTA 2722
QY 682 LysPheLysLeuAlaLysSerSerHisValValIleValIleValIleValIleValIle 701
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QY 702 TyrThrLysAsnLysSerLeuLysValValArgValGlyAspSerProSerGlyTyr 721
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QY 722 LeuLeuSerHisGluGluLeuLeuLysGlyIleGluLysSerGlnIleIleTyrSerArg 741
Db 2813 GTTTAGCGAAACAATCTAGATGTTAATGCAATCAAAACGAAATAAAGCAGAGCGGAACGA 2872
QY 742 LeuGluGluAsnSerSerLeuSerGluLysSerLysThrAsnLeuSerLeuGlySerGlu 761
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QY 782 LysTyrArgSerAsnHisProAspPheTyrSerGluThrAspPhePheAlaLeuMetAsp 801
Db 2984 GGAATGACTCAAGATTCAAGTGGATTAATTAATGATAGCTTAAGTGCAGCAATATATAGAA 3043
QY 802 LysSer-----GluLysAsnAspTyrSerGlyGluArgLysIleTyr 815
Db 3044 AAAGGCAAAAGTAATAATTAATTAACGTAATCCGACAGTGAACAAGTAAGAGAGC 3103
QY 816 AlaAlaMetGluValLysValTyrHisAspLeuLysAsnLysGlnSerGluLeuHisVal 835
Db 3104 GTTGCTAATCCACAACAAAGTCATACAGATTTACAAAATGCTCGAAT----- 3151
QY 836 AsnTyrAlaLeuAlaHisProTyrThrGlnLeuSerAsnGlu-----GluArg 851
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Db 3206 AGTATTAAACCAACAAACAGATACTACGCGCATGACTCAAGATTCGCTTAACAATTAAT 3265
QY 869 PheLysGlyValGlyLysPheLeuThrMetLysAlaIleLysSerLeuLysGlyHis 888
Db 3266 GATAAATTAGCAAAAGCTAGACAAAACCTTGAATAATATCTAAAGCTTTAGGTGCTCAA 3325
QY 889 LysIle-----AsnArgIleSerThrGluAlaIleAsnIleArgSerAlaAlaIle 905
Db 3326 CCTACTGTAGTGAATTAAGACAAATACAGATGAAGCAAAATGCACATAAACCAAGCATTA 3385

RESULT 6
US-10-821-234-245/c
; Sequence 245, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Labat, Ivan
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 245
; LENGTH: 3626
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-821-234-245

Alignment Scores:
Pred. No.: 0.000772 Length: 3626
Score: 163.50 Matches: 183
Percent Similarity: 33.41% Conservative: 116
Best Local Similarity: 20.45% Mismatches: 304
Query Match: 3.45% Indels: 293
DB: 6 Gaps: 44

US-10-647-956A-6 (1-915) x US-10-821-234-245 (1-3626)
QY 31 LeuArgThrGlnAlaAspGluAsnSerAspGluLeuIleThrPheTyrGluPheAsnIle 50
Db 3592 TTAGCCCACTAAAGTGTGATAACTGGA-----TGGACAAACGTTTTTGTGACTATGACAGT 3539
QY 51 ProGlyPheGlnValLysSerThrAspProArgLysAsnLysAsnGlnSerGlyProAsn 70
Db 3538 GAAGGT-----CGTCTGACAAATGTTAGTTTCCAACT 3506
QY 71 PheIleArgValPheAsnLeuAlaGlyGlnVal----- 81
Db 3505 GGAGTG---GTCAACAACCTGCATGGGACATCGCAAGGCTATCATCAGTGGACATTGAG 3449
QY 82 -----LeuArgGluGluSerValAspAlaGlyArgThrIleThrLeuAsnAspIleGlu 99
Db 3448 TCATCTAGCCGAGAGAGAA-----GATGTGAGCATCACTTCAAACTCTGCTCGATCGAT 3395
QY 100 Ser----- 101
Db 3394 TCTTTCTACCACTGGTTCAAGATCAGTTAAGAAACAGCTACAGATTGTTATGACGGC 3335
QY 102 ProValLeuIleAsnAlaThrGlyValArgGlnAsnHisArgTyrGluAspAsnThr 121
Db 3334 TCCTCAGAAATTAATCTACGCCAGTGGCCCTGAGCTACATACCAACACAGCGCAGCTT 3275
QY 122 LeuProGlyArg-----LeuLeuAlaIleThrGluGlnValGlnAlaGlyGluLys 138
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Db 3274 CTGGCTGGCAGCCGCTAATCCGACGGTTGCCAAAGAAACATGACTTTGGCTGGCGAGAAC 3215
Qy 139 ThrThrGluArgLeuIleThrPalaGlyAsnThrProGln---GluLysAspTyrAsnLeu 157
Db 3214 GGTCAAAACTTGGTGAATGAGATTCGAAAGAGCAAGCCCAAGGAAAGTCAATGTC 3155
Qy 158 AlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAsnSerLeuSer 177
Db 3154 TTTGGCCGCAAGCTCAGG-----GTTAATGGCAGAAACCTTCCTTCA 3113
Qy 178 LeuAlaGlyValValLeuSerGlnSerGlnGlnLeuThrAspAsnGlnAsp----- 195
Db 3112 GTTGACTTTGATCGAACACAAAGACAGCAAGAAAGATCTATGACGACCCCGTAAATTTCTA 3053
Qy 196 -----AlaAspTrpThrGlyGluAspGlnSerLeuTrp-----GlnGlnLysLeu 210
Db 3052 CTGAGGATCGCCTACGACACGCTCTGGGCACCGGACTCTCTGGCTGCCAAGCAGCAAGCTG 2993
Qy 211 SerSerAspValTyrIleThrGlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrGln 230
Db 2992 ATGGCC---GTCAATGTCACCTATTATCCACAGGTCAAAATTCGCAGATCCACGAGGC 2936
Qy 231 ThrAspAlaLysGlyAsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLeu----- 248
Db 2935 ACCACTAGC-----GAGAAAGTAGATTATGACGACAGGGGAGGATCGTGTCT 2888
Qy 249 -----LysGlySerTrpLeu 253
Db 2887 CGGGCTTTGCTGATGTTAAACATGAGGTATACACATATTTAGAAAAGTCCATGGTTCTT 2828
Qy 254 ThrLeuLysGlyGlnAlaGluGlnValle-----IleLysSer 266
Db 2827 CTGCTTCATACCGCAGCGCATACATCTCTCGAATACGATATGTGGGACCGCCTCTCTGCC 2768
Qy 267 LeuThrTyrSerAlaAlaGly-----GlnLysLeuArgGlu----- 278
Db 2767 ATCACCATGCCAGTGGCTCGCCACACACCATGCAGACCATCCGATCCATGGCTACTAC 2708
Qy 279 -----GluHisGlyAsnGlyIleValThrGluTyrSerTyrGlu 291
Db 2707 CGCAACATATACAAACCCCGGAAAGCAACGCCCTCCATCATCAGCGAGTACACAGGAGAA 2648
Qy 292 -----ProGluThrGlnArgLeuIleGlyIleThr 302
Db 2647 GGGCTGCTTCTACAAACAGCTTCTTGGGTACAAGTCGAGGGTCTTATTCAAATACAGA 2588
Qy 303 ArgArgProSerAspAlaLysValLeuGlnAsp-----LeuArgTyrGlnTyrAsp 319
Db 2587 AGGCAGACTAGGCTCTCAGAAATTTATATGATAGACACAGAGTCAGTTTTTACCTATGAT 2528
Qy 320 ProValGlyAsnValIleAsnIleArgAsn----- 329
Db 2527 GAAACAGCAGGAGTCTTAAAGACAGATAAACCTCCACAGTGTGTTTTATTTCACCATTT 2468
Qy 330 -----AspAlaGluAlaThrArgPheTrpArgAsnGln 340
Db 2467 AGATACAGGCAAAATGGTCCCTGATTCAGAGGAGAGATTTCCGCTTTAGTGAAGATGGG 2408
Qy 341 LysValAlaProGluAsnSerTyrThrTyrAspSer----- 352
Db 2407 ATGGTAAATCGAAGATTTTGATATAGCTATGACACAGCTTTTCGAGTGACCATGCAG 2348
Qy 353 -----LeuTyrGlnLeuIleSerAlaThrGly 361
Db 2347 GGTGTGATCAATGAACGCCACTGCTATTGATCTGTATGATAGTTGTGATGACATTTCTGGC 2288
Qy 362 Arg-----GluMetAlaAsnIleGlyGlnGlnAsnAsnGlnLeuProSer 376
Db 2287 ANAGTTGACGAGTTTGGAAAGTTTGGAGTTATATATTATGATATTATTAACCATCATTTCT 2228
Qy 377 ProAlaLeuProSerAspAsnAsnThrTyrThrAsn----- 388

Db 2227 ACAGCTGTA-----ATGACCTATACGAAGCACTTTTGATGCTCATGGCCGCTATC 2180
Qy 389 -----TyrThrArgSerTyrSerTyrAsp 396
Db 2179 AAGGAGATTCAATPATGAGATATTTCAGTCCGCTCATGCTATGGAATTCAAATTCAGTATGAT 2120
Qy 397 HisSerGlyAsnLeuThr-----GlnIleArgHisSerSerProAlaThrGlnAsnAsn 414
Db 2119 AACATGGTGGTAACTAACAGAGAGAGATTAATAATAGGCCCTTTTGCACACACCACAAA 2060
Qy 415 TyrThrValAlaIleThrLeuSerAsnArgSerAsnArgGlyValLeuSerThrLeuThr 434
Db 2059 TATGCTTATGAATATGATGTTGAT-----GGACAGCTTCCAAACAGTTTAC 2015
Qy 435 ThrAspProAsnGlnValAspThrLeu---PheAspAlaGlyGlyHisGlnThrSerLeu 453
Db 2014 CTCAAATGAAAAGATATATGTGGCGGTACAACTACGATCTGAATGGAACCTCCATTTACTG 1955
Qy 454 LeuProGlyGlnThrLeuIleTrpThrPro---ArgGlyGluLeuLysGlnValAsnAsn 472
Db 1954 AACCCAAGTAACAGTCGGCGCTCGACACCCCTTCGCTATGACCTCGGACAGACAGATCACT 1895
Qy 473 GlyProGlyAsnGluTrpTyrArgTyrAspSerAsnGly---MetArgGlnLeuLysVal 491
Db 1894 CGACTGGTGTATCTCAATATCGTTGGATGAAGATGGTTCTCTAGCTCAA----- 1844
Qy 492 SerGluGlnProThrGlnAsnThrThrGlnGlnArgValIleTyrLeuProGlyLeu 511
Db 1843 -----AGGGGCAAG 1835
Qy 512 GluLeuArgThrThrGlnSerAsnAlaThrThrThrGluGluLeuHisValIleThrLeu 531
Db 1834 GAAATCTTTGAATATAGTCCAAAGGGCTTCTAACT-----CGAGTTTACAGTAAA 1784
Qy 532 GlyGlu-AlaGlyArgAlaGlnValArgValLeuHisTrpGluSer-----GlyLys 548
Db 1783 GGCAGTGGCTGGACAGTGATCTACCGTTATGACGGCTCGGAAGGGGTGTTCTTAGCAAA 1724
Qy 548 sProGluAspValAsnAsnGlnLeuArgTyrSerTyrAspAsnLeuIle----- 565
Db 1723 ACCA-----GTCTA-GGACAGCACTGCGAGTTTTTATGCTGACCTTAACCTTATCCAC 1671
Qy 566 -----GlySerSerGln-----LeuGluLeuAspAs 574
Db 1670 TAGATTACTCATGCTACAAACCATTCGAGTTCAGAAATTAACCTCCCTGTTATTATGATCT 1611
Qy 574 nGlnGly-----GlnIleIleSerGluGluGluTyrTyrProPheGly-- 588
Db 1610 CCAAGGACATCTTTTGGCCATGGAAATCAGCAGTGGGGATGAATTTCTATATTGCATCGGA 1551
Qy 589 -----GlyThrAlaLeuTrpAlaAlaAsnSerGlnThrGluAlaSerTyrLysThrI1 606
Db 1550 TAACACAGGACACCACTG--GCTGTGTTTCAGTAGCAATGGGCTTATGCTGAACAGAT 1494
Qy 606 eArgTyrSer----- 609
Db 1493 TCAGTACACTGCATATGGGAAATCTATTTTGACTCTAATATTGACTTTTCACTGGTAAT 1434
Qy 610 -----GlyLysGluArgAspAlaThrGlyLeuTyrTyrGlyTyrArgTy 625
Db 1433 TGGATTTTCATGGTGGCTGTATGACCCACTCACCAAAATTAATCCACTTTTGAGAAAGAGA 1374
Qy 625 rTyrGlnProTrpAlaGlyArgTrp-----LeuSe 635
Db 1373 TTATGACATTTTGGCAGGCGGTGGACCAACCTGCATAGAAATCTGGAAAAGAAATGG 1314
Qy 635 rAlaAspProAlaGlyThrIleAspGlyLeuAsnLeuTyrArgMetValArgAsnAsnPr 655
Db 1313 GAAGGACCAAGCT-----CCTTTTAACCTGTACATGTTTAGGAATAACACCC 1266
Qy 655 oValSer---LeuGlnAspGluAsnGlyLeuAlaProGluLysGlyLysTyrThrLysG1 674
Db 1265 TGCAAGCAAAATCCATGACGTGAAAGATTATACATCACAGATGTTAAACAGCTGGCTGGTGAC 1206

Qy 674 uValAsnPhe-----PheAspGluLeuLysPheLysLeuAl 686
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Db 1205 ATTGGTTTCCATCTGCACAAATGCTATTCTCGGATTCCTGTTCCCAAAATTGATTAAAC 1146
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RESULT 7
US-11-096-051-3
; Sequence 3, Application US/11096051
; Publication No. US20050244869A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: MacLachlan, Timothy K
; APPLICANT: Rastelli, Luca
; APPLICANT: Vernet, Corine
; APPLICANT: Etenberg, Seth
; TITLE OF INVENTION: Ten-M3 Polypeptides and Polynucleotides and their Methods of Use
; FILE REFERENCE: Attorney Docket No. Cura 967
; CURRENT APPLICATION NUMBER: US/11/096,051
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: 10/038,854
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 10/455,772
; PRIOR FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: 60/557,978
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 3
; LENGTH: 7786
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (476)..(7603)
US-11-096-051-3
Alignment Scores:
Pred. No.: 0.0022 Length: 7786
Score: 163.50 Matches: 183
Percent Similarity: 33.41% Conservative: 116
Best Local Similarity: 20.45% Mismatches: 304
Query Match: 3.45% Indels: 293
DB: 9 Gaps: 44
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Qy 51 ProGlyPheGlnValLysSerThrAspProArgLysAsnLysAsnGlnSerGlyProAsn 70
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Qy 71 PheIleArgValPheAsnLeuAlaGlyGlnVal----- 81
|||
Db 4442 GGAGTG---GTCACAAACCTGCGATGGGGACATGGACAAAGCTATCACAGTGGACATTGAG 4498
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Qy 82 -----LeuArgGluGluSerValAspAlaGlyArgThrIleThrLeuAsnAspIleGlu 99
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Db 4499 TCATCTAGCCGAGAA-----GATGTGAGCATCACTTCAAACTGTGCTCTGATCGAT 4552
|||
Qy 100 Ser-----Arg 101
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Qy 102 ProValLeuIleIleAsnAlaThrGlyValArgGlnAsnHisArgTyrGluAspAsnThr 121
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Qy 122 LeuProGlyArg-----LeuLeuAlaIleThrGluGlnValGlnAlaGlyGluLys 138
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Db 4673 CTGGCTGGCACCGCTAATCCGACGGTTGCCAAAGAAACATGACTTTGCTGCGGAGAAC 4732
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Qy 139 ThrThrGluArgLeuIleTrpAlaGlyAsnThrProGln---GluLysAspTyrAsnLeu 157
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Db 4733 GGTCAAAACTTGGTGGAAATGGAGATTCCGAAAGACAGACCCCAAGGAAAGTCAATGTC 4792
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Qy 158 AlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAsnSerLeuSer 177
|||
Db 4793 TTTGGCCGCAAGCTCAGG-----GTTAATGGCAGAAACCTCTTCA 4834
|||
Qy 178 LeuAlaGlyValValLeuSerGlnSerGlnLeuLeuThrAspAsnGlnAsp----- 195
|||
Db 4835 GTTGACTTTGATCGAACACAAAGACAGAAAGATCTATGACGACCAACCGCTAAATTTCTA 4894
|||
Qy 196 -----AlaAspTrpThrGlyGluAspGlnSerLeuTrp-----GlnGlnLysLeu 210
|||
Db 4895 CTGAGATCGCCTACGACACGCTGGGACCCGACCTCTCTGGTGCCACAGCAGCAAGCTG 4954
|||
Qy 211 SerSerAspValTyrIleThrGlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrGln 230
|||
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|||
Qy 231 ThrAspAlaLysGlyAsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLeu----- 248
|||
Db 5012 ACCACTAGC-----GAGAAAGTAGATTATGACGACGAGGAGGATCGTGCT 5059
|||
Qy 249 -----LysGlySerTrpLeu 253
|||
Db 5060 CGGGTCTTTGCTGATGTTAAACATGGAGTTACACATATTTAGAAAGTCCATGGTCTT 5119
|||
Qy 254 ThrLeuLysGlyGlnAlaGluGlnValIle-----IleLysSer 266
|||
Db 5120 CTGCTTCATGACGCGGCGAGTACATCTTCGAATACGATATGCGGACCGCCTGTCTGCC 5179
|||
Qy 267 LeuThrTyrSerAlaAlaGly-----GlnLysLeuArgGlu----- 278
|||
Db 5180 ATCACCATGCCAGTGTGGCTGCCACACCATGACAGACCATCGATTCGCTACTAC 5239
|||
Qy 279 -----GluHisGlyAsnGlyIleValThrGluTyrSerTyrGlu 291
|||
Db 5240 CGCAACATATACAAACCCCGGAAAGCAACGCCCTCCATCATCGGACTACACAGGAA 5299
|||
Qy 292 -----ProGluThrGlnArgLeuIleGlyIleThrThr 302
|||
Db 5300 GGCTCTCTTACAAACAGCTTCTTGGGTGACAAAGTCGAGGGTCTTATTCAATACAGA 5359
|||
Qy 303 ArgArgProSerAspAlaLysValLeuGlnAsp-----LeuArgTyrGlnTyrAsp 319
|||
Db 5360 AGGCAGACTAGGCTCTCAGAAATTTTATGATAGCACAAGAGTACAGTTTACCTATGAT 5419
|||
Qy 320 ProValGlyAsnValIleAsnIleArgAsn----- 329
|||
Db 5420 GAAACAGCAGGAGTCTTAAAGACAGATAAACCTCCAGAGTGATGTTTTTATTCACCACT 5479
|||
Qy 330 -----AspAlaGluAlaThrArgPheTyrAspAsnGln 340
|||
Db 5480 AGATCAGGCAAAATGGTCCCTGATGACAGCAGATTTCGCTTTAGTGAAGATGGG 5539
|||
Qy 341 LysValAlaProGluAsnSerTyrThrTyrAspSer----- 352
|||
Db 5540 ATGTTAATGCAAGATTGCTGACTATAGCTATGACAAACAGCTTTCGAGTGACCATGCGAG 5599
|||
Qy 353 -----LeuTyrGlnLeuIleSerAlaThrGly 361
|||
Db 5600 GGTGTGATCAATGAAACGCCACTGCGCTTATGATCTGTATCAGTTTGTGATTCCTGCGC 5659
|||
Qy 362 Arg-----GluMetAlaAsnIleGlyGlnAsnAsnGlnLeuProSer 376
|||
Db 5660 AAAGTTGAGCAGTTTGGAAAGTTTGGAGTTATATATATATATATATATATATATATATAT 5719
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QY 377 ProAlaLeuProSerAspAsnAsnThrTyrThrAsn----- 388
Db |||:|:|
5720 ACAGCTGTA-----ATGACCTATACGAAGACACCTTTGTGATGCTCATGGCGGTATC 5767
QY 389 -----TyrThrArgSerTyrSerTyrAsp 396
Db |||:|:|
5768 AAGGAGATTCAATATGAGATATTACAGGTGCGTCTATGCTATGCTGATTAACAATTCAGTATGAT 5827
QY 397 HisSerGlyAsnLeuThr-----GlnIleArgHisSerSerProAlaThrGlnAsnAsn 414
Db |||:|:|
5828 AACATGGGTGGGTAACCAAGAGAGAGATTAAATAGGGCCCTTTGGCCAAACACCACCAAA 5887
QY 415 TyrThrValAlaIleThrLeuSerAsnArgSerAsnArgGlyValLeuSerThrLeuThr 434
Db |||:|:|
5888 TATGCTTATGATATGATGTTGAT-----GGACAGCTCCAAACAGTTTAC 5932
QY 435 ThrAspProAsnGlnValAspThrLeu-----PheAspAlaGlyGlyHisGlnThrSerLeu 453
Db |||:|:|
5933 CTCAATGAAGAATAATGTGGCGGTACAACTACGATCTGMAATGGAAACCTCCATTACTG 5992
QY 454 LeuProGlyGlnThrLeuIleThrPro-----ArgGlyGluLeuLysGlnValAsnAsn 472
Db |||:|:|
5993 AACCAAGTAACAGTGGCGGTCTGACACCCCTTCGCTATGACCTGCGAGACAGAACTCACT 6052
QY 473 GlyProGlyAsnGluTyrTyrArgTyrAspSerAsnGly---MetArgGlnLeuLysVal 491
Db |||:|:|
6053 CGACTGGGTGATGTTCAATATCGGTGGATGAAGATGGTTTCCTACGTCAA----- 6103
QY 492 SerGluGlnProThrGlnAsnThrThrGlnGlnArgValIleTyrLeuProGlyLeu 511
Db |||:|:|
6104 -----AGGGGCACG 6112
QY 512 GluLeuArgThrThrGlnSerAsnAlaThrThrThrGluGluLeuHisValIleThrLeu 531
Db |||:|:|
6113 GAAATCTTTGAATATAGTCTCCAAAGGGGCTTCTAACT-----COCGTTTACAGTAAA 6163
QY 532 GlyGlu-AlaGlyArgAlaGlnValArgValLeuHisTyrGluSer-----GlyLy 548
Db |||:|:|
6164 GGCAGTGGCTGGACAGTATCTACCGTTATACGGCTGGAGAGCGGTGTTCTAGCAAA 6223
QY 548 sProGluAspValAsnAsnAsnGlnLeuArgTyrSerTyrAspAsnLeuIle----- 565
Db |||:|:|
6224 ACCA-----GTCTA-GGACAGCACCTGCAGTCTTTTATGCTGCTAACTTATCCAC 6276
QY 566 -----GlySerSerGln-----LeuGluLeuAspAs 574
Db |||:|:|
6277 TAGGATTACTCATGTTCTAACACCATTCAGTTCAGAAATTAACCTCCCTGTTATATGATCT 6336
QY 574 nGlnGly-----GlnIleIleSerGluGluTyrTyrProPheGly-- 588
Db |||:|:|
6337 CCAAGGACATCTTTTGGCCATGGGAAATCAGCAGTGGGGATGAATCTATATGTCATCGGA 6396
QY 589 -----GlyThrAlaLeuTrpAlaAlaAsnSerGlnThrGluAlaSerTyrLysThrIl 606
Db |||:|:|
6397 TAACACAGGGACACCACTG---GCTGTGTTTCAGTAGCAATGGGCTTATGCTGAAACAGAT 6453
QY 606 eArgTyrSer----- 609
Db |||:|:|
6454 TCAGTACACTGCATATGGGGAATCTATTTTGACTCTAATATGACTTTCACTGCTGAAT 6513
QY 610 -----GlyLysGluAArgAspAlaThrGlyLeuTyrTyrGlyTyrArgTyr 625
Db |||:|:|
6514 TGGATTTTCATGGTGGCCCTGTATGACCCACTCACCAAAATTAATCCACTTTGGAGAAAGAGA 6573
QY 625 rTyrGlnProTrpAlaGlyArgTrp-----LeuSe 635
Db |||:|:|
6574 TTATGACATTTTGGCAGGACGGTGCAACACCTGCATAGATAATCTCGAAAAAGAAATTGG 6633
QY 635 rAlaAspProAlaGlyThrIleAspGlyLeuAsnLeuTyrArgMetValArgAsnAsnPr 655
Db |||:|:|
6634 GAAGGACCCAGCT-----CCTTTTAAACTTTGTACATGTTTAGGAATAACACCC 6691
QY 655 oValSer---LeuGlnAspGluAsnGlyLeuAlaProGluLysGlyLysTyrThrLysG1 674
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Db 6682 TGCAGCAAAAATCCATGACGCTGAAAGATTACATCAGAGATTAAACAGCTGGCTGTGAC 6741
QY 674 uValAsnPhe-----PheAspGluLeuLysPheLysLeuAl 686
Db 6742 ATTTGGTTTCCATCTGCACAAATGCTATCTCTGATTCCTGTTCCCAAAATTTGATTTAAC 6801
QY 686 aAlaLysSerSerHisValValLys-----TrpAsnGlu 697
Db |||:|:|
6802 AGAACCTTCTTACGAACCTTGTGAAGAGTCCAGCAGTCGGATGAT 6844

RESULT 8
US-11-096-051-1
; Sequence 1, Application US/11096051
; Publication No. US20050244868A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: MacLachlan, Timothy K
; APPLICANT: Rastelli, Luca
; APPLICANT: Vernet, Corine
; APPLICANT: Eitenberg, Seth
; TITLE OF INVENTION: Ten-M3 Polypeptides and Polynucleotides and their Methods of Use
; FILE REFERENCE: Attorney Docket No. Cura 967
; CURRENT FILING DATE: 2005-03-30
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 10/038,854
; PRIOR FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: 60/557,978
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 1
; LENGTH: 8362
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (71)..(8215)
US-11-096-051-1

Alignment Scores:
Pred. No.: 0.00243 Length: 8362
Score: 163.50 Matches: 183
Percent Similarity: 33.41% Conservative: 116
Best Local Similarity: 20.45% Mismatches: 304
Query Match: 3.45% Indels: 293
DB: 9 Gaps: 44

US-10-647-956A-6 (1-915) x US-11-096-051-1 (1-8362)

QY 31 LeuArgThrGlnAlaAspGluAsnSerAspGluLeuIleThrPheTyrGluPheAsnIle 50
Db |||:|:|
4967 TTAGCCACTAAAAGTCATGAAGAACTGGA-----TGGACAACGTTTTTTGATATGACAGT 5020
QY 51 ProGlyPheGlnValLysSerThrAspProArgLysAsnLysAsnGlnSerGlyProAsn 70
Db |||:|:|
5021 GAAGGT-----CGTCTGACAAATGTTACGTTTCCAACT 5053
QY 71 PheIleArgValPheAsnLeuAlaGlyGlnVal----- 81
Db |||:|:|
5054 GGAGTG---GTCACAAACCTGTCATGGGACATGACCAAGGCTATCAGTGGACATTGAG 5110
QY 82 -----LeuArgGluGluSerValAspAlaGlyArgThrIleThrLeuAsnAspIleGlu 99
Db |||:|:|
5111 TCATCTACCGCAGAGAA-----GATGTCAGCATCACTTCAAATCTGTCTCGATCGAT 5164
QY 100 Ser-----Arg 101
Db |||:|:|
5165 TCTTTTACACCATGGTTCAGATCAGTTAAGAAACAGCTACCAGATTGGTTATGACGGC 5224
QY 102 ProValLeuIleIleAsnAlaThrGlyValArgGlnAsnHisArgTyrGluAspAsnThr 121
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Qy 655 oValSer---LeuGlnAspGluAsnGlyLeuAlaProGluLysGlyLysTyrThrLysG1 674
Db 7294 TGCAGCAAAATCCATGACGTGAAAGATTACATACAGATGTTAAACAGCTGGCTGGTGAC 7353
Qy 674 uValAsnPhe-----PheAspGluLeuLysPheLysLeuA1 686
Db 7354 ATTGGTTTCCATCTGCACAATGCTATTCTCTGGATTCCCTGTTCCCAAAATTGATTAAAC 7413
Qy 686 aAlaLysSerSerHisValVallys-----TyrAsnGlu 697
Db 7414 AGAACCTTCTTACCAACTTGTGAAGAGTCAGCAGCTGGGATCAT 7456

RESULT 9
US-11-096-051-9
; Sequence 9, Application US/11096051
; Publication NO. US20050244868A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: MacLachlan, Timothy K
; APPLICANT: Rastelli, Luca
; APPLICANT: Vernet, Corine
; APPLICANT: Eitenberg, Seth
; TITLE OF INVENTION: Ten-M3 Polypeptides and Polynucleotides and their Methods of Use
; FILE REFERENCE: Attorney Docket No. Cura 967
; CURRENT APPLICATION NUMBER: US/11/096,051
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: 10/038,854
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 10/455,772
; PRIOR FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: 60/557,978
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 9
; LENGTH: 8645
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (151)..(8313)
US-11-096-051-9

Alignment Scores:
Pred. No.: 0.00254 Length: 8645
Score: 163.50 Matches: 183
Percent Similarity: 33.41% Conservative: 116
Best Local Similarity: 20.45% Mismatches: 304
Query Match: 3.45% Indels: 293
DB: 9 Gaps: 44

US-10-647-956A-6 (1-915) x US-11-096-051-9 (1-8645)
Qy 31 LeuArgThrGlnAlaAspGluAsnSerAspGluLeuLeuThrPheTyrGluPheAsnIle 50
Db 5065 TTAGCCCTAAAGTAGTAACTCGGA-----TGGACACGTTTTTGTGATGATGACAGT 5118
Qy 51 ProGlyPheGlnVallysSerThrAspProArgLysAsnLysAsnGlnSerGlyProAsn 70
Db 5119 GAAGGT-----CGTCTGACAAATGTTACGTTTCCAAC 5151
Qy 71 PheLeuArgValPheAsnLeuAlaGlyGlnVal----- 81
Db 5152 GGAGTG---GTCAAAACCTCATGGGACATGGACAGGCTATCACAGTGGACATTGAG 5208
Qy 82 -----LeuArgGluGluSerValAspAlaGlyArgThrIleThrLeuAsnAspIleGlu 99
Db 5209 TCATCTAGCCCGAAGAA-----GATGTACGATCACTTCAAAATCTGTCTCTCGATCAT 5262
Qy 100 Ser-----Arg 101
Db 5263 TCTTCTTACACCATGGTTTCAAGATCAGTTTAAGAAACAGCTACCAGATTGGTTTATGACGGC 5322
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Qy 102 ProValLeuIleAsnAlaThrGlyValA:GlnAsnHisArgTyrGluAspAsnThr 121
Db 5323 TCCTCAGAAATTATCTACGCCAGTGGCTGGACTACACTACCAACAGAGCCGACGTT 5382
Qy 122 LeuProGlyArg-----LeuLeuAlaIleThrGluGlnValGlnAlaGlyGluLys 138
Db 5383 CTGGCTGGCACCCTAATCCGACGGTTGCCAAAAGAAACATGACTTTGCTCGCGAGAAC 5442
Qy 139 ThrThrGluArgLeuIleTrpAlaGlyAsnThrProGln---GluLysAspTyrAsnLeu 157
Db 5443 GGTCAAAACCTTGGTGAATGGAGATTCCGAAAAGAGCAAGCCCAAGGGAAGATCAATGTC 5502
Qy 158 AlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAsnSerLeuSer 177
Db 5503 TTTGGCCCAAGCTCAGG-----GTTAATGGCAGAAACCTCTCTTCA 5544
Qy 178 LeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAspAsnGlnAsp----- 195
Db 5545 GTTGACTTTGATCGAACAACAAAGACAGAAAGATCTATGACGACCACCGTAAATTTCTA 5604
Qy 196 -----AlaAspTrpThrGlyGluAspGlnSerLeuTrp-----GlnGlnLysLeu 210
Db 5605 CTGAGGATCGCTTACGACAGCTCTGGGCACCCGACTCTCTGGCTGCCAAGCAGCAAGCTG 5664
Qy 211 SerSerAspValTyrIleThrGlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrGln 230
Db 5665 ATGCCC---GTCAATGTCACTATTTCACACAGTCAATTCACAGCATCCAGCAGGC 5721
Qy 231 ThrAspAlaLysGlyAsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLeu----- 248
Db 5722 ACCACTAGC-----GAGAAAGTAGATTATGACGACAGGGGAGGAGCTGTCT 5769
Qy 249 -----LysGlySerTrpLeu 253
Db 5770 CGGGTCTTTGCTGATGGTAAACATGGAGTTACACATATTTAGAAAGTCCATGGTCTT 5829
Qy 254 ThrLeuLysGlyGlnAlaGluGlnValIle-----IleLysSer 266
Db 5830 CTGCTTCATAGCCAGCGGAGTACATCTTCGAATAGATATGTGGACCGCCTGTCTGCC 5889
Qy 267 LeuThrTyrSerAlaAlaGly-----GlnLysLeuArgGlu----- 278
Db 5890 ATCACCATGCCAGTGTGGCTGCCACACCATCCAGACCATCCGATTCCTACTAC 5949
Qy 279 -----GluHisGlyAsnGlyIleValThrGluTyrSerTyrGlu 291
Db 5950 CGCAACATATACAAACCCCGGAAAGCAAGCCCTCCATCATCAGGACTACACGAGGAA 6009
Qy 292 -----ProGluThrGlnArgLeuIleGlyIleThrThr 302
Db 6010 GGGCTGCTTCTCAAAACAGCTTCTTGGGTGACAGTCCGAGGGTCTTATTCAATACAGA 6069
Qy 303 ArgArgProSerAspAlaLysValLeuGlnAsp-----LeuArgTyrGlnTyrAsp 319
Db 6070 AGCAGACTAGGCTCTCAGAAATTTATATAGTACACAGAGTCACTTTTACCTATGAT 6129
Qy 320 ProValGlyAsnValIleAsnIleArgAsn----- 329
Db 6130 GAAACACAGCAGGATCTCTAAAGACAGATAAACCTCCAGAGTGATGGTTTTATTGACCAT 6189
Qy 330 -----AspAlaGluAlaThrArgPheTrpArgAsnGln 340
Db 6190 AGATACAGGCAAAATGGTCCCTGATGTTGACAGGAGATTTCGCTTTTAGTGAAGATGG 6249
Qy 341 LysValAlaProGluAsnSerTyrThrTyrAspSer----- 352
Db 6250 ATGTTAAATCAAGATTGACTATAGCTATAGTATGACACAGCTTTCGAGTGACCATGAG 6309
Qy 353 -----LeuTyrGlnLeuIleSerAlaThrGly 361
Db 6310 GGTGTGATCAATGAAAGCCCACTGCCTATTGATCTGTATCATGTTGTATGATCACTTCTG 6369
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Db 5275 TCITTTACACCATGGTTCAAGATCAGTTAAGAAACAGCTACCAGATTGGTTTATGACGGC 5334
Qy 102 ProValLeuIlelleAenAlaThrGlyValArgGlnAenHisArgTyrGluAenAsnThr 121
Db 5335 TCCTCAGAAATTATCTACGGCAGTGGCTGGATCTCACACTACCAAAACAGACCGCACGTT 5394
Qy 122 LeuProGlyArg-----LeuLeuAlaIleThrGluGlnValGlnAlaGlyGluLys 138
Db 5395 CTGGCTGGCACCGCTAATCCGACGGTTGCCAAAGAAAGAAACATGATTTGGCTTGGCGAGAAC 5454
Qy 139 ThrThrGluArgLeuIleThrAlaGlyAsnThrProGln---GluLysAspTyrAsnLeu 157
Db 5455 GGTCAAAACTTGGTGGATGGAGATTCGGAAGAGCAAGCCCAAGGAAAGTCATGTC 5514
Qy 158 AlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAenSerLeuSer 177
Db 5515 TTTGGCCGCAAGCTCAGG-----GTTAATGGCAGAAACCTCTCTTCA 5556
Qy 178 LeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAspAenGlnAsp----- 195
Db 5557 GTTGACTTTGATCGAACAACAGACAGAAAGATCTATGACGACCAACCGTAAATTTCTA 5616
Qy 196 -----AlaAspTTPThrGlyGluAspGlnSerLeuTrp-----GlnGlnLysLeu 210
Db 5617 CTGAGGATCGCTACGACAGCTCTGGGCACCCGACTCTCTGGCTGCCAAGCAGCAAGCTG 5676
Qy 211 SerSerAspValTyrIleThrGlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrGln 230
Db 5677 ATGGCC---GTCAATGTCACTATTATCCACAGGTCAAAATTTGCCAGCATCCAGCGAGGC 5733
Qy 231 ThrAspAlaLysGlyAenIleGlnArgLeuAlaTyrAspValAlaGlyGlnLeu----- 248
Db 5734 ACCACTAGC-----GAGAAAGTATTACGCGACAGCGGAGGATCGTGCT 5781
Qy 249 -----LysGlySerTrpLeu 253
Db 5782 CGGCTCTTGTGATGGTAAACATGGAGTTACACATATTAGAAAGTCCATGGTCTT 5841
Qy 254 ThrLeuLysGlyGlnAlaGluGlnValIle-----IleLysSer 266
Db 5842 CTGCTTCATACCCAGCGCATACATCTTCAATACGATATGTGGACCGCTCTCTGCC 5901
Qy 267 LeuThrTyrSerAlaAlaGly-----GlnLysLeuArgGlu----- 278
Db 5902 ATCACCATGCCAGTGGCTGGCCACACCATGACAGACCATCCATCCATGGCTACTAC 5961
Qy 279 -----GluHisGlyAenGlyIleValThrGluTyrSerTyrGlu 291
Db 5962 CGCAACATATACACCCCGGAAAGCAACGCTCCATCATCATCAGGACTACACAGGAA 6021
Qy 292 -----ProGluThrGlnArgLeuIleGlyIleThr 302
Db 6022 GGGCTGCTTCTACAAACAGCTTTCTGGGTACAAGTCGGAGGTCTTATTCAAAATACAGA 6081
Qy 303 ArgArgProSerAspAlaLysValLeuGlnAsp-----LeuArgTyrGlnTyrAsp 319
Db 6082 AGGCAGACTAGGCTCTCAGAAATTTTATGATAGCACAGAGTCAGTTTACCTATGAT 6141
Qy 320 ProValGlyAenValIleAsnIleArgAen----- 329
Db 6142 GAAACAGCAGGATCTCTAAGACACAGTAACCTCCAGAGTGATGGTTTATTGACCATTT 6201
Qy 330 -----AspAlaGluAlaThrArgPheTrpArgAenGln 340
Db 6202 AGATACAGGCAAAATGGTCCCTGATTGACAGGAGATTTTCCGCTTTAGTGAAGATGGG 6261
Qy 341 LysValAlaProGluAenSerTyrThrAspSer----- 352
Db 6262 ATGTTAAATGCAAGATTGATAGCTATGATGATGACAAACAGCTTTTCGAGTGACCGATGAG 6321
Qy 353 -----LeuTyrGlnLeuIleSerAlaThrGly 361
Db 353 -----LeuTyrGlnLeuIleSerAlaThrGly 361

Db 6322 GGTGTGATCAATGAAGAACGCCACTGCTTATGATCTGTATGATTTGATGACATTTCTTGGC 6381
Qy 362 Arg-----GluMetAlaAenIleGlyGlnAenAenGlnLeuProSer 376
Db 6382 AAAGTTGACAGATTGGAAAGTTTGGAGTTATATATATGATATTAACAGATCATTTCT 6441
Qy 377 ProAlaLeuProSerAspAenAenThrTyrAsn----- 388
Db 6442 ACAGCTGTA-----ATGACCTATACGACCACTTTTGTATGCTCATGSCCGCTATC 6489
Qy 389 -----TyrThrArgSerTyrSerTyrAsp 396
Db 6490 AAGGATTCATATATGAGATATTCAGTGGCTCATCTTCTGATTAACAATTCAGATGAT 6549
Qy 397 HisSerGlyAsnLeuThr-----GlnIleArgHisSerSerProAlaThrGlnAenAen 414
Db 6550 AACATGGTGGGTAAACCAAGAGAGATTAATAATAGGGCCCTTTCGCAACACCACAAA 6609
Qy 415 TyrThrValAlaIleThrLeuSerAsnArgSerAsnArgGlyValLeuSerThrLeuThr 434
Db 6610 TATGCTTATGAATATGATGTTGAT-----GGACAGCTCCAAACAGTTTAC 6654
Qy 435 ThrAspProAenGlnValAspThrLeu-----PheAspAlaGlyGlyHisGlnThrSerLeu 453
Db 6655 CTCAATGAAGAGATAATGTGGCGGTACAACTACGATCTGAATGGAACCTCCATTTACTG 6714
Qy 454 LeuProGlyGlnThrLeuIleThrPro---ArgGlyGluLeuLysGlnValAenAen 472
Db 6715 AACCCAGTAACAGTGGCGTCTGACCCCTTCGCTATGACCTGGAGAGACAGAACTACT 6774
Qy 473 GlyProGlyAsnGluTrpTyrArgTyrAspSerAsnGly---MetArgGlnLeuLysVal 491
Db 6775 CGACTGGGTGATGTTCAATATCGTTGGATGAAGATGGTTTCTCTACGTCAA----- 6825
Qy 492 SerGluGlnProThrGlnAenThrThrGlnGlnArgValIleTyrLeuProGlyLeu 511
Db 6826 -----AGGCGCACG 6834
Qy 512 GluLeuArgThrThrGlnSerAenAlaThrThrGluGluLeuHisValIleThrLeu 531
Db 6835 GAAATCTTGAATATAGTCCAAAGGGCTTCTAACT-----CGAGTTTACAGTAAA 6885
Qy 532 GlyGlu-AlaGlyArgAlaGlnValArgValLeuHisTrpGluSer-----GlyLys 548
Db 5886 GGCAAGTGGCTGGACAGTATCTACCTTATGACGGCTGGAGAGCGTGTCTTAGCAAA 6945
Qy 548 sProGluAspValAenAenGlnLeuArgTyrSerTyrAspAenLeu----- 565
Db 6946 ACCA-----GTCTA-GGACAGCACCTGCAGTGTCTTATGCTGACTTAACCTATCCAC 6998
Qy 566 -----GlySerSerGln-----LeuGluLeuAspAs 574
Db 6999 TAGGATTACTGCTCTACACCATTCGAGTTAGAAATTAACCTCCTCTGATTATGATCT 7058
Qy 574 nGlnGly-----GlnIleIleSerGluGluGluTyrTrpPheGly-- 588
Db 7059 CCAAGGACATCTTTTGGCCATGGAATCAGCACTGGGATGATTTCTATATTGATCGGA 7118
Qy 589 -----GlyThrAlaLeuTrpAlaAlaAenSerGlnThrGluAlaSerTyrLysThrI 606
Db 7119 TAACACAGGGGACCACTG---GCTGTGTTTCTAGTAGCAATGGGCTTATGCTGAACAGAT 7175
Qy 606 eArgTyrSer----- 609
Db 7176 TCAGTACACTGCATATGGGAAATCTATTTTGTACTCTAATATTGACTTTCACTGGTAAT 7235
Qy 610 -----GlyLysGluArgAspAlaThrGlyLeuTyrTyrGlyTyrArgTy 625
Db 7236 TGGATTTTCATGGTGGCTGTATGACCCACTCACCAATTAATCCACTTTGAGAGAGAGA 7295
Qy 625 rTyrGlnProTrpAlaGlyArgTrp-----LeuSe 635
Db 7296 TTATGACATTTTGGCAGGCGGTGGACCAACACCTGACATAGAAATCTGGAAAGAAATTGG 7355

QY 635 rAlaAspProAlaGlyThrIleAspGlyLeuAsnLeuTyrArgMetValArgAsnAsnPr 655
Db 7356 GAAGGACCAGCT-----CCTTTAACTTGTACATGTTTAGGAATAACAACC 7403
QY 655 oValSer---LeuGlnAspGluAsnGlyLeuAlaProGluLysGlyIlyTyrThrIysGI 674
Db 7404 TGAAGCAAAATCCATGACGTGAAGATTACATCACAGATGTTTAAACAGCTGGCTGTGAC 7463
QY 674 uValAsnPhe-----PheAspGluLeuLysPheLysLeuAl 686
Db 7464 ATTGGTTCCTCTGCACATGCTATTCTCTGATTCCCTGTTCCCAATTTGATTTAAC 7523
QY 686 aAlaLysSerSerHisValVallys-----TyrAsnGlu 697
Db 7524 AGAACCTTCTTACGAACCTTGTGAAGATCAGCAGTGGGATGAT 7566

RESULT 11
US-10-793-626-3824/c
; Sequence 3824, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3824
; LENGTH: 3068
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3824

Alignment Scores:
Pred. No.: 0.0314 Length: 3068
Score: 144.00 Matches: 194
Percent Similarity: 36.29% Conservative: 174
Best Local Similarity: 19.13% Mismatches: 389
Query Match: 3.04% Indels: 258
DB: 6 Gaps: 53

US-10-647-956A-6 (1-915) x US-10-793-626-3824 (1-3068)

QY 3 SerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsnArgLys 22
Db 2929 GCGTATAATATGCACTTAACAAAGCGGAGACATTAATTAACAGCTCAATCTCTAAC 2870
QY 23 LeuAsnValArgThrLeuArgThrLeuArgThrGlnAlaAspGluAsnSerAspGluLeu 42
Db 2869 TTAATGTCACAGACATT-----ACTAATGCTTTAAATAAT----- 2834
QY 43 IleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspProArgLys 62
Db 2833 ATTAACACACACAGATAACCTTCATGGAGCTCAA---AAATTAACAGCAAGCAAAAAT 2777
QY 63 AsnLysAsnGlnSerGlyProAsnPheIleArgValPheAsnLeuAlaGlyGlnValLeu 82
Db 2776 ACACTAATCAGCATTGGTAC-----TTAATCATCTTAATCAACCTCAA 2729
QY 83 ArgGluSerValAspAlaGlyArgThrIleThrLeuAsnAspIleGluSerArgPro 102
Db 2728 AAAGATCGCTTATACAGCT-----ATTAATGAGCTACATCTAGGAC 2684
QY 103 ValLeuIleIleAsnAlaThrGlyValArgGlnAsnHisArgTyrGluAspAsnThrLeu 122
Db 2683 CAAGTT-----GCAGAAAACTTAAAGAGCGCCGAGCGCTT 2648

QY 123 ProGlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGlyGluLysThrThrGluArg 142
Db 2647 GATGAAGCTATGAACAACACTTGAAGATCAAGTGAATCAAGATGATCAAAATTTCAATAGC 2588
QY 143 LeuIleTyrAlaGly---AsnThrProGlnGluLysAspTyrAsnLeuAlaGlyGlnCys 161
Db 2587 AGCCCAATTCATAATGAAGACTCAGACAACAACAAACTTATAAT----- 2543
QY 162 ValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAsnSerLeuSerLeuAlaGlyVal 181
Db 2542 -----GATAAAATCCAAGCTGCAAAAGAA 2519
QY 182 ValLeuSerGlnSerGlnGlnLeuLeuThrAspAsnGlnAspAlaAspTrpThrGlyGlu 201
Db 2518 ATAATTAATCAAAACATCTAATCAACCTTAGATAAACAACAAATTTGCTGATACACTTCAA 2459
QY 202 AspGlnSerLeuTyrGlnGlnLysLeuSerAspValTyrIleThrGlnSerAsnThr 221
Db 2458 AATATTAAAGATGCGAGTGAATATTTACATGGTGATCAAAATTTACTCAATCTAAACAA 2399
QY 222 AspAlaThrGly----- 225
Db 2398 GACGCTAATAATCAATTAATCATTTAGATGACTTAACCGAAGACAAACAAACCACTTTT 2339
QY 226 ---AlaLeuLeuThrGlnThrAspAlaLysGlyAsnIleGlnArgLeuAlaTyrAspVal 244
Db 2338 AAACCGTTAATAATTAATGCTGATCTCGAGATGAGGTAATAA---CAACTAGAGATT 2282
QY 245 AlaGlyGlnLeuLysGlySerTrpLeuThrLeu-----LysGlyGln 258
Db 2281 GCTAAACAATTAATGGTGATGATGAGTACACTTCATAAAGTCATAAATGATAAGATCAA 2222
QY 259 AlaGluGlnValIleIleLysSerLeuThrTyrSerAlaAlaGlyGlnLysLeuArgGlu 278
Db 2221 ATTCAACATTTA-----ACCAATTACATTAAATGCTGATGATAATGATAAACAACAA 2174
QY 279 GluHisGlyAsnGlyIleValThrGluTyrSerTyrGluProGluThrGlnArgLeuIle 298
Db 2173 AATTATGATAATGCTATT-----AAAGAAGCTGAGGATTTAATT 2135
QY 299 GlyIleThrThrArgArgProSer-----AspAlaLysValLeuGlnAspLeuArgTyr 316
Db 2134 -----CATAATCATCCAGATACATTAGATCATATAAGCATTAACAAGATTTATTAAAC 2084
QY 317 GlnTyrAspProValGlyAsnValIle----- 325
Db 2083 AGATAGACCAAGCGCATACCGAATTAATGGAGATCCAGATTTAAACAGCGCTTTAGAC 2024
QY 326 AsnIleArgAsnAspAlaGluAlaThrArgPheTrpArgAsnGlnLysValAlaProGlu 345
Db 2023 AATGCTTTAAACGACATAGATAGCTTA-----AACAGTCTCAATGTTCACAA 1976
QY 346 AsnSerTyrThrTyrAspSerLeuTyrGlnLeu-----IleSerAlaThrGlyArgGlu 363
Db 1975 CGTCAAACTGTTAAGGATAACATCAACCATGTGACAACTCTAGAAAGTTTAGCTCAAGAA 1916
QY 364 MetAlaAsnIleGlyGlnGlnAsn-----AsnGlnLeuProSer 376
Db 1915 TTCGAAAGCAAAAGAGCTTAATGCTGCTATCAAGCAATGAGAGATGATGATTAATGAAT 1856
QY 377 ProAlaLeuProSerAspAsnAsnThrTyrThrAsn-----TyrThrArgSerTyrSer 394
Db 1855 CAAGACAAATTCGTAATAATAGCAATTAATGAGAGCTTAGCTCAACAAATGCC 1796
QY 395 TyrAspHisSer---GlyAsnLeuThrGlnIleArgHisSerSerProAlaThr----- 411
Db 1795 TATAATCATGCGATAGATATAATAACATATTATTGGTGAAGACAAATGCGAGATGGAT 1736
QY 412 -----GlnAsnAsnTyrThrValAlaIleThrLeuSerAsnArgSerAsn 426
Db 1735 CCTCAATAATCAACACCAAGCACTCAAGATATAAATACAGCTATAAATGATTAATATGGA 1676

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Qy 427 ArgGlyValLeuSerThrLeuThrThrAspProAsnGlnValAspThrLeuPheAspAla 446
Db 1675 GATCAAAACTTCNAGATGCAACAGACAGATGCTAAACAAACAATTAATCTT-----1622
Qy 447 GlyGlyHisGlnThrSerLeuLeuProGlyGln-----ThrLeuLeu---460
Db 1621 -----ACTGGTTTAACCTGAACCAACAAACAAAGCATTTGGAAAAACATCATTAAC 1574
Qy 461 ---TrrPrrProArgGlyGluLeu---LysGlnValAsnAsnGlyProGlyAsnGluTrr 478
Db 1573 CAACAAAGTAGAGCAAAATGTTGCTAAACAGTTAAGTCTGCT-----1529
Qy 479 TyrArgTyrAspSerAsnGlyMetArgGlnLeuLysVal-----491
Db 1528 ---AAATCTTAAATGGAAGAAATGGAAGAAATTAAGTTGCAGTAGCCAAAGCGCTATTA 1472
Qy 492 -----SerGlnPrrProThrGlnAsnThrThrGlnGlnGln 503
Db 1471 GTAAGACAAAATAGTAATATATTAATGAAGATGCTCTGAAAAGAAAGCATATGAACAA 1412
Qy 504 ArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAlaThrThr 523
Db 1411 GCTATT-----GCAAAAGGTGAGGAAATTAATTAATTCAGAAATTAATCCAAACAATAGT 1358
Qy 524 GluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArgValLeuHis 543
Db 1357 AGTACTGATATCATCTGATCAATTCAGAAATTAATGATGCTGAA---CAAAATCTTCAT 1301
Qy 544 TrpGluSer-----GlyLysProGluAspValAsnAsnGlnLeuArgTyrSerTyr 561
Db 1300 GGTGAAAATAAATTAAGACACAGACAGGAAATTCGAAAGAAATGAATAACAA-----1250
Qy 562 AspAsnLeuIleGlySerSerGlnLeuGluLeuAspAsnGlnGlyGlnIleIleSerGlu 581
Db 1249 ---AATCTAGACGGATTAATTTACGCTCAAAATTAACAAATTAATCCAGATATAGGCAGA 1193
Qy 582 GluGluTyrTyrProPheGlyGlyThrAlaLeuTrrPrrAlaAlaAsnSerGlnThrGluAla 601
Db 1192 ACAACAATAAATCTGAGTAACTCAGAACTCAGAACTAGAAAGCAAAAGCAATAAACCAAGCT 1133
Qy 602 SerTyrLysThrIleArgTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyr 621
Db 1132 ---ATGCAACAACATTAACCAAAAGTATAGCCGATAAGGATGCTACT-----1091
Qy 622 GlyTyrArgTyrTyrGlnProTrrPrrAlaGlyArgTrrPrrLeuSerAlaAspProAlaGlyThr 641
Db 1090 -----CTAAATTTCTAGTAACTATCTCAATGAAGAT-----1061
Qy 642 IleAspGlyLeuAsnLeuTyrArgMetValArgAsnAsnProValSerLeuGlnAspGlu 661
Db 1060 -----TCTGAGAAAAGTTAGCTAGCATATGCTGTAGCCAGCTGAACAA 1013
Qy 662 AsnGlyLeuAlaProGlyLysGlyLysTyrThrLysGluValAsnPheAspGluLeu 681
Db 1012 -----CTCATAATCAACTTAACGCCCACTATGATATAGTAATATTAATCAAGCTATT 959
Qy 682 LysPheLys---LeuAlaAlaLysSer-----HisValValLysTrrAsn 696
Db 958 ACTCAAAAGGTTCATTCAAGCAAAAGATTCATTGCGCGTGCAGTAATAAATTCGACAAAAT 899
Qy 697 GluLysGluSerSerTyrThrLysAsnLysSerLeuLysValValArgValGlyAspSer 716
Db 898 CAACGATTCAAATTTAATAATAATAATCAATCA-----ACAAATTTAATGATAAA 848
Qy 717 AspProSerGlyTyr-----LeuLeuSerHisGluGluLeuLysGlyIleGluLys 734
Db 847 CAAAAGCAAGCATTAATGACTTAATTAATCATGCTCAA-----ACTAAA 803
Qy 735 SerGlnIleIleTyrSerArgLeuGluGluAsnSerSerLeuSerGluLysSerLysThr 754
Db 802 CAGCAAGTGGCA-----GAAATAATTTGACCAAGCTTAATAGTTA 764
Qy 755 AsnLeuSerLeuGlySerGluIleSerGlyTyrMetAlaArgThrIleGlnAspThrIle 774
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Db 763 AATAACGAAATGGGCACA-----CTAAAAACACTCGTAGAAGAACAG 722
Qy 775 SerGluTyrAlaGluGluHisLysTyrArgSerAsnHisPro-----AspPheTyr 791
Db 721 TCAACAGTTTCATCAACAAAGTAATATATTAATGAAGATCCGCAAGTTCAAAATATTTAT 662
Qy 792 SerGlu-----ThrAspPhePheAlaLeu 799
Db 661 AATGACTCCATTCAAAAAGTCGAGAAATATTAAACGGCACTACAGATGATGTTTTAAAC 602
Qy 800 MetAspLys-----SerGluLysAsnAspTyrSerGly 810
Db 601 AACATAAATAATAGCAGATGCCATTCAAAACATTCATTAACTAAAAACGATTTACATGGT 542
Qy 811 GluArgLysIleTyrAlaAlaMet-----GluValLysValTyrHisAsp 825
Db 541 GATCAAAAATTTACAAAAGCACAAACAGATGCAACCAATGAATTAACATTTTAAACAAAT 482
Qy 826 LeuLysAsn-----LysGlnSerGluLeuHisValAsnTyrAlaLeuAlaHisProTyr 843
Db 481 CTAACAATCTCAAAAGACAAACGAG---CATGATGAGATTAACTCTGCTCCTTCAGA 425
Qy 844 ThrGlnLeuSerAsnGlu-----GluArgAlaLeu-----LeuGlnGluThr 857
Db 424 ACTGAAGTTTCTAATGATTTAAATCATGCTAAAAGCACTTAATGAAGCTATGCGTCAACTT 365
Qy 858 GluProAlaIleAlaIleAspArgGluTyrAsnPheLysGlyValGlyLysPheLeuThr 877
Db 364 GAGAATGAAGTTGCTCTT-----GAAAACAGCTTTAAAAAATTAAGCGACTTTATCA-- 313
Qy 878 MetLysAlaIleLysLysSerLeuLysGlyHisLysIleAsn 891
Db 312 ATGAAG-----ATGAAGCGGCACAAAATGAAT 286

RESULT 12
US-10-793-626-2963
; Sequence 2963, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2963
; LENGTH: 15071
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-2963

Alignment Scores:
Pred. No.: 0.278 Length: 15071
Score: 144.00 Matches: 194
Percent Similarity: 36.29% Conservative: 174
Best Local Similarity: 19.13% Mismatches: 389
Query Match: 3.04% Indels: 258
DB: 6 Gaps: 53

US-10-647-956A-6 (1-915) x US-10-793-626-2963 (1-15071)

Qy 3 SerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsnArgLys 22
Db 4240 CGGTATAATAATGACATTTAAACAAACGCGGAAGACATTAATTAACAGCTCAAAATCCTAAC 4299
Qy 23 LeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAsnSerAspGluLeu 42
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QY 682 LysPheLys---LeuAlaAlaLysSerSer-----HisValValLysTrpAsn 696
Db 6211 ACTCAAAAGGTCATTCAAGCAAAAGATGTCGACGGTCGGAATAAACTTGCACAAAAT 6270
QY 697 GluLysGluSerSerTrpThrLysAsnLysSerLeuLysValValArgValGlyAspSer 716
Db 6271 CAACGATTCAAATTTAATAATAATCAATCA-----ACAAATTTAATGATATAA 6321
QY 717 AspProSerGlyTyr-----LeuLeuSerHisGluLeuLeuLysGlyIleGluLys 734
Db 6322 CAAAAGCAAGCATTAATGACTTAATTAATCATCTCAA-----ACTAAA 6366
QY 735 SerGlnIleIleTyrSerArgLeuGluLysSerSerLeuSerGluLysSerLysThr 754
Db 6367 CAGCAAGTGCCA-----GAAATAATTGCACCAAGCTAATAAGTTA 6405
QY 755 AsnLeuSerLeuGlySerGluIleSerGlyTyrMetAlaArgThrIleGlnAspThrIle 774
Db 6406 AATAACGAATGGGCACA-----CTAAAAACACTCGTAGAAGACAG 6447
QY 775 SerGluTyrAlaGluGluHisLysTyrArgSerAsnHisPro-----AspPheTyr 791
Db 6448 TCAACCGTTTCATCAACAAAGTAATATATTAAAGATCGCAAGTTCAAAAATATTAT 6507
QY 792 SerGlu-----ThrAspPhePheAlaLeu 799
Db 6508 AATGACTCCATTCAAAAAGGTCGAGAAATATTAAACGGCACTACAGATGATGTTTTAAAC 6567
QY 800 MetAspLys-----SerGluLysAsnAspTyrSerGly 810
Db 6568 AACATAAATAGCAGATGCCATTCAAAACATTTCAATTAAACGATTTACATGGT 6627
QY 811 GluArgLysIleTyrAlaAlaMet-----GluValLysValTyrHisAsp 825
Db 6628 GATCAAAAATATCAAAAAGCAACAACAGATGCAACCAATGAATTAATTAACAAAT 6687
QY 826 LeuLysAsn-----LysGlnSerGluLeuHisValAsnTyrAlaLeuAlaHisProTyr 843
Db 6688 CTAAACAAATTTCTCAAGACAAAGCGAG---CATGATGAGATTAACTCTGCTCTCTTCAAGA 6744
QY 844 ThrGlnLeuSerAsnGlu-----GluArgAlaLeu-----LeuGlnGluThr 857
Db 6745 ACTGAAGTTCTAATGATTTAATATCATGCTAAAGCACTTAATGAAGCTATGCGTCAACTT 6804
QY 858 GluProAlaIleAlaLysAspArgGluTyrAsnPhelysGlyValGlyLysPheLeuThr 877
Db 6805 GAGAATGAAGTTGCTCTT-----GAAAACAGTGTAAAAAATTAAGCGACTTTATCA-- 6856
QY 878 MetLysAlaIleLysLysSerLeuLysGlyHisLysIleAsn 891
Db 6857 ATGAAG-----ATGAAGCGGCACAAAATGAAT 6883

RESULT 13
US-11-113-424-13
; Sequence 13, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29

; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-113-424-13

Alignment Scores:
Pred. No.: 0.137 Length: 8354
Score: 143.50 Matches: 219
Percent Similarity: 31.19% Conservative: 126
Best Local Similarity: 19.80% Mismatches: 392
Query Match: 3.03% Indels: 373
DB: 7 Gaps: 55

US-10-647-956A-6 (1-915) x US-11-113-424-13 (1-8354)
QY 31 LeuArgThrClnAlaAspGluAsnSerAspGluLeuIleThrPheTyrGluPheAsn--- 49
Db 5078 CTGGCAACCAAAAGCAATGAAACCGA-----TGGACAAACATTTATGATGACGACAGC 5131
QY 50 -----IleProGlyPheGlnValLysSer----- 57
Db 5132 TTGGCGCGCTGACAAATGTGACCTTCCCTACTGGCCAGGTGAGCAGTTTCCGGAAGTGAT 5191
QY 58 ThrAspPro-----Arg 61
Db 5192 ACAGACAGTTTCAGTGCATGTCCAGGTAGACACCTCCAGCAAGGATGATGTACCATAACC 5251
QY 62 LysAsnLysAsnGlnSerGlyProAsnPheIleArgValPheAsnLeuAlaGlyGlnVal 81
Db 5252 ACCAACTGTCTGCCCTCAGCGCTTCTACACACTG-----CTGCAAGACCAAGTC 5302
QY 82 LeuArgGluGluSerValAspAlaGly-----ArgThrIleThrLeuAsnAspIle 98
Db 5303 CGGAACAGCTACTACATCGGGCGCGATGGCTCTTGGCGTCTGCTGGCCAAAGCGCATG 5362
QY 99 Glu-----SerArgProValLeuIleIleAsnAlaThrGlyValArgGlnAsn 114
Db 5363 GAGGTGGCGCTGCAGACTGAGCCCACTTCTGCTG-----GCTGGCAC-CGTCAACCC 5412
QY 115 HisArgTyrGluAspAsnThrLeuProGlyArgLeuLeuAlaIleThrGlnGlnValGln 134
Db 5413 CACCGTGGGCAA-----GAGGAATGTCCAC 5436
QY 135 AlaGlyGluLysThrThrGluArgLeuIleTrpAlaGlyAsnThrProGlnGlu----- 152
Db 5437 GCTGCCCA-TCGACACGGCTCAACTGTGGAGTGGCCCGCCAGCGCAAGAGCAGGCTC 5495
QY 153 -----LysAspTyrAsnLeuAlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeu 170
Db 5496 GGGCGCAGGTCACTGTCTTTGGCGCGCGTGC-----GGGTGC 5534
QY 171 ThrGlnLeuAsnSerLeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeu 190
Db 5535 ACAACCGA-AATCTCTTATCTCTGGACTTTGATCGCGTAAACCGCACAGAGAAGTCTAT 5593
QY 191 ThrAspAsnGlnAsp-----AlaAspTrpThrGlyGluAspGlnSer 204
Db 5594 GATGACCAACCGCAAGTTCACCTTCGGATTTCTGTACGACCGCGGGGGCGG---CCCGAGC 5650
QY 205 LeuTrpGln---GlnLysLeuSerSerAspValTyrIleThrGlnSerAsnThrAspAla 223
Db 5651 CTCTGGTCACCCAGCAGCGGTGAATGGTGTCAACGTGACATACTCC----- 5698
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224 ThrGlyAlaLeuLeuThrGlnThrAspAlaLysGlyAsnIleGlnArgLeuAlaTyrAsp 243
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5699 CTTGGGGGTTACATTGCTGCATCCAGAGGGCATCATGCTCGAAGAAATGGAATACGAC 5758
244 ValAlaGlyGlnLeu----- 248
5759 CAGGCGGGCCGCATCATCCAGAGTCTTCGCTGATGGGAAGACATGGAGCTACACATAC 5818
249 -----LysGlySerTrpLeuThrLeuLysGlyGlnAlaGlnValIle----- 263
5819 TTAGAGAGTCCATGGTGTCTACTACAGCAGGCGAGTATATCTTTGATGTTGAC 5878
264 -----IleYysSerLeuThrTyr---SerAlaAlaGlyGlnLysLeuArgGlu 278
5879 AAGAATGACCGCTCTCTCTGTCAGCATGCCCAAGCTGGCGGCGAGACACTAGAGACC 5938
279 GluHisGlyAsnGlyIleValThrGluTyrSerTyrGluProGlnThrGlnArgLeuIle 298
5939 ATCCGCTCAGTGGGCTACTACAGAAACATCTATCAGCCCCCTCAG----- 5983
299 GlyIleThrThrArgProSerAspAlaLysValLeuGlnAspLeuArg----- 315
5984 -----GCAATGCCCTCAGTCATACAGGACTTCCTAGGATGGG 6022
316 -----TyrGlnTyrAspPro 320
6023 CACCTCTTCCACACCTTCTACCTGGGCACCTGGCGGAGGTGATATACAAATGCGCAA 6082
321 ValGlyAsnValIleAsnIleArgAsnAspAlaGluAlaThrArgPheTrpArgAsnGln 340
6083 CTCTCAAAGCTG-----GCAGAGCGCTCTATGACACCCACC 6118
341 LysValAlaProGluAsnSerTyrThrTyrAspSerLeuTyrGlnLeuIleSerAlaThr 360
6119 AAGGTC-----AGTTTCACCTATGACAG-----ACG 6145
361 GlyArgGluMetAlaAsnIleGlyGlnGlnAsnGlnLeuPro----- 375
6146 GCAGGCGATGCTGAAGACCATCAACCTACAGAAATGAGGGCTTCCCTGCACCATCCGCTAC 6205
376 -----SerProAlaLeuProSerAspAsnThrTyrThr----- 387
6206 CGTCAGATTGGGCCCTGATGACCGACAGATCTCCGCTTCTACTGAGGAAGCATGGTC 6265
388 AsnTyrThrArgSerTyrSerTyrAspHisSerGlyAsnLeuThrGlnIleArg----- 405
6266 AACCCCGTTTGACTCAACTATGACACAGCTTCCGGGTGACCGAGCATGGAGGCTGTG 6325
406 ---HisSerProAlaThrGlnAsnAsnTyrThrValAlaIleThrLeuSerAsnArg 424
6326 ATCAACGAGACCCACCTGCCCATTTGATCTCTATCGCTATGATGATGTCAGGCAAGACA 6385
425 SerAsnArgGlyValLeuSerThrLeuThrThrAspProAsnGlnValAspThrLeu--- 443
6386 GAGCAGTTTGGGAAGTTTGGTGTCTTACTATGACATTAACAGAGATCATCACCACAGCT 6445
444 -----PheAspAlaGlyGlyHisGln----- 450
6446 GTCATGACCCACCAAGCATTTTGTGTCATGATGGCAGGATGAAGGATGTCAGATGAG 6505
451 -----ThrSerLeuLeuProGlyGlnThrLeuIleTrpThrProArgGlyGluLeu--- 467
6506 ATCTTCCGCTCGCTCATGTACTGATGATCGCTCCAGTATGATTAACATGGGCGGAGTAGTG 6565
468 ---LysGlnValAsnAsnGlyPro-----GlyAsnGluTrpTyrArgTyrAsp 482
6566 AAGAAGGAGCTGAAGGTAGGACCCCTACGCCAATACCACTCGCTACTCTCTATGATGATGAT 6625
483 SerAsnGlyMetArgGln---LeuLysValSerGluGlnPro----- 495
6626 GCTGACGGCGAGTGCAGACAGTCTCCATCAATGACAAGCCACTCTGGCGCTACAGCTAC 6685

496 -----ThrGlnAsnThrThrGln----- 501
6686 GACCTCAATGGGAACCTGCACCTACTGAGCCCTGGGAACAGTGCACGGCTCACACCACCTA 6745
502 -----GlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGln 517
6746 CGGTATGACATCCGCGACCGCATCTCGCTGGGTGGGTGCGTGCATACAAATACAGATGAG 6805
518 SerAsnAlaThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGly----- 535
6806 GATGGCTTCTCAGGCGAGCGGGCGGTATATCTTTGAGTACAACTCAGCTGCGCTGCTC 6865
536 ---ArgAlaGlnValArgValLeuHisTrpGluSerGlyLysProGluAspValAsnAsn 554
6866 ATCAAGGCTTCAACCGGCTGGAGCTGG----- 6895
555 AsnGlnLeuArgTyrSerTyrAspAsnLeu-----IleGlySer----- 567
6896 ---AGTGTGAGTACCGCTACCGTGGCGGCGGTGTCCAGCAAGAGCAGCCAC 6952
567 ----- 567
6953 AGCCACCACCTGCAGTTCTTCTATGCAGACCTGACCAACCCCAAGGTACCCACCTG 7012
568 -----SerGlnLeuGluLeuAspAsnGlnGly----- 576
7013 TACAACCACTCCAGCTCTGAGATCACTCCCTCTACTACGACTTGCAGAGACACCTCTTT 7072
577 -----GlnIleIleSerGluGluTyrTyr----- 585
7073 GCCATGGAGCTGAGCAGTGTGTGATGATTTTACATAGCTTGTGACAACATCGGAGCCCT 7132
586 ---ProPheGlyGlyThrAlaLeuTrpAlaAlaAsn----- 596
7133 CTTGTGCTCTTGTGGAACAGGTTTGTGATGATCAAGCAAACTCTGTACACAGCCTATGGG 7192
597 -----SerGlnThrGluAlaSerTyrLysThrIle-----ArgTyrSerGlyLys 611
7193 GAGATCTACATGGATACCAACCCCACTTTCAGATCATCATAGCTTACCATGTGGCCTC 7252
612 GluArgAspAlaThrGlyLeuTyrTyrGlyTyrArgTyrTyrGlnProTrpAlaGly 631
7253 TATGATCTCACTCAACAGCTTGTCCACATGGCGCGGAGATTTATGATGTGTGCGCGGA 7312
632 ArgTrpLeuSerAlaAsp-----ProAlaGlyThrIleAspGly 644
7313 CGCTGAGCTAGCCACACCGAGCTGTGGAAGCACCTTAGTAGCAGCAACGTGATGCT 7372
645 LeuAsnLeuTyrArgMetValArgAsnAsnProValSer----- 657
7373 TTTAATCTCTATATGTTCAAAAACAACAACCCCATCAGCAACTCCAGGACATCAAGTGC 7432
658 ---LeuGlnAspGluAsn---GlyLeuAlaProGluLysGlyLysTyrThrLysGluVal 675
7433 TTCATGACAGATGTTAAAGCTGGCTGCACCTTTGGATTCCAGGTACACA----- 7484
675 lAsnPhePheAspGluLeuLysPheLysLeuAlaLysSerSerHisValValLysTr 695
7485 -----ACGTGATCCCTGGTTATCCCAACACAGACATGGATGCCATG 7525
695 pAsnGluLysGluSerSerTyrThr-----LysAsnLysSerLeuLysValValAr 712
7526 GAACCCCTCTACGAGCTATCCACACACAGATGAAAACCGCAGAGGTGGGCAACAGCAAG 7585
712 gValGlyAspSerAspProSerGlyTyrLeuLeuSerHisGluGlu----- 727
7586 TCTATCC-----TCGGGGTACAGTGTGAAGATACAGAGCAGCTCAAGGCCCTT 7633
728 -----LeuLeuLysGlyIleGluLysSerGlnIleIleTyrSerArgLe 742
7634 GTCACCTTAGAACGGTTTGNACAGCTCTATGGCTCCACAATACCAGCTGCCAGCAGCT 7693
742 uGluGluAsnSerSerLeuSerGluLysSerLysThrAsnLeuSerLeuGlySerGluI 762

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Db 7694 CCAAGACCAAGAAGTTTGATCCAGCGCTCAG---TCITTGCAAGGGGTCAGATT 7750
Qy 762 eSerGlyTyrMetAlaArgThrIleGlnAspThrIleSerGluTyrAlaGluGluHisLy 782
Db 7751 GCCTTGAAGGATGCG-CGAGTGACACAGACATCATCAGTGTGGCCAATGAGGATGGCG 7809
Qy 782 sTyrArgSer-----AsnHisProAspPheTyrSer----- 792
Db 7810 AAGGGTTCCTGCCATCTTGAAACCATGCCACTACCTAGAGAACTCGCACTTCACCATGA 7869
Qy 793 -----GluThrAspPheAlaLeuMetAspLysSerGluLysAsnAspTyrSer-- 809
Db 7870 TGGGGTGGATACCATCTACTTGTGAACACGAGACCTTCAGAA---CGTGACCTGGCCAT 7926
Qy 810 -----GlyGluArgLysIleTyrAlaAlaMetGluValLysValTyrHi 824
Db 7927 CCTGGGCTCAGTGGGGGGCGGCGAACCCCTGGAGAATGGGGTCAACGCTCACTGTG---- 7981
Qy 824 sAspLeuLysAsnLysGlnSerGluLeuHisValAsnTyrAlaLeu-----AlaHi 841
Db 7982 -----TCCAGATCAACACACAGTACTTAATGGCAGGACTAG 8016
Qy 841 sProTyrThrGlnLeuSerAsnGluArgAlaLeuGlnGluThrGluProAlaI 861
Db 8017 ACGCTACACACATCCAGCTCCAGTACGGGGCACTGTGCTTGACACACGCTACGGGAC 8076
Qy 861 eAlaIleAspArgGlu 866
Db 8077 AACGTTGGATGAGGAG 8092

RESULT 14
US-10-793-626-4075
; Sequence 4075, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4075
; LENGTH: 3055
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-4075

Alignment Scores:
Pred. No.: 0.142 Length: 3055
Score: 136.50 Matches: 127
Percent Similarity: 35.28% Conservative: 121
Best Local Similarity: 18.07% Mismatches: 254
Query Match: 2.88% Indels: 201
DB: 6 Gaps: 27

US-10-647-956A-6 (1-915) x US-10-793-626-4075 (1-3055)
Qy 251 SerTrpLeuThrLeuLysGlyGlnAlaGluGlnValIleIleLysSerLeuThrTyrSer 270
Db 1022 AGCATGTTGAATCAAAAACACAGATGATCAGACAATTATAGAAAATTTTATAAAAT 1081
Qy 271 AlaAlaGlyGlnLysLeuArgGluGluHisGlyAsnGlyIleValThrGluTyrSerTyr 290
Db 1082 ATGACAGATCAACATCTGAGTCAAGTTCATCAATCAGACAAAATAAAGCACTTGTAAAGTTT 1141
Qy 291 GluProGluThrGlnArgLeuIleGlyIleThrThrArgArgProSerAspAlaLysVal 310
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Db 1142 -----ATATTGGATAGGAGGGGTAAAGATTTTGAAGCCT 1174
Qy 311 LeuGlnAspLeuArgTyrGlnTyrAspPro---ValGlyAsnValIleAsnIleArgAsn 329
Db 1175 TTACATATATAGTTATGGAGAACTTTGGCCCTTTATTATAAAGAACTATGATTTTGACAA 1234
Qy 330 AspAlaGluAlaThrArgPheTrpArgAsnGlnLysValAlaProGluAsnSerTyrThr 349
Db 1235 GTTGAACCTGATCACTCTTTTAAATTAGTGGTAAACCTGGATCTCGTAAACACATGATT 1294
Qy 350 TyrAsp-----SerLeuTyrGlnLeuIleSerAlaThrGlyArgGluMetAla 365
Db 1295 TTTGATGCTATAGTATACGCAATTATACGCTATGCTTCGACCAAACTAGAAAAAGAGGA 1354
Qy 366 AsnIleGlyGlnGlnAsnAsnGlnLeuProSerPro-----AlaLeuPro 380
Db 1355 GATTTAAGAAGTCAATTTTGCAGACGGTAAATCGCCAATGCTGTAAATTTATCAATTTAAA 1414
Qy 381 SerAspAsnAsnThrTyrThrAsnTyrThrArgSerTyrSerTyrAspHisSerGlyAsn 400
Db 1415 GTTAAATAATCAAACTTTTAAATTCAT---AGAGAAGCCGCATTTATTAAAGAGGGGAAT 1471
Qy 401 LeuThrGlnIleArg-----HisSerSerProAlaThrGlnAsnAsnTyrThrVal 417
Db 1472 ATAACTAAACACACACCAAGTTAAATATATATATAGTATGATTAATCAATTTGAATTA 1531
Qy 418 AlaIleThrLeuSerAsnArgSerAsnArgGlyValLeuSerThrLeuThrThrAspPro 437
Db 1532 AGAGAAAAGTAAAGTGAATCAAGGTAATCAATTTATCGTCAATTTATAGCGTAAATGCT 1591
Qy 438 AsnGlnValAspThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuProGlyGln 457
Db 1592 GAACAATTTTCGTCAATTAATTT----- 1612
Qy 458 ThrLeuIleTrpTrpProArgGlyGluLeuLysGlnValAsnAsnGlyProGlyAsnGlu 477
Db 1613 -----ATTTTGCTCAAGAGAAATTTAAAGTTT----- 1642
Qy 478 TrpTyrArgTyrAspSerAsnGlyMetArgGlnLeuLysValSerGluGlnProThrGln 497
Db 1643 -----CTTCAG 1648
Qy 498 AsnThrThrGlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGln 517
Db 1649 TCAAATAGTAAAGACAAACAATCGATT-----CTTAGAACACTTTT 1690
Qy 518 SerAsnAlaThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAla 537
Db 1691 AATAGTGCGGATTTGATGAGATTGACATCTACTTGTGA----- 1729
Qy 538 GlnValArgValLeuHisTrpGluSerGlyLysProGluAspValAsnAsnAsnGlnLeu 557
Db 1730 -----GAAAATGTAAAGCAAGAAAAGTA-----CAAAAT 1759
Qy 558 ArgTyrSerTyrAspAsnLeuIleGlySerSerGlnLeuGluLeuAspAsnGlnGlyGln 577
Db 1760 GAAAAATAGATAC-----ACTCAAAATGAA----- 1783
Qy 578 IleIleSerGluGluGluTyrTyrProPheGlyGlyThrAlaLeuTrp----- 593
Db 1784 -----AATTATGAATGATATAGAT 1804
Qy 594 AlaAlaAsnSerGlnThrGluAlaSerTyrLysThrIleArgTyrSerGlyLysGluArg 613
Db 1805 ACATTTAAATAATGATCAATGGCCCTTATATAAAGAAATTAGAGAGTTCTCAGACAGATAAA 1864
Qy 614 AspAlaThrGlyLeuTyrTyrTyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTrp 633
Db 1864 ----- 1864
Qy 634 LeuSerAlaAspProAlaGlyThrIleAspGlyLeuAsnLeuTyrArgMetValArgAsn 653
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Db 1865 -----ATGATTGAAAAATTCACCAATTT 1888
Qy 654 AsnProValSerLeuGlnAspGluAsnGlyLeuAlaProGluLysGlyLysTyrThrLys 673
Db 1889 AATGATTATGATGCAAAATTCCTCAAGTCATTTGAAGACGCTAAGATAAATAAATACTAAG 1948
Qy 674 GluValAsnPhePheAspGluLeuLysPheLysLeuAlaLysSerHisValVal 693
Db 1949 GAATTA-----GATGATTTA-----AATCATAAATAT 1975
Qy 694 LysTrpAsnGluLysGluSerTyrThrLysAsnLysSerLeuLysValValArgVal 713
Db 1976 AAGTGAATTTGAATTAAGTAGAGATACATACTATTTTACTAGGTTACAAAGTTTAAAAAAGATAA 2155
Qy 714 GlyAsp---SerAspProSerGlyTyrLeuLeuSerHisGluLeuLysGlyIle 732
Db 2036 GACGATTTGAAAAAGAACAAATTTATGATAAATTAAGCAAGATTTAAAAATGATT 2095
Qy 733 GluLysSerGlnIlelle-----TyrSerArgLeu----- 742
Db 2096 CAGGAATCTAAAGTATTAATCACTATTTTACTAGGTTACAAAGTTTAAAAAAGATAA 2155
Qy 743 GluGluAsnSerSerLeuSerGluLysSerLysThrAsn---LeuSerLeuGlySerGlu 761
Db 2156 GATGAATTTAGTGCTCCTCATGAGCAATCAAAATTAACGAAACAACTATCATCAATGAA 2215
Qy 762 IleSerGlyTyrMetAlaArg-----ThrIleGlnAspThrIleSerGlu 776
Db 2216 ATTAAAGTTTTCAAAACAACTCGACATTTATCAACAGAGAAATGAATTAACCTCAA 2275
Qy 777 TyrAlaGluGluHisLysTyrArgSerAsnHisProAspPheTyrSerGluThrAspPhe 796
Db 2276 TTT-----AATCAGTATCTAGAAAAAACCAGTTTCTTCAATCAATTAGAT--- 2323
Qy 797 PheAlaLeuMetAspLysSerGluLysAsnAspTyrSerGlyGluArgLysIleTyrAla 816
Db 2324 -----AAGATTATTAGTAGTTTATCAACAAAAACCGGTAATT 2359
Qy 817 AlaMetGluValLys-----ValTyrHisAspLeuLysAsnLysGlnSerGlu 832
Db 2360 GAAGAAGAAATATAAAGATTATACAGTGAATATAATGATTTAATACCAAAAAAGAGAA 2419
Qy 833 Leu-----HisValAsnTyrAlaLeuAlaHisProTyrThrGln 845
Db 2420 TTGACGAAAGAAATGAACAACAAGAACAAAGATTTTGCATTTATGAACATTAACCTGAA 2479
Qy 846 LeuSerAsnGluGluArgAlaLeuLeuGlnGluThrGluProAlaIleAlaIleAspArg 865
Db 2480 GAGATTTTAAAGCTGAAAAAGATTATAGATGAATCTGAAAAAGACAAAAAAGGATGAGAAA 2539
Qy 866 GluTyrAsnPheLysGlyValGlyLysPheLeuThrMetLysAlaIleLysLysSerLeu 895
Db 2540 TTATTTGATAAATTACAACTAGATAATCATCTTATCTTAGCAAAATTAAGAAG- 2593
Qy 886 LysGlyHisLysIleAsnArgIleSerThrGluAlaIleAsnIleArgSerAlaIle 905
Db 2594 AAGAAACACAGTTAAATGAATGAATTCATCAATCAATCAATATAGATGCGACTTAATT 2653
Qy 906 AlaGluAsn 908
Db 2654 GATTTGAAT 2662
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RESULT 15

US-10-623-155-117

; Sequence 117, Application US/10623155

; Publication No. US20050261166A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Peckham, David W.

; APPLICANT: Retter, Marc W.

; APPLICANT: Fanger, Gary R.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

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; FILE REFERENCE: 210121.455C20
; CURRENT APPLICATION NUMBER: US/10/623,155
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 117
; LENGTH: 6921
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-623-155-117

Alignment Scores:
Pred. No.: 0.531 Length: 6921
Score: 135.50 Matches: 220
Percent Similarity: 34.29% Conservative: 151
Best Local Similarity: 20.33% Mismatches: 395
Query Match: 2.86% Indels: 317
Db: 6 Gaps: 51
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US-10-647-956A-6 (1-915) x US-10-623-155-117 (1-6921)

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Qy 4 TyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsnArgLysLeu 23
Db 932 TATGAACCTAACTGTGTGAAGAGAGAGCAGTTATAGCTGACAGAATAATATTGAGAAT 991
Qy 24 AsnValArgThrIleuGluTyrLeuArgThrGlnAlaAspGluAsn----- 38
Db 992 CTAATAAGTACTTTAAAGCAATGGAGATCTGAAGTAGATCAAAAGACAGAGGTATTCAT 1051
Qy 39 -----SerAspGluLeuIleThrPheTyr 46
Db 1052 GCCTTAGAGATGAGTTGCAGAAAGCTAAAGCCATCAGTGTGTAATGTTTAAACGTAT 1111
Qy 47 GluPheAsnIleProGlyPheGlnValLysSerThrAspProArgLysAsnLysAsnGln 66
Db 1112 AAAGAACGGGACCTTGATTT-----GACTGGCACAAGAAAA----- 1150
Qy 67 SerGlyProAsnPheIleArgValPheAsnLeuAlaGlyGlnValLeu---ArgGluGlu 85
Db 1151 -----GCAGATCAATTAGTTGAAGAGTGGCAA 1177
Qy 86 SerValAspAlaGlyArgThrIleThrLeuAsnAspIleGluSerArgProValLeuIle 105
Db 1178 AATGTTTCATGTGCAGATTGCACACAGGTTACCGGACTTAG----- 1219
Qy 106 IleAsnAlaThrGlyValArgGlnAsnHisArgTyrGluAspAsnThrLeuProGlyArg 125
Db 1220 -----GGCATTGGCAAAATCCTGAAGTACTACAGACACTTACCAT----- 1261
Qy 126 LeuLeuAlaIleThrGluGlnValGlnAlaGlyLysIleThrThrGluArgLeuIleTyr 145
Db 1262 -----CCTTTAGATGATCGATCCAGCAGGTTGAA---ACTACTCAGAGAAAGATT--- 1309
Qy 146 AlaGlyAsnThrProGlnGluLysAspTyrAsnLeuAlaGlyGlnCysValArgHisTyr 165
Db 1310 CAGGAAAAATCAGCCT---GAAAAATAGTAAACCCCTAGCCACACAGTTGAATCAACAGAA- 1365
Qy 166 AspThrAlaGlyLeuThrGlnLeuAsnSerLeuSerLeuAlaGly----- 180
Db 1366 GAT---GCTGTGTGCGAAATGAATGAACAGACAAATGGACGAGTGTCAANAATA 1422
Qy 181 -----ValValLeuSerGlnSerGlnLeuLeuThrAspAsnGlnAspAlaAspTyr 198
Db 1423 TGCAGAACAGTACTCAGCTACAGTGAAGGACTATGAATTAACAACAATGACCTACCGGGC 1482
Qy 199 ThrGlyGluAspGlnSerLeuTyrGlnGlnLysLeuSerSerAspVal-TyrIleThrGln 218
Db 1483 CATGGTAGA-----TTCAACAACAAAAATCTCCAGTGAAGACCGCGAAGAAATGCA 1530
Qy 218 nSerAsnThrAspAlaThrGlyAlaLeuLeuThrGln-----ThrAspAlaLysGlyAs 236
Db 1531 GAGTTCAGCAGAT-----CTCATTTTCAAGAGTTTCATGGACCTAAGGACTCG 1578
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Db      3454  ACAGCTCAGGTGCAAGAGTTAATAACAGGTTCAAAAAAGTACAGACGAATTACAC-- 3511
Qy      835   lAsnTyzAlaLeuAlaHisProTyrThrGlnLeuSerAsnGluGluArgAlaLeuLeuG1 855
Db      3512  -----TTAAAGACCATAGAGGAGCAGATGACCCACAGAAAGATGGTCTCTTTCA 3561
Qy      855   nGluThrGluProAlaIleAlaIleAspArgGluTyrAsnPheIysGlyValGlyLysPh 875
Db      3562  GGAAGAATCTGGTAAATTCAACAATCAGCAGAGGAGTTTCGGGAAGAAGATGGAAAAAATT 3621
Qy      875   eLeuThrMetIysAlaIle---LysLysSerLeuLysGlyHisLysIleAsnArgIleSe 894
Db      3622  AATGAGTCCAAAGTCATCACTGAAATGATATTTCAGGCATTAGGCTTGACTTGTGTC 3681
Qy      894   rThrGluAlaIleAsnIleArgSerAlaAlaIleAlaGluAsnLeuGlyMetArgArgTh 914
Db      3682  TCITCAACAAGAAAACCTCTAGAGCC-----CAAGAAATGCTAAGCTTTGTGAAC 3732
Qy      914   rSer 915
Db      3733  AAAC 3736
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Job time : 420 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame plus p2n model

Run on: December 14, 2005, 10:30:03 ; Search time 10168 Seconds
(without alignments)
5115.240 Million cell updates/sec

Title: US-10-647-956A-6

Perfect score: 4740

Sequence: 1 MSYNSAIDQKTPSIKVLND.....EAINIRSAIAENLGMRRTS 915

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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ALIGNMENTS

RESULT 1 AR427909 AR427909 2745 bp DNA linear PAT 18-DEC-2003
LOCUS Sequence 5 from patent US 6639129.
DEFINITION AR427909
ACCESSION AR427909
VERSION AR427909.1 GI:40186940
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2745)
AUTHORS ffrench-Constant,R.H., Bowen,D.J., Rocheleau,T.A. and
TITLE Waterfield,N.R.
JOURNAL DNA sequences from photorhabdus luminescens
Patent: US 6639129-A 5 28-OCT-2003;
Wisconsin Alumni Research Foundation and University of Bath;
Madison, WI
FEATURES Location/Qualifiers
source
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/organism="unknown"
/mol_type="genomic DNA"

SUMMARIES

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1	4740	100.0	2745	6	AR427909 Sequence
2	4686	98.9	127816	1	AF346500 Photorhab
3	4429	93.4	349519	1	BX571862 Photorhab

Alignment Scores: 2.5e-248 Length: 2745
Pred. No.: 4740.00 Matches: 915
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0
US-10-647-956A-6 (1-915) x AR427909 (1-2745)			
QY	1	MetSerSerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn	20
DB	1	ATGAGCAGTTACAAATCTGCAATTGACCAAAAGACCCCTCGATTAAAGGTATTAGATAAC	60
QY	21	ArgLysLeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAsnSerAsp	40
DB	61	AGGAAATTAATGCTACGTACTTTAGATAATCTACGCACCTCAAGCTGACGAAACAGTGAT	120
QY	41	GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro	60
DB	121	GAATTAATACGTTCTATGATGTTCAATATTCCGGGATTTTCAGGTAAAGACACCGATCCT	180
QY	61	ArgLysAsnLysAsnGlnSerGlyProAsnPheIleArgValPheAsnLeuAlaGlyGln	80
DB	181	CGTAAAAATAAAAACACGAGCGGCCCAAAATTCATTCTGTCTTTAATCTTGGCGGTCAA	240
QY	81	ValLeuArgGluGluSerValAspAlaGlyArgThrIleThrLeuAsnAspIleGluSer	100
DB	241	GTTTTACGTGAAGAAAGTGTGATGCGCGTCCGACTATTACCTCTAATGATATTGAAAGT	300
QY	101	ArgProValLeuIleIleAsnAlaThrGlyValArgGlnAsnHisArgTyrGluAspAsn	120
DB	301	CGCCCGGTGTGTATCATCAATGCAACCGGTGTCGCCAANAACCATCGTTATGAAGATAAC	360
QY	121	ThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGlyGluLysThrThr	140
DB	361	ACCTTTCCCGTGTGTCTGCTCGCTATCCAGAACAGTACAGCAGAGAGAGAAAACGACC	420
QY	141	GluArgLeuIleTrpAlaGlyAsnThrProGlnGluLysAspTyrAsnLeuAlaGlyGln	160
DB	421	GAACGTCTTATCTGGGCGCGCAATACGCCGCAAGAAAAAGATTACAACTCGCGCGGTACG	480
QY	161	CysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAsnSerLeuLeuAlaGly	180
DB	481	TGTGTCCGCTATTACGATACCGGGGACTTACTCACTCAATAGCCCTTTCTCTGGCTGGC	540
QY	181	ValValLeuSerGlnSerGlnGlnLeuLeuThrAspAsnGlnAspAlaAspTrpThrGly	200
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QY	201	GluAspGlnSerLeuTrpGlnGlnLysLeuSerSerAspValTyrIleThrGlnSerAsn	220
DB	601	GAAGACCAGAGCTCTGGCAACAAAACTGAGTAGTGATGCTATATATACCCAAAGTAAAC	660
QY	221	ThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGlyAsnIleGlnArgLeu	240
DB	661	ACTGATGCCACCGGGCTTTACTGACCACAGACCGATGCCAAAGGCAACATTTCAGCGGCTG	720
QY	241	AlaTyrAspValAlaGlyGlnLeuLysGlySerTrpLeuThrLeuLysGlyGlnAlaGlu	260
DB	721	GCCTATGATGTGGCCGGCAGCTAAAGGGAGTTGGTTTAACACTCAAAAGGTACGGCCGAA	780
QY	261	GlnValIleIleLysSerLeuThrTyrSerAlaAlaGlyGlnLysLeuAspGluGluHis	280
DB	781	CAGGTGATTATCAATCGCTAACTACTCTCCGCCCGCGGCAAAAAATTTACGTGAAGAGCAC	840
QY	281	GlyAsnGlyIleValThrGluTyrSerTyrGluProGluThrGlnArgLeuIleGlyIle	300
DB	841	GGTAACCGGATGTGCTACTGAATACAGTACAGAACCGGAAACCCCAACCGGCTTATCGGCATT	900
QY	301	ThrThrArgArgProSerAspAlaLysValLeuGlnAspLeuArgTyrGlnTyrAspPro	320
DB	901	ACCACTCCCGCTCATCAGACCCAGCGTGTGCAAGACCTACGCTATCATATATGACCCA	960
QY	321	ValGlyAsnValIleAsnIleArgAsnAspAlaGluAlaThrArgPheTrpArgAsnGln	340
DB	961	GTAGGCAATGTCTATTAAATATCCGTAATGATGCGGAAGCCACTCGCTTTTGGCGCAATCAG	1020
QY	341	LysValAlaProGluAsnSerTyrThrTyrAspSerLeuTyrGlnLeuIleSerAlaThr	360
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QY	361	GlyArgGluMetAlaAsnIleGlyGlnGlnAsnAsnGlnLeuProSerProAlaLeuPro	380
DB	1081	GGCGCGAAATGGCCAAATATCGGTACGAAACCAACCAACTTCCCTCCCTCGGCTACCT	1140
QY	381	SerAspAsnAsnThrTyrThrAsnTyrThrArgSerTyrSerTyrAspHisSerGlyAsn	400
DB	1141	TCGTGACAAACAATACCTACACTACTCGCAGCTACAGCTATGATCAGTGGTAAT	1200
QY	401	LeuThrGlnIleArgHisSerSerProAlaThrGlnAsnAsnTyrThrValAlaIleThr	420
DB	1201	CTGACCGAAATTCGGCACAGCTCGCCAGCTACCCAGAACACTACACCGTGGGTATCACC	1260
QY	421	LeuSerAsnArgSerAsnArgGlyValLeuSerThrLeuThrAspProAsnGlnVal	440
DB	1261	CTCTCAACCGCAGCAATCGGGGTGTTCTCAGTACGTAAACCACCGATCCAAATCAAGTG	1320
QY	441	AspThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIle	460
DB	1321	GATACGTTGTTGATCCGCTGGTCCACAAACCAAGTTTATTACCCGGACAGACTTATC	1380
QY	461	TrpThrProArgGlyGluLeuLysGlnValAsnAsnGlyProGlyAsnGluTyrTyrArg	480
DB	1381	TGGACACACGAGAGAGTTAAAGCAGGTTAATATNGGCCGGGAAATGAGTGGTACCGC	1440
QY	481	TyrAspSerAsnGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAsnThrThr	500
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QY	501	GlnGlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAla	520
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QY	521	ThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArg	540
DB	1561	ACAAACAAACGAGAGTTACAGTTATCACCTCGTGAAGCCGCTCGCGCACAGGTACGG	1620
QY	541	ValLeuHisTrpGluSerGlyLysProGluAspValAsnAsnAsnGlnLeuArgTyrSer	560
DB	1621	GTCTTGCACCTGGGAGAGCGGTAAAGCAGAAAGATGTCAACAAATATCAACTACGTTACAG	1680
QY	561	TyrAspAsnLeuIleGlySerSerGlnLeuGluLeuAspAsnGlnGlyGlnIleIleSer	580
DB	1681	TACGATAANTCTGATCGGCTCCAGCCAGCTTGAACTGGACAAACCAAGGACAAATTTATCAG	1740
QY	581	GluGluGluTyrTyrProPheGlyGlyThrAlaLeuTrpAlaAlaAsnSerGlnThrGlu	600
DB	1741	GAGAAAGATATTATTCATTTGGCGGACAGCCGCTGTGGCAGCAACACAGCCAAACAGAA	1800
QY	601	AlaSerTyrLysThrIleArgTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyr	620
DB	1801	GCCAGCTATAAAACGATTCGCTATTCCGCAAAAGACGAGATGCCACCGGTTGTATTAT	1860
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Qy	721	TyrLeuLeuSerHisGluGluLeuLeuLysGlyLeuGlySerGlnIleIleTyrSer	740
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Db	2221	CGACTTGAGAAAAACAGCTCCCTTCAGAAAAATCAAAAACGATCTTCTTTAGGATCT	2280
Qy	761	GluIleSerGlyTyrMetAlaArgThrIleGlnAspThrIleSerGluTyrAlaGluGlu	780
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Qy	781	HisIysTyrArgSerHisProAspPheTyrSerGluThrAspPhePheAlaLeuMet	800
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Qy	801	AspLysSerGluLysAsnAspTyrSerGlyGluArgLysIleTyrAlaAlaMetGluVal	820
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Qy	861	IleAlaIleAspArgGluTyrAsnPheLysGlyValGlyLysPheLeuThrMetLysAla	880
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VERSION	AF346500.2	GI:27479637	
KEYWORDS			
SOURCE	Photorhabdus luminescens		
ORGANISM	Photorhabdus luminescens		
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AUTHORS	Waterfield,N.R., Bowen,D.J., Fetherston,J.D., Perry,R.D. and french-Constant,R.H.		
TITLE	The tc genes of Photorhabdus: a growing family		
JOURNAL	Trends Microbiol. 9 (4), 185-191 (2001)		
PUBMED	11286884		
REFERENCE	2	(bases 1 to 127816)	
AUTHORS	Waterfield,N.R., Daborn,P.J. and french-Constant,R.H.		
TITLE	Genomic islands in Photorhabdus		
JOURNAL	Trends Microbiol. 10 (12), 541-545 (2002)		
PUBMED	12564983		
REFERENCE	3	(bases 1 to 127816)	
AUTHORS	french-Constant,R.H., Bowen,D.J. and Waterfield,N.R.		
TITLE	Direct Submission		
JOURNAL	Submitted (19-JAN-2001) Biology and Biochemistry, University of Bath, Claverton Down, Bath BA2 7AY, UK		
REFERENCE	4	(bases 1 to 127816)	

AUTHORS	Waterfield,N.R. and french-Constant,R.H.
TITLE	Direct Submission
JOURNAL	Submitted (22-AUG-2002) Biology and Biochemistry, University of Bath, Claverton Down, Bath BA2 7AY, UK
REMARK	Sequence update by submitter
COMMENT	On Jan 3, 2003 this sequence version replaced gi:16416925.
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QY	221	ThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGlyAsnIleGlnArgLeu	240	581	GluGluGluTyrTyrProPheGlyGlyThrAlaLeuTrpAlaAlaAsnSerGlnThrGlu	600
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QY	441	AspThrLeuPheAspAlaGlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIle	460	801	AspLysSerGluLysAsnAspTyrSerGlyGluArgLysIleTyrAlaAlaMetGluVal	820
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KEYWORDS
SOURCE
ORGANISM
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Photorhabdus luminescens

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

Enterobacteriaceae; Photorhabdus.

REFERENCE

1. French-Constant, R. H. and Waterfield, N. R.

Dna sequences from tcd genomic region of photorhabdus luminescens

Patent: WO 200404217-A 15 27-MAY-2004;

UNIVERSITY OF BATH (GB)

FEATURES

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ACCESSION CQ854091
VERSION CQ854091.1 GI:51510128
KEYWORDS
SOURCE Photorhabdus luminescens
ORGANISM Photorhabdus luminescens
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
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REFERENCE
AUTHORS Hey,T.D., Schleper,A.D., Bevan,S.A., Bintrim,S.B., Mitchell,J.C.,
Li,Z.S., Ni,W., Zhu,B., Merlo,D.J. and Apel-Birkhold,P.C.
TITLE Mixing and matching tc proteins for pest control
JOURNAL Patent: WO 2004067727-A 57 12-AUG-2004;
Dow Agrosciences LLC (US)
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ACCESSION BX571873 BX470251
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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REFERENCE
1 Duchaud,B., Rusniok,C., Frangeul,L., Buchrieser,C., Taourit,S.,
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Derzelle,S., Freyssinet,G., Gaudriault,S., Givaudan,A., Glaser,P.,
Medigue,C., Lanois,A., Powell,K., Siguier,P., Wingate,V.,
Zouine,M., Boenare,N., Danchin,A. and Kunst,F.
Complete genome sequence of the entomopathogenic bacterium
Photorhabdus luminescens
Nat. Biotechnol. 11 (1) (2003) In press
2
Duchaud,B., Frangeul,L., Rusniok,C. and Kunst,F.
Direct Submission
Submitted (23-APR-2003) L. Frangeul, Institut Pasteur, Genopole, 25
rue du Docteur Roux, 75724 Paris Cedex 15, FRANCE. E-mail:
lfrangeul@pasteur.fr, fkunst@pasteur.fr
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RBS

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JOURNAL	Patent: WO 200404217-A 11 27-MAY-2004; UNIVERSITY OF BATH (GB)
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DEFINITION Sequence 46 from Patent WO200406727.
ACCESSION CQ854080
VERSION CQ854080.1 GI:51510119
KEYWORDS Photorhabdus luminescens

ORGANISM Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.

REFERENCE 1
AUTHORS Hey, T.D., Schleper, A.D., Bevan, S.A., Bintrim, S.B., Mitchell, J.C.,
Li, Z.S., Ni, W., Zhu, B., Merlo, D.J. and Apel-Birkhold, P.C.
TITLE Mixing and matching c proteins for pest control
JOURNAL Patent: WO 2004/067727-A 46 12-AUG-2004;
Dow Agrosciences LLC (US)
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Alignment Scores:
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US-10-647-956A-6 (1-915) x CQ854080 (1-2883)

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CQ824620

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LOCUS CQ824620
DEFINITION Sequence 13 from Patent WO200404217.
ACCESSION CQ824620
VERSION CQ824620.1
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SOURCE Photorhabdus luminescens
ORGANISM Photorhabdus luminescens
          Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
          Enterobacteriaceae; Photorhabdus.
REFERENCE 1
AUTHORS French-Constant,R.H. and Waterfield,N.R.
TITLE Dna sequences from tcd genomic region of photorhabdus luminescens
JOURNAL Patent: WO 200404217-A 13 27-MAY-2004;
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	DEFINITION		Sequence 11 from patent US 6281413.	
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	VERSION		ARI166758.1	GI:16242227
	KEYWORDS			Unknown.
	SOURCE			Unknown.
	ORGANISM			Unknown.

Unclassified.	
REFERENCE 1 (bases 1 to 37948)	
AUTHORS Kramer, V. Cary., Morgan, M. Kent., Anderson, A. Robert., Hart, H. Prim., Warren, G. W., Dunn, M. M. and Chen, J. Shong.	
TITLE Insecticidal toxins from Photorhabdus luminescens and nucleic acid sequences coding therefor	
JOURNAL Patent: US 6281413-A 11 28-AUG-2001;	
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QY	651	ValArgAsnProValSerLeuGlnAspGluAsnGlyLeuAlaPro	666
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Db	17265	ACAAACGTAGCGATAAATATCCCGCCGCGGTAGCACCAAAACCTACC-----TTACCCAA	17321
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Db	17442	ATATCTCTTCCA-----GAAAGCACTCAA-----AGC	17468
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DEFINITION			Insecticidal toxin from Photobhabdus.
ACCESSION	BD136648		
VERSION	BD136648.1	GI:23231593	
KEYWORDS	JP 2002504336-A/6.		
SOURCE	Photobhabdus luminescens		
ORGANISM	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Photobhabdus.		
REFERENCE	1 (bases 1 to 37948)		
AUTHORS	Kramer, V.C., Morgan, M.K., Anderson, A.R., Hart, H.P., Warren, G.W., Dunn, M.M. and Chen, J.S.		
TITLE	Insecticidal toxin from Photobhabdus		
JOURNAL	Patent: JP 2002504336-A 6 12-FEB-2002;		
COMMENT	NOVARTIS AG		
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	PF 18-FEB-1998 US 2000532529		
	PR 20-FEB-1998 US 09/027080, 20-JAN-1999 US 60/116439 PI		
	VANCE CARY KRAMER, MICHAEL KENT MORGAN, ARNE ROBERT ANDERSON, PI		
	HOPE PRIM HART,		
	PI GREGORY WAYNE WARREN, MARTHA MARY DUNN, JENG SHONG CHEN PC		
	.C12N15/09,A01H5/00,A01N63/02,C07K14/24,C12N1/15,C12N1/19 PC		
	.C12N1/21,C12N5/10.		
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Location/Qualifiers

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Percent Similarity:	74.33%	Conservative:	103
Best Local Similarity:	61.74%	Mismatches:	159
Query Match:	52.77%	Indels:	51
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CQ854059
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DEFINITION CQ854059
ACCESSION CQ854059.1 GI:51510104
VERSION CQ854059.1
KEYWORDS Photorhabdus luminescens
SOURCE Photorhabdus luminescens
ORGANISM Photorhabdus luminescens
REFERENCE 1 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
AUTHORS Enterobacteriaceae; Photorhabdus.
TITLES Hey, T.D., Schleper, A.D., Bevan, S.A., Bintrim, S.B., Mitchell, J.C.,
JOURNAL Li, Z.S., Ni, W., Zhu, B., Merio, D.J. and Apel-Birkhold, P.C.
MIXING and matching to proteins for pest control
PATENT: WO 200406772-A 25 12-AUG-2004;
Dow Agrosciences LLC (US)
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DB: 6 Gaps: 5

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RESULT 14

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DEFINITION Sequence 60 from patent US 6528484.
ACCESSION AR285426
VERSION AR285426.1 GI:29722605
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KEYWORDS

SOURCE Unknown.

ORGANISM

Unknown.

REFERENCE

1 (bases 1 to 3132)

Ensign, J. C., Bowen, D. J., Petell, J., Fatig, R., Schoonover, S.,
ffrench-Constant, R. H., Rocheleau, T. A., Blackburn, M. B., Hey, T. D.,
Marlo, D. J., Orr, G. L., Roberts, J. L., Strickland, J. A., Guo, L.,
Cliche, T. A., and Sukhapinda, K.

TITLE

Insecticidal protein toxins from *Photobacterium*

Patent: US 6528484-A 60 04-MAR-2003;

Wisconsin Alumni Research Foundation; Madison, WI

FEATURES

source

1..3132

Location/Qualifiers

/organism="unknown"

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 Best Local Similarity: 52.05% Indels: 18
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US-10-647-956A-6 (1-915) x AR285426 (1-3132)

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

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7	2960	62.4	2817	12	ADN61384
8	2956	62.4	2817	12	ADP18627
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15	2578.5	54.4	2898	10	ACF71155
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XX	
KW	Gene; db; toxin A; toxin B; TcdA; protoxin; TcdB; TccC2; transgenic;
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601 AlaSerTyrLysThrIleArgTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyr 620
1801 GCCAGCTATAAACGATTCCGCTATTCGGCAAGAACGAGATGCCACCGGTTGATTAT 1860
621 TyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTrpLeuSerAlaAspProAlaGly 640
1861 TACGGTTATCGTTATTACCAACCGTGGCGGCGAGATGGTTAAGCGCGACCGCGCAGGA 1920
641 ThrIleAspGlyLeuAsnLeuTyrArgMetValArgAsnAsnProValSerLeuGlnAsp 660
1921 ACCATTGATGGGCTGAATCTATACCGAATGGTAAAGAAATAATCCTGTGAGTTTACAAAT 1980
661 GluAsnGlyLeuAlaProGluLysGlyLysTyrThrLysGluValAsnPheAspGlu 680
1981 GAAATGGATTAGCGCCAGAAAGGAAATATACCAAGAGGTAATTTCTTTGATGAA 2040
681 LeuIlePheLysLeuAlaLysSerSerHisValValLysTrpAsnGluLysGluSer 700
2041 TTAATAATTCAAATTGGCAGCCAAAGTTTACATGTTGTCAAAATGGAAACGAGAAAGAGC 2100
701 SerTyrThrIleAsnLysSerLeuLysValValArgValGlyAspSerAspProSerGly 720
2101 AGTTATACAAAAATAAATCAATTGAAGTGGTTCTGGTGGTATTCAGATCCGTCGGGT 2160
721 TyrLeuLeuSerHisGluGluLeuLeuLysGlyIleGluLysSerGlnIleIleTyrSer 740
2161 TATTTCTAAGCCACGAGGTTACTTAAAGGTATAGAAAAAGTCAATCATATATAGC 2220
741 ArgLeuGluAsnSerSerLeuSerGluLysSerLysThrAsnLeuSerLeuGlySer 760
2221 CGACTTGAAGAAACAGCTCCCTTTTCAGAAAAATCAAAAAACGAATCTTTCTTTAGGATCT 2280
761 GluIleSerGlyTyrMetAlaArgThrIleGlnAspThrIleSerGluTyrAlaGluGlu 780
2281 GAAATATCCGGTTATATGGCAAGAACCATACAGATACAGATATCAGAAATATGCCGAAGAG 2340
781 HisLysTyrArgSerAsnHisProAspPheTyrSerGluThrAspPheAlaLeuMet 800
2341 CATAAATATAGAAGTAAATACCTGATTTTATTTCAGAAACCACTTCCTTTGGCTTAAG 2400
801 AspLysSerGluLysAsnAspTyrSerGlyGluArgLysIleTyrAlaAlaMetGluVal 820
2401 GATAAAGTCAAAAAATGATTATTCGGTGAAGAAAAATTTATCGCGCAATGGAGGTT 2460
821 LysValTyrHisAspLeuLysAsnLysGlnSerGluLeuHisValAsnTyrAlaLeuAla 840
2461 AAGGTTTATCATGATTATAAAAAATAAACAATCAGAAATTATCATGTCACTATGCAATTGGCC 2520
841 HisProTyrThrGlnLeuSerAsnGluGluArgAlaLeuLeuGlnGluThrGluProAla 860
2521 CATCCCTATACGCAATTAGTATGAAGAAAGAGCGCTGTTCAGAAACCAAGAACCCGCT 2580
861 IleAlaIleAspArgGluTyrAsnPheLysGlyValGlyLysPheLeuThrMetLysAla 880

2581 ATTGCAATAGATAGAGATAATAATTTCAAGGTGTTGGCAATTTCTGCAATGAAGCA 2640
881 IleLysLysSerLeuLysGlyHisLysIleAsnArgIleSerThrGluAlaIleAsnIle 900
2641 ATTAAAAAATCATTTGAAAGGACATAAAATTAATAGGATATCAACAGAGGCTATTAAAT 2700
901 ArgSerAlaAlaIleAlaGluAsnLeuGlyMetArgArgThrSer 915
2701 CGCTCTGGCGTATCGCTGAGAAATTTAGGAATTCGCGAGAATCTTCA 2745

RESULT 2

ADN61381
ID ADN61381 standard; DNA; 2748 BP.
XX
AC ADN61381;
XX
XX 01-JUL-2004 (first entry)
DT
XX
DE Photorhabdus strain W14 tccC2 toxin complex DNA.
KW
KW Cry; toxic; lepidopteran pest; toxin complex; insecticide; strain W14;
KW ds; tccC2.
XX
OS Photorhabdus sp.
XX
PN WO2004002223-A2.
PD
XX 08-JAN-2004.
XX
PF 27-JUN-2003; 2003WO-US020082.
XX
PR 28-JUN-2002; 2002US-0392633P.
PR 21-JAN-2003; 2003US-0441647P.
XX
XX (DOWC) DOW AGROSCIENCES LLC.
PA
XX
PI Bintrim SB, Bevan SA, Zhu B, Merlo DJ;
XX
XX WPI; 2004-082821/08.
XX
XX Screening a culture of Paenibacillus isolate for Cry protein or toxin
PT complex protein, useful for controlling lepidopterans, comprises
PT obtaining DNA or protein from the culture and assaying the presence of
the gene or protein.
XX
XX Example 12; SEQ ID NO 45; 220pp; English.
XX
XX The invention relates to a novel method for screening a culture of a
CC Paenibacillus isolate for a gene encoding a protein selected from a Cry
CC protein that is toxic to a lepidopteran pest and a toxin complex protein.
CC The method comprises obtaining DNA from the culture and assaying the DNA
CC for the presence of the gene or obtaining a protein produced by the
CC culture and assaying the presence of a protein that indicates the
CC presence of the gene in the isolate. The method of the invention has
CC insecticide applications and may be useful for screening Paenibacillus
CC sp. for toxin complex (TC)-like genes and proteins which may themselves
CC be used to enhance or potentiate the activity of a stand-alone
CC Xenorhabdus toxin protein. The method may also be useful for screening
CC Paenibacillus sp. and others for insecticidal thiaminase genes and
CC proteins for controlling insects, particularly lepidopterans. The current
CC sequence is that of the Photorhabdus strain W14 tccC2 toxin complex DNA
CC of the invention.
XX
SQ Sequence 2748 BP; 907 A; 621 C; 608 G; 612 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 2748
Score: 4686.00 Matches: 902
Percent Similarity: 99.23% Conservative: 6
Best Local Similarity: 98.58% Mismatches: 7
Query Match: 98.86% Indels: 0
DB: 12 Gaps: 0

US-10-647-956A-6 (1-915) x ADN61381 (1-2748)		
Qy	1 MetSerSerTyrAenSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn	20
Dd		
Dd	1 ATGAGCAGTTACAAATCTCGCAATTGACCAAAAGACCCCTCGATTAAAGGTATTAGATAAC	60
Qy		
Dd	21 ArgLysLeuAenValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAenSerAsp	40
Dd		
Dd	61 AGGAAATTAATGTPACGTACTTTAGAAATATCTACGCACTCAAGCTGACGAAACAGTGAT	120
Qy		
Dd	41 GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro	60
Dd		
Dd	121 GAATTAATTAAGTCTATAGTTCAATATATCCGGGATTTTCAGGTAAAGACCCGATCCT	180
Qy		
Dd	61 ArgLysAenLysAenGlnSerGlyProAenPheIleArgValPheAenLeuAlaGlyGln	80
Dd		
Dd	181 CGTAAATAAACCAGAGCGGCCCAATTTCAATTCGTGTCTTTAAATCTTGGCGGTCAA	240
Qy		
Dd	81 ValLeuArgGluGluSerValAspAlaGlyArgThrIleThrLeuAenAspIleGluSer	100
Dd		
Dd	241 GTTTTACGTGAAGAAAGTTGTGATGCCGTCGGACTATTTACCTCAATGATATTGAAAGT	300
Qy		
Dd	101 ArgProValLeuIleIleAsnAlaThrGlyValArgGlnAenHisArgTyrGluAspAsn	120
Dd		
Dd	301 CGCCCGGTGTTGATCATCAATGCAACCGGTGTCGCCCAAAACCATCGTTATGAAGATAAC	360
Qy		
Dd	121 ThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGlyGluLysThrThr	140
Dd		
Dd	361 ACCCTCCCGTCTGCTCGCTATCACCAACAGTACAGGAGGAGAGAAACGACC	420
Qy		
Dd	141 GluArgLeuIleTrpAlaGlyAenThrProGlnGluLysAspTyrAenLeuAlaGlyGln	160
Dd		
Dd	421 GAACGTCTTATCTGGCGCGCAATACGCCGCAAGAAAAGATTACAACCTCGCCGGTCAG	480
Qy		
Dd	161 CysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAenSerLeuSerLeuAlaGly	180
Dd		
Dd	481 TGTGTCGCCATTACGATACCGCGGACTTACTCAACTCAATAGCCTTCTCGCTGCG	540
Qy		
Dd	181 ValValLeuSerGlnSerGlnLeuLeuThrAspAenGlnAenAlaAspTrpThrGly	200
Dd		
Dd	541 GTCGTGCTATCACAACTCTCAGCAACTACTCTCGATGATATAAAATGCTGACAGGT	600
Qy		
Dd	201 GluAspGlnSerLeuTrpGlnLysLeuSerSerAspValTyrIleThrGlnSerAsn	220
Dd		
Dd	601 GAACACCAAGCCCTCTGCACAAAACTGACGAGTGATGCTATACACCCAAATATAA	660
Qy		
Dd	221 ThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGlyAenIleGlnArgLeu	240
Dd		
Dd	661 GCCGATGCCACCGGGCTTTATTGACCCAGACCGATGCCAAAGGCAACATCCACGCTG	720
Qy		
Dd	241 AlaTyrAspValAlaGlyGlnLeuLysGlySerTrpLeuThrLeuLysGlyGlnAlaGlu	260
Dd		
Dd	721 GCCTACGACGTAGCGGGCAGCTAAAGGCTGTGTTGGTTGACACTCAAGGTCAGCGCGAG	780
Qy		
Dd	261 GlnValIleIleLysSerLeuThrTyrSerAlaAlaGlyGlnLysLeuArgGluLysHis	280
Dd		
Dd	781 CAAGTGATTATCAATTCGCTGACCTTAAAGGCTGTGTTGGTTGACACTCAAGGTCAGCGCGAG	840
Qy		
Dd	281 GlyAenGlyIleValThrGluTyrSerTyrGluProGluThrGlnArgLeuIleGlyIle	300
Dd		
Dd	841 GGTAACGGGTTATCACTGAATACAGCTATGAACCCAGAAACCCCAACCGCTTATCGGTATT	900
Qy		
Dd	301 ThrThrArgProSerAspAlaLysValLeuGlnAenLeuArgTyrGlnTyrAspPro	320
Dd		
Dd	901 GCCACCGCGCTCGCTCAGACGCCAAAGTTGCAAGACTTACGCTATCAATATGACCCG	960
Qy		
Dd	321 ValGlyAenValIleAenIleArgAenAspAlaGluAlaThrArgPheTrpArgAenGln	340
Dd		
Dd	961 GTAGCAATGATCAATATCCGTAATGATCGGAAGCCACCCGCTTTTGGCGCAATCAG	1020
Qy		
Dd	341 LysValAlaProGluAenSerTyrThrTyrAspSerLeuTyrGlnLeuIleSerAlaThr	360
Dd		

Dd	1021 AAAGTGGTCCCGAGAAATAGCTATATACCTACGACTCCCTGTGTATCAGCTTATCAGTGGCCACC	1080
Qy		
Dd	361 GlyArgGluMetAlaAenIleGlyGlnGlnAenAenGlnLeuProSerProAlaLeuPro	380
Dd		
Dd	1081 GGGCGGGAATGGCTAANTATAGTTCAGCAAAATACCAACTGCCCTCCCTCGGCTACCT	1140
Qy		
Dd	381 SerAspAenAenThrTyrThrAenTyrThrArgSerTyrSerTyrAspHisSerGlyAen	400
Dd		
Dd	1141 TCTGCAACAATACCTACACTAACTATCTCGCAGCTACAGCTATGATCACAGTGGTAAT	1200
Qy		
Dd	401 LeuThrGlnIleArgHisSerSerProAlaThrGlnAenAenTyrThrValAlaIleThr	420
Dd		
Dd	1201 CTGACGCAAAATCGGCACAGCTCGCCAGCTACCCAGAACACTACACCGTGGCTATCACC	1260
Qy		
Dd	421 LeuSerAenArgSerAenArgGlyValLeuSerThrLeuThrThrAspProAenGlnVal	440
Dd		
Dd	1261 CTCTCAACCGCAGCAATCGGGTGTCTCAGTACGCTAACCCAGATTCAAATCAAGTG	1320
Qy		
Dd	441 AspThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIle	460
Dd		
Dd	1321 GATACGTTGTTGATGCCGTGGTCAACCAACCCAGTTTATTACCCGAGACACACTTATC	1380
Qy		
Dd	461 TrpThrProArgGlyGluLeuLysGlnValAenAenGlyProGlyAenGluTrpTyrArg	480
Dd		
Dd	1381 TGGACACACGAGAGAGTTAAAGCAGGTTAATAATGGCCCGGAAATGAGTGGTACCGC	1440
Qy		
Dd	481 TyrAspSerAenGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAenThrThr	500
Dd		
Dd	1441 TAGCAGCAACCGCATGAGCAACCTGAAGTGATGGAACAGCAACCCAGCAATACTACG	1500
Qy		
Dd	501 GlnGlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAenAla	520
Dd		
Dd	1501 CAGCAACACGGGTAACTTATTTGCCGGACTGGAGCTACGCACACCCAGAGCAACGCC	1560
Qy		
Dd	521 ThrThrThrGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArg	540
Dd		
Dd	1561 ACAACAACGGAAGAGTTACACGTTATCACACTCGGTGAAGCCGCTCGCCACAGGTACGG	1620
Qy		
Dd	541 ValLeuHisTrpGluSerGlyLysProGluAspValAenAenGlnLeuArgTyrSer	560
Dd		
Dd	1621 GTGTTGCACCTGGGAGAGCGGTAAAGCAGAGATGTCAACAATTAATCAACTACGTTACAGC	1680
Qy		
Dd	561 TyrAspAenLeuIleGlySerSerGlnLeuGluLeuAspAenGlnGlyGlnIleLeSer	580
Dd		
Dd	1681 TACGATAATCTGATCGCTCCAGCCAGCTTGAACTCGACCAACCAAGAGCAAAATATCAGC	1740
Qy		
Dd	581 GluGluGluTyrTyrProPheGlyGlyThrAlaLeuTrpAlaAlaAenSerGlnThrGlu	600
Dd		
Dd	1741 GAGGAAGAGTATTATTCATTGCGGGGACAGCGCTGTGGGACAGCAACAGCCAAACAGAA	1800
Qy		
Dd	601 AlaSerTyrLysThrIleArgTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyr	620
Dd		
Dd	1801 GCAGCTTATAAACAATTCGCTATTCCGGCAAGAACAGAGATGCCACCGGGTTGTATTAT	1860
Qy		
Dd	621 TyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTrpLeuSerAlaAspProAlaGly	640
Dd		
Dd	1861 TACGTTATCGTTATTACCAACCGTGGCGGGCAGATGGTTAAGCGGAGCCCGCAGGA	1920
Qy		
Dd	641 ThrIleAspGlyLeuAenLeuTyrArgMetValArgAenAenProValSerLeuGlnAen	660
Dd		
Dd	1921 ACCATTGATGGGTGAATCTATACCGAATGGTAAGAAATAATCTGTGAGTTTTACAGAT	1980
Qy		
Dd	661 GluAenGlyLeuAlaProGluLysGlyLysTyrThrLysGluValAenPheAspGlu	680
Dd		
Dd	1981 GAAAAATGGATTACGCCGAGAAAAAGGAAATATACCAAGAGGTAATAATTTCTTTTATGAA	2040
Qy		
Dd	681 LeuLysPheLysLeuAlaAlaLysSerSerHisValValLysTrpAenGluLysGluSer	700
Dd		
Dd	2041 TTAATAATTCAAATGGCAGCCAAAGTTTCACATGTTGTCAAATGGAAACAGAGAGAGC	2100
Qy		
Dd	701 SerTyrThrLysAenLysSerLeuLysValValArgValGlyAspSerAspProSerGly	720
Dd		
Dd	2101 AGTTATACAAAAATAAATCATTTGAAAGTGGTTTCGTGTCGGTGATTTCCGATCCGTCGGGT	2160

QY 721 TyrLeuLeuSerHisGluGluLeuLeuLeuGlyLeGluLysSerGlnllelleTyrSer 740
Db 2161 TATTTGCTAGCCACGAAGAGTTACTAAAGAGGTATAGAAAAAGTCAAAATCATATATAGC 2220
QY 741 ArgLeuGluLeuSerSerLeuSerGluLysSerIleThrAsnLeuSerLeuGlySer 760
Db 2221 CGACTTGAAGAAACAGTCCCTTTTCAGAAAAATCAAAAACGAATCTTTCTTTAGGATCT 2280
QY 761 GluIleSerGlyTyrMetAlaArgThrIleGlnAspThrIleSerGluTyrAlaGluGlu 780
Db 2281 GAATATCCGGTTATATGGCAAGACCATACAGATACGATATCAGATATGCCGAAGAG 2340
QY 781 HisLysTyrArgSerAsnHisProAspPheTyrSerGluThrAspPheAlaLeuMet 800
Db 2341 CATAAATATAGAAGTAATCACCCCTGATTTTATTATTCAGAAACCGATTTCTTGGCTTAATG 2400
QY 801 AspLysSerGluLysAsnAspTyrSerGlyGluArgLysIleTyrAlaAlaMetGluVal 820
Db 2401 GATAAAAGTGAAAAAATGATTATTCGGTGAAGAAAAAATTTATCGGCAATGGAGGTT 2460
QY 821 LysValTyrHisAspLeuLysAsnLysGlnSerGluLeuHisValAsnTyrAlaLeuAla 840
Db 2461 AAGTTTATCATGATTAAAAAATAAACATCAGATTACATCTCAACTATGCTATGGCC 2520
QY 841 HisProTyrThrGlnLeuSerAsnGluGluArgAlaLeuLeuGlnGluThrGluProAla 860
Db 2521 CATCCCTATACGCAATAGTAATGAAGAAAGCGCTGTTCAAGAAACAGAACCCGCT 2580
QY 861 IleAlaIleAspArgGluTyrAsnPheLysGlyValGlyLysPheIleThrMetLysAla 880
Db 2581 ATTGCAATAGATAGAGAAATATAATTTCAAAGGTGTTGGCAAAATTCCTGCAATGNAAGCA 2640
QY 881 IleLysLysSerLeuLysGlyHisLysIleAsnArgIleSerThrGluAlaIleAsnIle 900
Db 2641 ATTAAAAAATCATTTGAAGACATATAAATTAATAGGATATCAACAGAGGCTATTATATT 2700
QY 901 ArgSerAlaAlaIleAlaGluAsnLeuGlyMetArgArgThrSer 915
Db 2701 CGCTCTCGCGCTATCGTGAGAAATTTAGGAATCGGAGAACTTCA 2745
RESULT 3
ACF69438
ID ACF69438 standard; DNA; 2748 BP.
AC ACF69438;
XX
DT 20-NOV-2003 (first entry)
XX Photorhabdus luminescens nucleotide sequence #7905.
XX
KW Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;
KW detection; food; gene expression; plant; animal; microorganism; toxin;
KW antibiotic; biopesticide; virulence factor; disease model; plague;
KW whooping cough; gene; ds.
XX
OS Photorhabdus luminescens.
XX
PN W020294867-A2.
XX
XX 28-NOV-2002.
XX
XX 07-FEB-2002; 2002WO-IB003040.
XX
XX 07-FEB-2001; 2001FR-00001659.
XX
XX (INSP) INST PASTEUR.
XX (CNRS) CNRS CENT NAT RECH SCI.
XX
XX Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;
XX Buchrieser C;
XX
XX WPI; 2003-148459/14.

XX
PT Genomic sequence of Photorhabdus luminescens and encoded polypeptides,
XX useful e.g. as therapeutic antimicrobials and agricultural pesticides.
XX
PS Claim 2; SEQ ID NO 7905; 1205pp; French.
XX
CC The invention relates to the isolation of genes and their encoded
CC proteins from Photorhabdus luminescens. The isolated sequences are
CC sources of probes and primers for detecting the genome of P. luminescens
CC and related species; to study polymorphisms; for gene analysis and for
CC detection/amplification of the genes. Antibodies (Ab) raised against the
CC polypeptides encoded by the genes are used for detection/identification
CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that
CC carry a gene-containing vector are used to select compounds that
CC modulate, regulate, induce or inhibit expression of the genes in plants,
CC animals or microorganisms other than P. luminescens and are able to alter
CC response or sensitivity to toxins and antibiotics produced by P.
CC luminescens. Cells transformed to express the genes are useful for
CC recombinant production of the proteins, particularly toxins and
CC antibacterials useful as insecticides, bactericides and fungicides. The
CC genes, proteins, vectors containing the genes and Ab are also useful
CC therapeutically (to treat microbial infection by bacteria or fungi that
CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as
CC biopesticides. Other uses of the genes and the proteins are as virulence
CC factors and for identifying targets of human diseases for which P.
CC luminescens is a model (particularly plague and whooping cough). This
CC sequence represents one of the isolated P. luminescens genes
XX
SQ Sequence 2748 BP; 914 A; 606 C; 615 G; 613 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0 Length: 2748
Score: 4429.00 Matches: 847
Percent Similarity: 95.96% Conservative: 31
Best Local Similarity: 92.57% Mismatches: 37
Query Match: 93.44% Indels: 0
DB: 10 Gaps: 0
US-10-647-956A-6 (1-915) x ACF69438 (1-2748)
QY 1 MetSerSerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn 20
Db 1 ATGAGCAGTTATCGTTCTGAAATTTGACAAAAAACACCAATTAATCAGTGTATTGGATAAC 60
QY 21 ArgLysLeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAsnSerAsp 40
Db 61 AGAGGTTAAATGTACGTACTTTAGAAATATCTACGTACTCAAGCTGATGAAACAGTGAT 120
QY 41 GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro 60
Db 121 GAATTGATCACACTCTATGAGTTCAATATTCAAGGATTTGAGGTAAAAAGTACTGATCCT 180
QY 61 ArgLysAsnLysAsnGlnSerGlyProAsnPheIleArgValPheAsnLeuAlaGlyGln 80
Db 181 CGTAGAATAAAAAATCAGAGCGGCCGGAATTTCAATTCGGCTCTTTAATCTCGCGGTGAG 240
QY 81 ValLeuArgGluGluSerValAspAlaGlyArgThrIleThrLeuAsnAspIleGluSer 100
Db 241 GTTCTACGTGAAGAGGGGTTCATCCGGTCGAACTATCATCTCAACGATGTTGAAGGT 300
QY 101 ArgProValLeuIleIleAsnAlaThrGlyValArgGlnAsnHisArgTyrGluAspAsn 120
Db 301 CGCCCGGTATTAAACCATCAATGCAACCGGTGTCCGCAAGACTTATCACTACCAAGATAAC 360
QY 121 ThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGlyGluIleThrThr 140
Db 361 ATCTTACCGGTGCGTTACTTGTCTATCCAGCAACAGGTGCGAGCAGAGAGAAATGACC 420
QY 141 GluArgLeuIleIlePheAlaGlyAsnThrProGlnGluLysAspTyrAsnLeuAlaGlyGln 160
Db 421 GAGCGCTTATCTGGGCCGCAATAGCCGCGCAAGAAAAAGATACACCTTCTGCTGTCAG 480
QY 161 CysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAsnSerLeuSerLeuAlaGly 180

|||||
481 TGTCTCGCCACTACGATACCGCTGGACTCACTCAACTCAACAGCCCTTCTCTGGCTGGC 540
Db
|||||
181 ValValLeuSerGlnSerGlnGlnLeuLeuThrAspAsnGlnAspAlaAspTrpThrGly 200
Qy
|||||
541 GTCGTGCTATCACAACTCTCAACAACCTGCTGCTGATGATCAAAATGCGGACTGACAGGT 600
Db
|||||
201 GluAspGlnSerLeuTrpGlnGlnLysLeuSerSerAspValTyrIleThrGlnSerAsn 220
Qy
|||||
601 GAAGATCAAGCCCTCTGGCAGCAAAACTGAGAGTGTGTATATACCAACCAAAATAGC 660
Db
|||||
221 ThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGlyAsnIleGlnArgLeu 240
Qy
|||||
661 ACTGATGCCACCGGGCTTTACTTATCCAGACCAGTGCMAAGGCAACATCCAGCGTCTG 720
Db
|||||
241 AlaTyrAspValAlaGlyGlnLeuLysGlySerTrpLeuThrLeuLysGlyGlnAlaGlu 260
Qy
|||||
721 GCCATATGATGAGCGGGCAGCTAAAGGCTGTGGTTAACTCAACTCAAAAGGTCAAAGCCGAA 780
Db
|||||
261 GlnValIleIleLysSerLeuThrTyrSerAlaAlaGlyGlnLysLeuArgGluGluHis 280
Qy
|||||
781 CAAGTGATTCAAACTCGCTGACCTACTCTGCCCGCGGACAAAATTCAGTGAAGAGCAC 840
Db
|||||
281 GlyAsnGlyIleValThrGluTyrSerTyrGluProGluThrGlnArgLeuIleGlyIle 300
Qy
|||||
841 GGTAAACGGGTATCACCGAATACAGCTATGAACAGAAACCAACCGCTTATTGGTATC 900
Db
|||||
301 ThrThrArgAspProSerAspAlaLysValLeuGlnAspLeuArgTyrGlnTyrAspPro 320
Qy
|||||
901 ACTACCGCGCTCGCTCAGATCAACAGGTGTGCAAGACTTACGCTATCAATATGATCCG 960
Db
|||||
321 ValGlyAsnValIleAsnIleArgAsnAspAlaGluAlaThrArgPheTrpArgAsnGln 340
Qy
|||||
961 GTAGGCAATGATCAATATCCGTAACTGCGTGGAGCCACCGCTTTGGCGCAATCAG 1020
Db
|||||
341 LysValAlaProGluAsnSerTyrThrTyrAspSerLeuTyrGlnLeuIleSerAlaThr 360
Qy
|||||
1021 AAAGTGGTCCCGGAGATAGCTATCTACGACTCCCTGTACCAGCTTATCAGTGTACT 1080
Db
|||||
361 GlyArgGluMetAlaAsnIleGlyGlnGlnAsnAsnGlnLeuProSerProAlaLeuPro 380
Qy
|||||
1081 GGGCGTGAATGGCCAAATATAGGTGAGCAAAATATCAACTGCCCTCCCTCGCCCTACCT 1140
Db
|||||
381 SerAspAsnAsnThrTyrThrAsnTyrThrArgSerTyrSerTyrAspHisSerGlyAsn 400
Qy
|||||
1141 TCCGACAACTACTACACTAACTATACTCGCGCTACAGTTATGATCAGCGGTAAAT 1200
Db
|||||
401 LeuThrGlnIleArgHisSerSerProAlaThrGlnAsnAsnTyrThrValAlaIleThr 420
Qy
|||||
1201 CTGACGCAAAATTCGGCACAGTTCTATCGGCTACCCCAAAATACTACACCACCGCTATCACC 1260
Db
|||||
421 LeuSerAsnArgSerAsnArgGlyValLeuSerThrLeuThrThrAspProAsnGlnVal 440
Qy
|||||
1261 ATCTCGAATCGCAGTAACCGGGCGGTCTCTAGTACGCTGACAAACAGATCCAAATCAAGTG 1320
Db
|||||
441 AspThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIle 460
Qy
|||||
1321 GATACGTTATTGATCCCGGTGGTCACCAACCCAGTTTATTACCGGTGACACTGGTC 1380
Db
|||||
461 TrpThrProArgGlyGluLeuLysGlnValAsnAsnGlyProGlyAsnGluTrpTyrArg 480
Qy
|||||
1381 TGGACATCACGAGGAGAGTTAAAGCAGGTCAATACCGTTCCAGGAATGAATGGTACCGA 1440
Db
|||||
481 TyrAspSerAsnGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAsnThrThr 500
Qy
|||||
1441 TACGCAGCAACCGGAATGAGCAACTGAAAGTGAGTGAACAGCCCAACCCAGAACTACG 1500
Db
|||||
501 GlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAla 520
Qy
|||||
1501 CAGCAGCAGCGGGTAACTATCTCTCGCGGGGTGGAACTTACGCACAAACCCAGAACGACAC 1560
Db
|||||
521 ThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArg 540
Qy
|||||

1561 ACAACAACAGAGAGTTACACGTGATCACACTAGGTGAAGCGGGTCCGCGCACAGGTGCGG 1620
Db
|||||
541 ValLeuHisTrpGluSerGlyLysProGluArgValAsnAsnAsnGlnLeuArgTyrSer 560
Qy
|||||
1621 GTCTGCACTGGAGAGCGGTAAACCAAGAGGTATCAACAACATCAGTACTACGTTACAGC 1680
Db
|||||
561 TyrAspAsnLeuIleGlySerSerGlnLeuGluLeuAspAsnGlnGlyGlnIleLeuSer 580
Qy
|||||
1681 TACGATAATCTGATCGCTCCAGCCAGCTTGAACTCGACAACCAAGGGCAGATTATTAGT 1740
Db
|||||
581 GluGluGluTyrTyrProPheGlyGlyThrAlaLeuTrpAlaAlaAsnSerGlnThrGlu 600
Qy
|||||
1741 GAGCAAGAGTATTATTCATTCGGCGGCACAGCGATGTGGCAGCCCAATAGCCAAACAGAA 1800
Db
|||||
601 AlaSerTyrLysThrIleArgTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyr 620
Qy
|||||
1801 GCCAATATATAAACTATTTCGTATTGAGCAAGAAGCGGATACCAACCGGGCTGTATTAT 1860
Db
|||||
621 TyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTrpLeuSerAlaAspProAlaGly 640
Qy
|||||
1861 TACGGTTACCGCTATTATCAACCGTCGGCGGCAGATGGTTAAGCGCGATCCGGCAGGA 1920
Db
|||||
641 ThrIleAspGlyLeuAsnLeuTyrArgMetValArgAsnAsnProValSerLeuGlnAsp 660
Qy
|||||
1921 ACCATTGATGGGTGAATCTATACCGAATGGTGAGAAATAATCCAGTAAGTTTGCAGGAT 1980
Db
|||||
661 GluAsnGlyLeuAlaProGluLysGlyLysTyrThrLysGluValAsnPhePheAspGlu 680
Qy
|||||
1981 GAAATGGGATTAGCACAGAAAGGAAATAATATCTAAAGAGGTGAATTTCTTGATGAA 2040
Db
|||||
681 LeuLysPheLysLeuAlaLysSerSerHisValValLysTrpAsnGluLysGluSer 700
Qy
|||||
2041 TTAATAATTCBAATTCGCAGCCCAAAATTCACATGTTGTCAAAATGGAACAGAGAAAGAT 2100
Db
|||||
701 SerTyrThrLysAsnLysSerLeuLysValValArgValGlyAspSerAspProSerGly 720
Qy
|||||
2101 AGTTATACAAAAATAAATCAATTCATGAAAGTGGTTTCGGGTCCGTGATTCGCGTCCGGGT 2160
Db
|||||
721 TyrLeuLeuSerHisGluGluLeuLeuLysGlyIleGluLysSerGlnIleIleTyrSer 740
Qy
|||||
2161 TATTTGCTAAGCCACCAAGAGTTACTTAAAGGGCTAGAAAAAGCCCAATATATATAGC 2220
Db
|||||
741 ArgLeuGluGluAsnSerSerLeuSerGluLysSerLysThrAsnLeuSerLeuGlySer 760
Qy
|||||
2221 CGGCTCGAAGAAACAGATCCCTTTTCAGAAAAATCAAAACAAATCTTTCTTTGGGATCT 2280
Db
|||||
761 GluIleSerGlyTyrMetAlaArgThrIleGlnAspThrIleSerGluTyrAlaGluGlu 780
Qy
|||||
2281 GAAATATCCGGTTATATGGCAAAACGATAAAAGATACGATATCAGAAATATACAGAAGG 2340
Db
|||||
781 HisLysTyrArgSerSerAsnHisProAspPheTyrSerGluThrAspPheAlaLeuMet 800
Qy
|||||
2341 CATAGGTATAGAGCAATCATCCGATTTTATGCGACCAACAGATTTCTTTGCTTTAATG 2400
Db
|||||
801 AspLysSerGluLysAsnAspTyrSerGlyGluArgLysIleTyrAlaAlaMetGluVal 820
Qy
|||||
2401 GATAAAGTCAAAAAATGATTATTCGGGTGAAAGAAAAATTTATCGCGCAATAGAGGTT 2460
Db
|||||
821 LysValTyrHisAspLeuLysAsnLysGlnSerGluLeuHisValAsnTyrAlaLeuAla 840
Qy
|||||
2461 AAGGTTTATCATGATTTAAAAATAAACCAATCAGAAATTACATGCTCAACTATGCACTGGCT 2520
Db
|||||
841 HisProTyrThrGlnLeuSerAsnGluAlaArgAlaLeuGlnGlnThrGluProAla 860
Qy
|||||
2521 CATCCCTATACGCAATTGAGTAATGAGAGAGAGCGCTGGTGCAAGAAACAGAACCCGCT 2580
Db
|||||
861 IleAlaIleAspArgGluTyrAsnPheLysGlyValGlyLysPheLeuThrMetLysAla 880
Qy
|||||
2581 ATTGCAATAATAGAGNAATATAATTTCAAAGGGCTTGGTAAATTCCTGGCAATGAAAGCA 2640
Db
|||||
881 IleLysLysSerLeuLysGlyHisLysIleAsnArgIleSerThrGluAlaIleAsnIle 900
Qy
|||||
2641 ATTAATAAATCAATGAAAGGGCAGAGATCAATAAAAAATATCAACAGAGGCTATTATATT 2700
Db

Qy 901 ArgSerAlaIleAlaGluAenLeuGlyMetArgArgThrSer 915
Db 2701 CGCTCTGGCTATCGCTAAGAAATTTAGGAATCGGAGAGCTTCA 2745

RESULT 4

Continuation (24 of 57) of ACF67367 from base 2300001 (Photorhabdus luminescens nucleotide)

WP Sequence split into 57 fragments LOCUS ACF67367 Accession ACF67367

Fragment Name	Begin	End
WP ACF67367_00	1	110000
WP ACF67367_01	100001	210000
WP ACF67367_02	200001	310000
WP ACF67367_03	300001	410000
WP ACF67367_04	400001	510000
WP ACF67367_05	500001	610000
WP ACF67367_06	600001	710000
WP ACF67367_07	700001	810000
WP ACF67367_08	800001	910000
WP ACF67367_09	900001	1010000
WP ACF67367_10	1000001	1110000
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WP ACF67367_50	5000001	5110000
WP ACF67367_51	5100001	5210000
WP ACF67367_52	5200001	5310000
WP ACF67367_53	5300001	5410000
WP ACF67367_54	5400001	5510000
WP ACF67367_55	5500001	5610000
WP ACF67367_56	5600001	5648894

Alignment Scores:

Pred. No.:	1.03e-315	Length:	110000
Score:	4429.00	Matches:	847
Percent Similarity:	95.96%	Conservative:	31
Best Local Similarity:	92.57%	Mismatches:	37

Query Match:	93.44%	Indels:	0
DB:	10	Gaps:	0
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Qy 1 MetSerSerTyrAsnSerAlaIleAepGlnLysThrProSerIleLysValLeuAAspAen 20			
Db 100781 ATGAGCAGTTATCGTCTCGAAATTGCAAAAAAACCACTTATATAGTGTATTGGATTAAC 100840			
Qy 21 ArgLysLeuAenValArgThrLeuGluTyrLeuArgThrGlnAlaAAspGluAenSerAAsp 40			
Db 100841 AGGAGGTTAAATGTAGCTACTTTAGAAATATCTACGTACTCAAGCTGATGAATAACAGTGAT 100900			
Qy 41 GluLeuIleThrPheTyrGluPheAenIleProGlyPheGlnValLysSerThrAAspPro 60			
Db 100901 GAATTGATCACACTCTATGAGTTCAATATTCAAGGATTTGAGGTAAATAAGTACTGATCCT 100960			
Qy 61 ArgLysAenLysAenGlnSerGlyProAenPheIleArgValPheAenLeuAlaGlyGln 80			
Db 100961 CGTAAGAAATAAAATCAGAGCGGCCGGAATTCATTCCGGCTCTTTTAACTCTCGCGGGTCAG 101020			
Qy 81 ValLeuArgGluGluSerValAAspAlaGlyArgThrIleThrLeuAAspIleGluSer 100			
Db 101021 GTTCTACGTGAAGAGGGGTTGATGCCGTCGAACCTATCATCTCAACGATGTTGAAGT 101080			
Qy 101 ArgProValLeuIleIleAenAlaThrGlyValArgGlnAAsnHisArgTyrGluAAspAen 120			
Db 101081 CGCCCGGTATTAAACCATCAATGCAACCGGTGTCCGCAAGACTATCATCTACGAAGATAAC 101140			
Qy 121 ThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGlyGluTyrThrThr 140			
Db 101141 ATCTACCCGGTCGCTTACTTGTATACCGCAACAGGTGAGCAGCAAGAGAAATGACC 101200			
Qy 141 GluArgLeuIleTrpAlaGlyAAsnThrProGlnGluLysAAspTyrAAsnLeuAlaGlyGln 160			
Db 101201 GAGCGCTTATCTGGCCGCGCAATAGCCGCGCAAGAAAGAGTACAACTTGTGTGTGTCAG 101260			
Qy 161 CysValArgHisTyrAAspThrAlaGlyLeuThrGlnLeuAAsnSerLeuSerLeuAlaGly 180			
Db 101261 TGTGTCCGCACATACGATACCGCTGAGCTCACTCAACTCAACAGCCCTTCTCTGGCTGGC 101320			
Qy 181 ValValLeuSerGlnSerGlnGlnLeuThrAAspAenGlnAAspAlaAAspTrpThrGly 200			
Db 101321 GTCGTGCTATCAATCTCAACAACCTGCTCGATGATCAAAATGCCAGCTGAGCAGGT 101380			
Qy 201 GluAAspGlnSerLeuTrpGlnGlnLysLeuSerSerAAspValTyrIleThrGlnSerAAsn 220			
Db 101381 GAAGATCAAAAGCCTCTGGCAGCAAAAACCTGAGCAGTGATGTCTATACCAACCAAAATAGC 101440			
Qy 221 ThrAAspAlaThrGlyAlaLeuLeuThrGlnThrAAspAlaLysGlyAenIleGlnArgLeu 240			
Db 101441 ACTGATGCCACCGGGCTTTACTTATCCAGACCGATGCCAAGGCAACATCCAGCGCTCTG 101500			
Qy 241 AlaTyrAAspValAlaGlyGlnLeuLysGlySerTrpLeuThrLeuLysGlyGlnAlaGlu 260			
Db 101501 GCCTATGATGTAGCCGGCAGCTTAAAGGCTGTGGTTAACTCAACTCAAGAGGTCAAGCCGAA 101560			
Qy 261 GlnValIleIleLysSerLeuThrTyrSerAlaAlaGlyGlnLysLeuArgGluGluHis 280			
Db 101561 CAAGTGATTATCAATCCGCTGACCTACTCTGCCCGCGCAAAAATATTACGTGAAGAGCAC 101620			
Qy 281 GlyAAsnGlyIleValThrGluTyrSerTyrGluProGluThrGlnArgLeuIleGlyIle 300			
Db 101621 GGTAAACGGGGTTATATACCGAATACAGCTATGAACCAAGAAACCAACCGGCTATTGGTATC 101680			
Qy 301 ThrThrArgArgProSerAAspAlaLysValLeuGlnAAspLeuArgTyrGlnTyrAAspPro 320			
Db 101681 ACTACCCGCGCTCCGTCAGATACCAAGGTGTTGCAAGACTTACGCTATCAATATGATCCG 101740			
Qy 321 ValGlyAAsnValIleAAsnIleArgAAspAlaGluAlaThrArgPheTrpArgAAsnGln 340			
Db 101741 GTAGGCAATGTGATCAATATCCGTAACGATCGGGAAGCCACCCGCTTTTGGCGCAATCAG 101800			

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Qy 341 LysValAlaProGluAenSerTyrThrTyrAspSerLeuTyrGlnLeuIleSerAlaThr 360
Db 101801 AAAGTGGTCCGGAGAAATAGCTATACCTTACGACTCCCTGTACCAAGCTTATCAGTGGCTACT 101860
Qy 361 GlyArgGluMetAlaAenIleGlyGlnGlnAenGlnLeuProSerProAlaLeuPro 380
Db 101861 GGGCGTGAATGGCCAATATAGGTACGCAAAATAATCAACTGCCCTCCCTGGCGCTACCT 101920
Qy 381 SerAspAenAenThrTyrThrAsnTyrThrArgSerTyrSerTyrAspHisSerGlyAsn 400
Db 101921 TCCGACAAACAATACCTACACTAATCTACTCGCGCTACAGTTATGATCAAGCGGTAAT 101980
Qy 401 LeuThrGlnIleArgHisSerSerProAlaThrGlnAenAenTyrThrValAlaIleThr 420
Db 101981 CTGACGCAAAATTCGGCACAGTTTCATCGGCTACCCCAAAATAACTACACCGCTATCAC 102040
Qy 421 LeuSerAenArgSerAenArgGlyValLeuSerThrLeuThrThrAspProAenGlnVal 440
Db 102041 ATCTCGAATCGAGTACCGCGGGCTTCTCAGTACGCTGACAAACAGATCCAAATCAAGTG 102100
Qy 441 AspThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIle 460
Db 102101 GATACGTATTTGATCGCGGTGGTCACCAACCAAGTTTATTAACCGGTTCAGACACTGGCT 102160
Qy 461 TrpThrProArgGlyGluLeuLysGlnValAenAenGlyProGlyAenGluTyrTyrArg 480
Db 102161 TGGACATCACGAGAGAGAGTTAAAGCAGGTCAATTAACGGTTCAGGAATGAATGGTACCGA 102220
Qy 481 TyrAspSerAenGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAenThrThr 500
Db 102221 TACGGCAGCAACGGAAATGAGACAACTGAAAGTGAGTGAACAGCAACCCAGAACTACG 102280
Qy 501 GlnGlnAenArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAenAla 520
Db 102281 CAGCAGCAGCGGGTAAATCTATCTCGCGGGGTGAAACTACGCACAAACCCAGCAACGAC 102340
Qy 521 ThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArg 540
Db 102341 ACAACAACGAAGAGTTTACAGTGATACACTAGTGTAAGCGGTTCGGGCACAGGTGCGG 102400
Qy 541 ValLeuHisTrpGluSerGlyLysProGluAspValAenAenAenGlnLeuArgTyrSer 560
Db 102401 GTGCTGCACTGGAGAGCGGTAAACCAAGAGTATCAACAACATCAGTACGTTACAGC 102460
Qy 561 TyrAspAenLeuIleGlySerSerGlnLeuGluLeuAspAenGlnGlyGlnIleIleSer 580
Db 102461 TACGATATCTGATCGGCTCCAGCGAGCTTGAACCTGGCAACCAAGGCGCAGATTATTAGT 102520
Qy 581 GluGluGluTyrTyrProPheGlyGlyThrAlaLeuTrpAlaAlaAenSerGlnThrGlu 600
Db 102521 GAGGAAGAGTATTTATCCATTCCGGCGGCACAGCGATGTGGCGGAGCCAAATAGCCAAACAGAA 102580
Qy 601 AlaSerTyrLysThrIleArgTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyr 620
Db 102581 GCCAACTATAAACTATTTCCGTATTTACGGCAAAAGAACGGGATACACCGGCGCTGTATTAT 102640
Qy 621 TyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTrpLeuSerAlaAspProAlaGly 640
Db 102641 TACGGTTACCGCTATTTATCAACCGGTGGCGGCGCAGATGGTTAAGCGCGGATCCGGCAGGA 102700
Qy 641 ThrIleAspGlyLeuAenLeuTyrArgMetValArgAenAenProValSerLeuGlnAsp 660
Db 102701 ACCATTGATGGCTGAATCTTATACCGAATGGTGAGAAATAATCCAGTAAGTTTCAGGAT 102760
Qy 661 GluAenGlyLeuAlaProGluLysGlyLysTyrThrLysGluValAenAenPheAspGlu 680
Db 102761 GAAAAATGGATTAGCACCAAGAGAGAAAAATATACTAAAGAGGTGAATTTCTCTTGATGAA 102820
Qy 681 LeuLysPheLysLeuAlaAlaLysSerSerHisValValLysTrpAenGluLysGluSer 700
Db 102821 TTAATAATTCAAATTTGGCAGCCCAAAATTTACATGTTGTCAAAATGGAACGAGAAAAAGT 102880
Qy 701 SerTyrThrLysAenLysSerLeuLysValValArgValGlyAspSerAspProSerGly 720
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Db 102881 AGTTATACAAAAATAAATCAATTCATTTGAAGTGGTTCCGCTCGGTGATTCCGATCCGTCGGGT 102940
Qy 721 TyrLeuLeuSerHisGluGluLeuLeuLysGlyIleGluLysSerGlnIleIleTyrSer 740
Db 102941 TATTTGCTAAGCCACCAAGAGTTTACTAAAGGCGCATAGAAAAAGCCAAAATTTATATATAGC 103000
Qy 741 ArgLeuGluGluAenSerSerLeuSerGluLysSerLysThrAenLeuSerLeuGlySer 760
Db 103001 CGGCTCGAAGAAAACAGATCCCTTTTCAGAAAAAATCAAAAAAATCTTTCTTTGGGATCT 103060
Qy 761 GluIleSerGlyTyrMetAlaArgThrIleGlnAspThrIleSerGluTyrAlaGluGlu 780
Db 103061 GAAATATCCGTTATATGCAAAAACGATAAAAGATACGATATCAGATATACAGAAGGG 103120
Qy 781 HisLysTyrArgSerAenHisProAspPheTyrSerGluThrAspPhePheAlaLeuMet 800
Db 103121 CATAGGTATAGAAGCAATCATCCGATTTTATGCGACCAACAGATTTCTTTGCTTTAATG 103180
Qy 801 AspLysSerGluLysAenAspTyrSerGlyGluArgLysIleTyrAlaAlaMetGluVal 820
Db 103181 GATAAAGTGAAAAAATGATTATTCGGGTGAAAGAAAAAATTTATCGCGCAATAGAGGTT 103240
Qy 821 LysValTyrHisAspLeuLysAenLysGlnSerGluLeuHisValAenTyrAlaLeuAla 840
Db 103241 AAGGTTATCATGATTTAAAAAATAAACAATCAGAATTCATCTCAACTATGCACGTGCT 103300
Qy 841 HisProTyrThrGlnLeuSerAenGluGluArgAlaLeuLeuGlnGlnThrGluProAla 860
Db 103301 CATCCCTTATACGCAATTTGAGTAATGAAGAGAGAGCGCTGGTGCAGAAAACAGAACCCGCT 103360
Qy 861 IleAlaIleAspArgGluTyrAenPheLysGlyValGlyLysPheLeuThrMetLysAla 880
Db 103361 ATTGCAATAAATAGAGAAATATAATTTCAAAGGCGTTGGTAAATTCCTGGCAATGAAAGCA 103420
Qy 881 IleLysLysSerLeuLysGlyHisLysIleAenAsnArgIleSerThrGluAlaIleAenIle 900
Db 103421 ATTAAAAAATCATTTGAAGGCGCAGAGAGTCAATAAAATATCAACAGAGGCTATTAAATAT 103480
Qy 901 ArgSerAlaAlaIleAlaGluAenLeuGlyMetArgArgThrSer 915
Db 103481 CGCTCTCGCGCTATCGCTAAGAAATTTAGGAATTCGGAGAGAGCTTCA 103525
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RESULT 5

ACF67367_24

Continuation (25 of 57) of ACF67367 from base 2400001 (Photorhabdus luminescens nucleotide sequence split into 57 fragments) LOCUS ACF67367 Accession ACF67367

WP	Fragment Name	Begin	End
WP	ACF67367_00	1	110000
WP	ACF67367_01	100001	210000
WP	ACF67367_02	200001	310000
WP	ACF67367_03	300001	410000
WP	ACF67367_04	400001	510000
WP	ACF67367_05	500001	610000
WP	ACF67367_06	600001	710000
WP	ACF67367_07	700001	810000
WP	ACF67367_08	800001	910000
WP	ACF67367_09	900001	1010000
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WP	ACF67367_21	2100001	2210000
WP	ACF67367_22	2200001	2310000
WP	ACF67367_23	2300001	2410000
WP	ACF67367_24	2400001	2510000


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QY 521 ThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArg 540
Db 2341 ACAACAACAGAGAGTTACACGTGATCACACTAGGTGAGCGGTCCGGCACAGGTCCG 2400
QY 541 ValLeuHisTrpGluSerGlyLysProGluAspValAlaAsnAsnGlnLeuArgTyrSer 560
Db 2401 GTGCTGCACCTGGGAGACGGGTAAACACAGAGAGTATCAACAACATCAGCTACGTTACAGC 2460
QY 561 TyrAspAsnLeuIleGlySerSerGlnLeuGluLeuAspAsnGlnGlyGlnIleIleSer 580
Db 2461 TAGCATAATCTGATCGCTCCAGCCAGCTTTGAACCTGGACAAACCAAGGCGAGATTATTAGT 2520
QY 581 GluGluGluTyrTrpProPheGlyGlyThrAlaLeuTrpAlaAlaAsnSerGlnThrGlu 600
Db 2521 GAGGAAGAGTATTATTCATTCGGGGCGCACAGCGATGTGGCGAGCAATATGCCAAACAGAA 2580
QY 601 AlaSerTyrLysThrIleArgTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyr 620
Db 2581 GCCAACTATAAACTATTTCGCTATTACGCAAGAACGGGATACCACCGGGCTGTATTAT 2640
QY 621 TyrGlyTyrArgTyrTrpGlnProTrpAlaGlyArgTrpLeuSerAlaAspProAlaGly 640
Db 2641 TAGCGTTTACCGCTATTATCAACCGTGGCGCGGAGATGGTTAAGCGCGGATCCGGCAGGA 2700
QY 641 ThrIleAspGlyLeuAsnLeuTyrArgMetValArgAsnAsnProValSerLeuGlnAsp 660
Db 2701 ACCATTGATGGCTGGAATCTATACCGAATGGTGAAGAATAATCCAGTAAGTTTGCAGAT 2760
QY 661 GluAsnGlyLeuAlaProGluLysGlyLysTyrThrLysGluValAsnPhePheAspGlu 680
Db 2761 GAAATCGATTAGCACCAAGAGAGGAAATATATCTAAAGAGGTGAATTTCCITGTATGAA 2820
QY 681 LeuLysPheLysLeuAlaLysSerSerHisValLysTrpAsnGluLysGluSer 700
Db 2821 TTAATAATTCAAATTTGGCAGCAAAATTCACATGTTCTCAAAATGGAACGAGAAAGAAGT 2880
QY 701 SerTyrThrLysAsnLysSerLeuLysValValArgValGlyAspSerAspProSerGly 720
Db 2881 AGTTATACAAAATAAATAATCATTGAAAGTGGTTCGGCTCGGTGATCCCGATCCGTCGGGT 2940
QY 721 TyrLeuLeuSerHisGluGluLeuLysGlyIleGluLysSerGlnIleIleTyrSer 740
Db 2941 TATTTGTAAAGCCACGAAGAGTTACTAAAGGCATAGAAAAAGCCAAATATATATATAGC 3000
QY 741 ArgLeuGluAsnSerSerLeuSerGluLysSerLysThrAsnLeuSerLeuGlySer 760
Db 3001 CGGCTCGAAGAAAACAGATCCCTTTTCAGAAAAATCAAAAAACAATCTTTCTTTGGGATCT 3060
QY 761 GluIleSerGlyTyrMetAlaArgThrIleGlnAspThrIleSerGluTyrAlaGluGlu 780
Db 3061 GAAATATCCGGTTATATGGCAAAACGATAAAGATACGATATCAGATATACAGAAAGGG 3120
QY 781 HisLysTyrArgSerAsnHisProAspPheTyrSerGluThrAspPhePheAlaLeuMet 800
Db 3121 CATAGGTATAGAACCAATCATCCCGATTTTATGCAGCAACAGATTTCTTTGCTTTAATG 3180
QY 801 AspLysSerGluLysAsnAspTyrSerGlyGluArgLysIleTyrAlaAlaMetGluVal 820
Db 3181 GATAAAAGTGAATAAAATATGATTATCCGGTGAAGAAAAATTTATGCGGCAATAGAGGTT 3240
QY 821 LysValTyrHisAspLeuLysAsnLysGlnSerGluLeuHisValAsnTyrAlaLeuAla 840
Db 3241 AAGGTTTATCATGATTTTAAATAATAAACAATCAGAAATTCAGATTCACATATGCACTAGC 3300
QY 841 HisProTyrThrGlnLeuSerAsnGluGluArgAlaLeuLeuGlnGluThrGluProAla 860
Db 3301 CATCCCTATACGCAATTGAGTAAATGAAGAGAGAGCGCTGGTGCAGAAACAGAACCCGCT 3360
QY 861 IleAlaIleAspArgGluTyrAsnPheLysGlyValGlyLysPheLeuThrMetLysAla 880
Db 3361 ATTGCAATAAATAGAGAAATATAATTTCAAAGGCGTTGGTAAATTTCTGGCAATGAAAGCA 3420
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QY 881 IleLysLysSerLeuLysGlyHisLysIleAsnArgIleSerThrGluAlaIleAsnIle 900
Db 3421 ATTAAAAAATCATTGAAAGGCGCAGAGATCAATAAAATATCAACAGAGGCTATTAAATATT 3480
QY 901 ArgSerAlaAlaIleAlaGluAsnLeuGlyMetArgArgThrSer 915
Db 3481 CGCTCTCGCGCTATCGTCTAAGAATTTAGGAATTCGGAGAGACTTCA 3525
RESULT 6
ACF65386_4/c
Continuation (5 of 7) of ACF65386 from base 400001 (Photorhabdus luminescens nucleotide
WP Sequence split into 7 fragments LOCUS ACF65386 Accession ACF65386
Fragment Name Begin End
WP ACF65386_0 1 110000
WP ACF65386_1 100001 210000
WP ACF65386_2 200001 310000
WP ACF65386_3 300001 410000
WP ACF65386_4 400001 510000
WP ACF65386_5 500001 610000
WP ACF65386_6 600001 700779
Alignment Scores: 1.03e-315 Length: 110000
Pred. No.: 4429.00 Matches: 847
Score: 95.96% Conservative: 31
Percent Similarity: 92.57% Mismatches: 37
Best Local Similarity: 93.44% Indels: 0
Query Match: 10 Gaps: 0
DB:
US-10-647-956A-6 (1-915) x ACF65386_4 (1-110000)
QY 1 MetSerSerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn 20
Db 97845 ATGAGCAGTTATCGTCTCGAAATTGACAAAAAACCCATTATCTAGTGTATTGGATAAC 97786
QY 21 ArgLysLeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAsnSerAsp 40
Db 97785 AGCAGGTTAAATGTACGTACTTCTTAGAATATCTACGTACTCAAGCTGATGAAAAACAGTGAT 97726
QY 41 GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro 60
Db 97725 GAATGATCACACTCTATGAGTTCAATATTTCAAGGATTTTGAGGTAAGAAAGTACTGATCCT 97666
QY 61 ArgLysAsnLysAsnGlnSerGlyProAsnPheIleArgValPheAsnLeuAlaGlyGln 80
Db 97665 CGTAAGAAATAAAATCAGACGCGCCGGAATTTCAATTCGCGTCTTTAATCTTCGCGGTCAG 97606
QY 81 ValLeuArgGluGluSerValAspAlaGlyArgThrIleThrLeuAsnAspIleGluSer 100
Db 97605 GTTCTACGTGAAGAGGGTTGATCGCGTTCGAACATATCTCAACGATGTTGAAGGT 97546
QY 101 ArgProValLeuIleIleAsnAlaThrGlyValArgGlnAsnHisArgTyrGluAspAsn 120
Db 97545 CGCCCGGTATTAAACCATCAATGCAACCGGTGTCGCCCAAGACTATCTACGAAAGATAAC 97486
QY 121 ThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGlyGluLysThrThr 140
Db 97485 ATCCTACCCCGTTCGTTTACTTGTCTATCACCACAGGTGCGCAGGAGAGAAATGACC 97426
QY 141 GluArgLeuIleTrpAlaGlyAsnThrProGlnGluLysAspTyrAsnLeuAlaGlyGln 160
Db 97425 GAGCGCTTATCTGGCGCGCAATACGCCCAAGAAAAAGATACAACTTCTGCTGTCAG 97366
QY 161 CysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAsnSerLeuSerLeuAlaGly 180
Db 97365 TGTGTCGCCACTACGATACCGCTGGACTCACCTCAACTCAACAGCCCTTCTCTGGCTGGC 97306
QY 181 ValValLeuSerGlnSerGlnLeuLeuLeuThrAspAsnGlnAspAlaAspTyrThrGly 200
Db 97305 GTGCTGCTATCACATCTCAACCACTGCTGCTCGATGATCAAAATGCCGACTGGACAGGT 97246
QY 201 GluAspGlnSerLeuTrpGlnGlnLysLeuSerSerAspValTyrIleThrGlnSerAsn 220
Db 97246
```

Db 97245 GAAGATCAAAAGCCCTCTGGCAGCAAAAACGTAGCAGTGTCTATACCAACCCCAAAATAGC 97186
QY 221 ThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGlyAsnIleGlnArgLeu 240
Db 97185 ACTGATGCCACCGGGCTTTACTTATCCAGACCGATGCCAAGGCAACATCCAGCGCTCG 97126
QY 241 AlaTyrAspValAlaGlyGlnLeuLysGlySerTyrLeuThrLeuLysGlyGlnAlaGlu 260
Db 97125 GCCTATGATGTAGCCGGCAGCTAAAGGCTGTGTGGTTAACTCAAAAGTCAAGCCGAA 97066
QY 261 GlnValIleIleLysSerLeuThrTyrSerAlaAlaGlyGlnLysLeuArgGluGluHis 280
Db 97065 CAAGTGATTTCAATACGCTGACCTACTCTGCCCGCCGCAAAAATTACGTGAAGACAC 97006
QY 281 GlyAsnGlyIleValThrGluTyrSerTyrGluProGluThrGlnArgLeuIleGlyIle 300
Db 97005 GGTAAACGGGGTTATCACCGGNATACAGCTATGAACCAAGAACCCAAACGGCTTATGGTATC 96946
QY 301 ThrThrArgArgProSerAspAlaLysValLeuGlnAspLeuArgTyrGlnTyrAspPro 320
Db 96945 ACTACCGCGCTCCGTCAAGTATCAAGGCTGTTCGAAGACTTACGCTATCAATATGATCCG 96886
QY 321 ValGlyAsnValIleAsnIleArgAsnAspAlaGluAlaThrArgPheTyrArgAsnGln 340
Db 96885 GTAGGCAATGTGATCAATATCCGTAAACGATGCGGAAGCCACCCGCTTTTGGCGCAATCAG 96826
QY 341 LysValAlaProGluAsnSerTyrThrTyrAspSerLeuTyrGlnLeuIleSerAlaThr 360
Db 96825 AAGTGGTCCCGAGAAATAGCTATATCTTACGACTCCCTGTACAGCTTATCAGTGGTACT 96766
QY 361 GlyArgGluMetAlaAsnIleGlyGlnGlnAsnGlnLeuProSerProAlaLeuPro 380
Db 96765 GGGCGTGAAATGGCCAAATATAGTCCAGCAAAATAATCAACTGCCCTCCCTCGCGTACCT 96706
QY 381 SerAspAsnAsnThrTyrThrAsnTyrThrArgSerTyrSerTyrAspHisSerGlyAsn 400
Db 96705 TCCGCAACAACAAATACCTACATACTATCTACCTCGCGCTTACAGTTATGATCACACGCGTAAT 96646
QY 401 LeuThrGlnIleArgHisSerProAlaThrGlnAsnAsnTyrThrValAlaIleThr 420
Db 96645 CTGACCGAAATTCGGCACAGTTCATCGGTACCTACCCAAATACTACACCACCGCTATCAC 96586
QY 421 LeuSerAsnArgSerAsnArgGlyValLeuSerThrLeuThrThrAspProAsnGlnVal 440
Db 96585 ATCTCGAATCGCAGTAACCGCGCGTCTCAGTACGCTGACACAGATCCAAATCAAGTG 96526
QY 441 AspThrIleuPheAspAlaGlyGlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIle 460
Db 96525 GATACGTTATTGATCCGGTGGTCAACCAACAGTTTATTACCCCGGTCAACACTGGCT 96466
QY 461 ThrThrProArgGlyGluLeuLysGlnValAsnAsnGlyProGlyAsnGluTyrTyrArg 480
Db 96465 TGGACATCACGAGAGAGTTTAAGCAGGTCAATACGGTTCAGGAATGAAATGGTACCGA 96406
QY 481 TyrAspSerAsnGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAsnThrThr 500
Db 96405 TACGGCAGCAACGGAATGACAACTGAAAGTGAGTGAAACAGCAACCCAGAACTACTACG 96346
QY 501 GlnGlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAla 520
Db 96345 CAGCAGCAGCGGGTAAATCTATCTGCCGGGCTGGAATACGACTACGCAACCCCAAGCAGCACC 96286
QY 521 ThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArg 540
Db 96285 ACAACAACAAGAGATTACACGTGATCACACTAGGTGAACGGGTCCGCAACAGGTCGGG 96226
QY 541 ValLeuHisTyrGluSerGlyLysProGluAspValAsnAsnAsnGlnLeuArgTyrSer 560
Db 96225 GTCTGCACTGGGAGAGCGGTAAACCAAGAGGTATCAACAACAAATCAGCTACGTTACAGC 96166
QY 561 TyrAspAsnLeuIleGlySerSerGlnLeuGluLeuAspAsnGlnGlyGlnIleIleSer 580
Db 96165 TAGCATAATCTGATCGGCTCCAGCCAGCTTGAACCTGGACAACCAAGGCGCAGATTATTAGT 96106

QY 581 GluGluGluTyrTyrProPheGlyGlyThrAlaLeuLeuTyrAlaAlaAsnSerGlnThrGlu 600
Db 96105 GAGGAAGAGTATTATCCATTCCGCGCACAGCGATGCGGCGCAATAGCCAAACAGAA 96046
QY 601 AlaSerTyrLysThrIleArgTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyr 620
Db 96045 GCCAATTAATAACTATTTCGCTATTCCAGCAAGAAACGGGATACCAACCCGGCTGTATTAT 95986
QY 621 TyrGlyTyrArgTyrTyrGlnProTyrAlaGlyArgTyrLeuSerAlaAspProAlaGly 640
Db 95985 TACGGTTACGCTATTATCAACCGTGGCGGCGCAGATGTTAAGCGCGGATCCGCGCAGGA 95926
QY 641 ThrIleAspGlyLeuAsnLeuTyrArgMetValArgAsnAsnProValSerLeuGlnAsp 660
Db 95925 ACCATTGATGGCTGAATCTATACCGAATGGTGAGAAATAATCCAGTAAGTTTGCAGGAT 95866
QY 661 GluAsnGlyLeuAlaProGluLysGlyLysTyrThrLysGluValAsnPheAspGlu 680
Db 95865 GAAATGGGATTAGCACCAAGAGAGGAAATATACTAAAGAGGTGAATTTCTTGTATGAA 95806
QY 681 LeuLysPheLysLeuAlaAlaLysSerSerHisValValLysTyrAsnGluLysGluSer 700
Db 95805 TTAAATTCAAATTTGGCAGCCAAATTCACATGTTGTCAATGGACGAGAAAGAAAGT 95746
QY 701 SerTyrThrLysAsnLysSerLeuLysValValArgValGlyAspSerAspProSerGly 720
Db 95745 AGTTATACAAAAATAAATCATTTGAAGTGGTTCGCGTCCGTGATTCGATCCGTCGGT 95686
QY 721 TyrLeuLeuSerHisGluGluLeuLysGlyIleGluLysSerGlnIleIleTyrSer 740
Db 95685 TATTTGCTAAGCCACCAAGAGTTACTTAAAGGCGCATAGAAAAAGCCAAATTTATATATAGC 95626
QY 741 ArgLeuGluGluAsnSerSerLeuSerGluLysSerLysThrAsnLeuSerLeuGlySer 760
Db 95625 CGCTCGAAGAAAAACAGATCCCTTTTCAGAAAAATCAAAAAACAATCTTTCTTTGGGATCT 95566
QY 761 GluIleSerGlyTyrMetAlaArgThrIleGlnAspThrIleSerGluTyrAlaGluGlu 780
Db 95565 GAAATATCCGTTATATGCAAAAAACGATAAAAGATACGATATCAGATATACAGAAGGG 95506
QY 781 HisLysTyrArgSerAsnHisProAspPheTyrSerGluThrAspPhePheAlaLeuMet 800
Db 95505 CATAGGTATAGAGCAATCATCCCGATTTTATGCGACCAACAGATTTCTTTGCTTTAATG 95446
QY 801 AspLysSerGluLysAsnAspTyrSerGlyGluArgLysIleTyrAlaAlaMetGluVal 820
Db 95445 GATAAAGTGAAAAAATGATTATTCGGTGAAAGAAAAATTTATCGGCGCATAGAGTT 95386
QY 821 LysValTyrHisAspLeuLysAsnLysGlnSerGluLeuHisValAsnTyrAlaLeuAla 840
Db 95385 AAGTTTATCATGATTTTAAAAATAAACAATCAGAAATTACATGTCACATATGCACCTGGCT 95326
QY 841 HisProTyrThrGlnLeuSerAsnGluGluArgAlaLeuLeuGlnGluThrGluProAla 860
Db 95325 CATCCCTATACGCAATTTGAGTAATGAAGAGAGAGCGCTGCTGCAAGAAAAACAGAACCCGCT 95266
QY 861 IleAlaIleAspArgGluTyrAsnPheLysGlyValGlyLysPheLeuThrMetLysAla 880
Db 95265 ATTGCAATTAATAGAGAAATATAATTTCAAGGGCTGTGTAATTTCTTGGCAATGAAGCA 95206
QY 881 IleLysLysSerLeuLysGlyHisIleAsnArgIleSerThrGluAlaIleAsnIle 900
Db 95205 ATTAAAAATCATTTGAAGGCGCAGAGATCAATAAATAATATCAACAGAGCGCTATTATATT 95146
QY 901 ArgSerAlaAlaIleAlaGluAsnLeuGlyMetArgArgThrSer 915
Db 95145 CGCTCTCGCGCTATCGTAAAGAAATTTAGGAATTCGGAAATCGGAGAGCTTCA 95101
RESULT 7
ADN61384
ID ADN61384 standard; DNA; 2817 BP.
XX

AC ADN61384;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Photorhabdus strain W14 tccC5 toxin complex DNA.
 XX
 KW Cry; toxic; lepidopteran pest; toxin complex; insecticide; strain W14;
 KW ds; tccC5.
 XX
 OS Photorhabdus sp.
 XX
 PN WC2004002223-A2.
 XX
 PD 08-JAN-2004.
 XX
 XX 27-JUN-2003; 2003WO-US020082.
 XX
 XX 28-JUN-2002; 2002US-0392633P.
 PR 21-JAN-2003; 2003US-0441647P.
 XX
 XX (DOWC) DOW AGROSCIENCES LLC.
 PA
 XX Bintrim SB, Bevan SA, Zhu B, Merlo DJ;
 XX
 XX WPI; 2004-082821/08.
 DR
 XX
 XX Screening a culture of *Paenibacillus* isolate for Cry protein or toxin
 PT complex protein, useful for controlling lepidoptera, comprises
 PT obtaining DNA or protein from the culture and assaying the presence of
 PT the gene or protein.
 XX
 XX Example 12; SEQ ID NO 48; 220pp; English.
 PS
 XX The invention relates to a novel method for screening a culture of a
 CC *Paenibacillus* isolate for a gene encoding a protein selected from a Cry
 CC protein that is toxic to a lepidopteran pest and a toxin complex protein.
 CC The method comprises obtaining DNA from the culture and assaying the DNA
 CC for the presence of the gene or obtaining a protein produced by the
 CC culture and assaying the presence of a protein that indicates the
 CC presence of the gene in the isolate. The method of the invention has
 CC insecticide applications and may be useful for screening *Paenibacillus*
 CC sp. for toxin complex (TC)-like genes and proteins which may themselves
 CC be used to enhance or potentiate the activity of a stand-alone
 CC *Xenorhabdus* toxin protein. The method may also be useful for screening
 CC *Paenibacillus* sp. and others for insecticidal thiaminase genes and
 CC proteins for controlling insects, particularly lepidoptera. The current
 CC sequence is that of the *Photorhabdus* strain W14 tccC5 toxin complex DNA
 CC of the invention.
 XX
 XX Sequence 2817 BP; 902 A; 700 C; 614 G; 601 T; 0 U; 0 Other;
 SQ

Alignment Scores:
 Pred. No.: 4.98e-209 Length: 2817
 Score: 2960.00 Matches: 607
 Percent Similarity: 73.01% Conservative: 91
 Best Local Similarity: 63.49% Mismatches: 186
 Query Match: 62.45% Indels: 72
 DB: 12 Gaps: 13

US-10-647-956A-6 (1-915) x ADN61384 (1-2817)

Qy 1 MetSerSerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn 20
 Db 1 ATGGAAACATTGACCCCAAACTTTATCACCATACGCTACCGTCAGTGTTCACGATAAC 60
 Qy 21 ArgLysLeuAnValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAsnSerAsp 40
 Db 61 CGTGACTAGTATCCGTAATATTAGTTTTCACCGCACTACCGGAGAGCAATACCGAT 120
 Qy 41 GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro 60
 Db 121 ACCGGTATTACCGCCCAATATATATGCGCGGATATTTGAACCAAGCATTTGATCCT 180

61 Arg-----LysAsnLysAsnGlnSerGlyProAsnPheIleArgValPhe 75
 181 CGCCTGTATGACGCCAAACAGACTAACACGCTGTACAAACCGAATTTTATCTGGCGACAT 240
 Qy AsnLeuAlaGlyGlnValLeuArgGluSerValAspAlaGlyArgThrIleThrLeu 95
 241 AATTTGACCGCAATATCTGCGAAACAGAGAGCGTGCATCGCGTCCGACGATTACCTC 300
 Qy AsnAspIleGluSerArgProValLeuIleIleAsnAlaThrGlyValArgGlnAsnHis 115
 301 AACGATATTGAAGGCCCGCGGTGTGACCATCAATGACGCCGTCTCGGCAAAACCAT 360
 Qy ArgTyrGluAspAsnThrLeuProGlyArgLeuLeuAlaIleThrGlnValGlnAla 135
 361 CGCTACGAAGATAACACCTGCGCGTCTGCTGCTATCAGCAACAAGGACAGGCA 420
 Qy GlyGluLysThrThrGluArgLeuIleThrAlaGlyAsnThrProGlnGluLysAspTyr 155
 421 GAAGAGAAAACGACCGAGCGCTTATCTGGCGCGCAATACGCGCAAGAAAAGACCAC 480
 Qy AsnLeuAlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAsnSer 175
 481 AACCTTGGCGGTGAGTCCGCTACGATACCGAGGACTCACTCAACTCAACAGC 540
 Qy LeuSerLeuAlaGlyValValLeuSerGlnSerGlnLeuLeuThrAspAsnGlnAsp 195
 541 CTTCCTGACCGCGCGCTTCTATCACAATCTCAACACTGCTTACCGATAACAGGAT 600
 Qy AlaAspTyrThrGlyGluAspGlnSerLeuTyrGlnGlnLysLeuSerSerAspValTyr 215
 601 GCGCACTGGACAGGTGAAGACAGAGCGCTCTGGCAACAAAACCTAGTAGTGTCTAT 660
 Qy IleThrGlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGly 235
 661 ATCACCACAAAGTAACACTGATGCCCGGGCTTTTACTGACCAGACCGATGCAAGGC 720
 Qy AsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLysGlySerTyrLeuThrLeu 255
 721 AACATTACGGCGTGGCCTATGATGTGGCGGCGAGCTAAAGAGGAGTTGTTTAACACTC 780
 Qy LysGlyGlnAlaGluGlnValIleLysSerLeuThrTyrSerAlaAlaGlyGlnLys 275
 781 AAAGGTGAGCGGAAACAGGTGATTATCAATCGTAACCTACTCCGCGCGCGGCAAAA 840
 Qy LeuArgGluGluHisGlyAsnGlyIleValThrGluTyrSerTyrGluProGluThrGln 295
 841 TTACGTGAAGAGACCGGTAAACGGGATGTCACCTAGTAATACAGCTACGACCGAAACCAA 900
 Qy ArgLeuIleGlyIleThrThrArgArgProSerAspAlaLysValLeuGlnAspLeuArg 315
 901 CGCTTATCGCATTTACCACTCCGCTCCATCAGACGCCAAGGTGTTGCAAGACCTACGC 960
 Qy TyrGlnTyrAspProValGlyAsnValIleAsnIleArgAsnAspAlaGluAlaThrArg 335
 961 TATCAATATACCCAGTAGGCAATGTCATTAGTATCGTAATGATGCGAAGCCACTCGC 1020
 Qy PheTyrArgAsnGlnLysValAlaProGluAsnSerTyrThrTyrAspSerLeuTyrGln 355
 1021 TTTTGGCGCAATCAGAAAGTAGCCCGGAGAAATAGCTATACCTACGATTCCTGTATCAG 1080
 Qy LeuIleSerAlaThrGlyArgGluMetAlaAsnIleGlyGlnGlnAsnAsnGlnLeuPro 375
 1081 CTTATCAGCGCCACCGCGCGAGATGGCCAAATATCGTCCAGCAACCAACCACTTCCC 1140
 Qy SerProAlaLeuProSerAspAsnAsnThrTyrThrAsnTyrThrArgSerTyrSerTyr 395
 1141 TCTCGCGCGTACCTCTGATAACAATACCTACCACTATATCTACCTACCTTACTTAT 1200
 Qy AspHisSerGlyAsnLeuThrGlnIleArgHisSerSerProAlaThrGlnAsnAsnTyr 415
 1201 GACGTGGCGCAATTTGACGAAATTTACGATAGTTTACGACCGCGGCAAAATACTAC 1260
 Qy ThrValAlaIleThrLeuSerAsnArgSerAsnArgGlyValLeuSerThrLeuThrThr 435


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Db 1261 |||||.....|||||.....|||||.....|||||..... 1320
QY 436 ACACCGATATAACGGTTTCAAAATCGAGAACCGCGCGTACTAGCACATTGACCGCA 1320
Db 1321 |||||.....|||||.....|||||.....|||||..... 455
QY 456 AspProAsnGlnValAspThrLeuPheAspAlaGlyHisGlnThrSerLeuLeuPro 455
Db 1321 GATCCCAACTCAAGTCGATCGCTTATTTGATCGGGAGCCATCAACACGCTGTATCC 1380
QY 456 GlyGlnThrLeuLeuThrProArgGlyGluLeuLeuGlnValAsnAsnGlyProGly 475
Db 1381 GGCCTAAGTTCTTAATCTGGACCGCGAGCGAATTGAAACAGCCCAACATAGCGCAGGA 1440
QY 476 AsnGluTrpTyrArgTyrSerAspSerAsnGlyMetArgGlnLeuLeuValSerGluGlnPro 495
Db 1441 AATGAGTGGTATCGCTACGATAGCAACCGCATACCGCAGCTAAAGTGAATGAACACAA 1500
QY 496 ThrGlnAsnThrThrGlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThr 515
Db 1501 ACTCAGATATCCCGCAACCAACAAAGGTAACTTATCTACCGGGGTGGAAATACGTACA 1560
QY 516 ThrGlnSerAsnAlaThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGly 535
Db 1561 ACCCAGAACCAACCGCCCAACCAACAGAGAGTTACAGTTATCATCACTCGGTAAAGCGGC 1620
QY 536 ArgAlaGlnValArgValLeuHisTrpGluSerGlyLeuProGluAspValAsnAsn 555
Db 1621 CGCGCCAAAGTCCGATTTGCAATTCGGAGAGCGGTAAACCAACAGATATTAATCAAT 1680
QY 556 GlnLeuArgTyrSerTyrAspAsnLeuIleGlySerGlnLeuGluLeuAspAsnGln 575
Db 1681 CAGCTTCGTACAGCTACGATATCTTATTTGGTCCAGCCCACTCAATAGATAGCGAC 1740
QY 576 GlyGlnIleLeuSerGluGluGluTyrTyrProPheGlyGlyThrAlaLeuTrpAlaAla 595
Db 1741 GGCACAAATATCAGTGAAGAAGAAATATATCCATTTGGTGTACAGCGCTGTGGCGGCA 1800
QY 596 AsnSerGlnThrGluAlaSerTyrLeuThrIleArgTyrSerGlyLeuGluArgAspAla 615
Db 1801 AGGAATCAACCGAAGCCAGCTATAAACCCATTCGTTATTTCTGTAAAGCGCGGATGT 1860
QY 616 ThrGlyLeuTyrTyrTyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTrpLeuSer 635
Db 1861 ACCGGCTGTATTTATGCTACCGTACCGTTATACCAACCGTGGCGGCGAGATGTTAAGT 1920
QY 636 AlaAspProAlaGlyThrIleAspGlyLeuAsnLeuTyrArgMetValArgAsnAsnPro 655
Db 1921 GCAGACCCGCGCAGCAACCATTTGATGACGTGAATTTATATCGCATGTTGAGAAATAACCCG 1980
QY 656 ValSerLeuGlnAspGluAsnGlyLeuAlaPro----- 666
Db 1981 GTGACGCAATTTGATGTTTCAGGGATTTATCACCGGCCCAACAGAACAGAGCGATAATA 2040
QY 667 GluLeuGlyLeuTyrThrLeuGluValAsnPheAspGluLeuLeuPheLeuAla 686
Db 2041 AAACGGTTCCTTTACGGGA-----ATGGAAGAGCTGTTTATAAAAAAATG 2088
QY 687 AlaLys-----SerSerHisValValIleValIleValIleValIle 700
Db 2089 GCTAAACCTCAAACTTTCAACCGCCAAAGAGCTATCGTCCGCCAAACAGAGCAAGAGCC 2148
QY 701 -----SerTyrThrLysAsnLysSerLeuLysValValArgValGlyAspSerAspPro 718
Db 2149 CATGAATCATTTGACCAACCAACCTAGTGTAGATATT-----AGCCCAAT 2193
QY 719 SerGlyTyrLeuLeuSerHisGluGluLeuLeuLysGlyIleGluLysSerGlnIleIle 738
Db 2194 AAAAATACACCAAGATAGCTCACAAATTAATGCGCGGATAAGGAAATCGTATTACG 2253
QY 739 TyrSerArgLeuGluGluAsnSerSerLeuSerGluLysSerLysThrAsnLeuSerLeu 758
Db 2254 CCAGCAGTGAAGATTAGACCGCCACATTTATCTCCCTACAAGATAGACAAATGAGGGTA 2313
QY 759 GlySerGluLeuSerGlyTyrMetAlaArgThr----- 769
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Db 2314 ACTTATCGGGTATGACCTATGTAGTAATTCACGCCATCGCCTGGGCACTGCCACAG 2373
QY 770 -----IleGlnAspThrIleSerGluTyrAla-----Glu 779
Db 2374 GAAGGAATAGTATTAAATGTTGTTGATATCGTTTCGGATAACGCTTATTATTATCAACATCG 2433
QY 780 GluHisLysTyrArgSerAsn-----HisProAspPheTyrSerGluThrAspPhePhe 797
Db 2434 GCCCATCGTGGTTCCTGAATTTTGTTCACAAAAAGAACCAAGTGAACCTCGATACGTC 2493
QY 798 AlaLeu-----MetAspLysSerGluLysAsnAspTyr 808
Db 2494 AGATGGCATTTTAAACGAATCGGGTGTCAATGTCTCAGCAGCATCTATGTATATAAT 2553
QY 809 SerGlyGluArgLysIleTyrAlaAlaMetGluValLysValTyrHisAspLeuLysAsn 828
Db 2554 GCTGGCGAGGAGCAAGTATTAAATG-----GATTTAAACGAT 2592
QY 829 LysGlnSerGluLeuLeuHisValAsnTyrAlaLeuAlaHisProTyrThrGlnLeuSerAsn 848
Db 2593 TCAAGAAAAAGCGCTTCTGCTGAAAAAATTAAACCTAAGAGTCAGTGACCAACATCGGCACAA 2652
QY 849 GluGluArgAlaLeuLeuGlnGluThrGluProAlaIleAlaIleAspArgGluTyrAsn 868
Db 2653 GCGGAATATTACTACCTAGGGAACACACAGTTGCGAAGTTGTT-----TCAATGAAA 2703
QY 869 PheLysGlyValGlyLysPheLeuThrMetLysAlaIleLysLysSerLeuLysGlyHis 888
Db 2704 CATCAGGCGAGAGATACCTATGTATTATTGCAAGATATTAAACCAATCCGCGACCATCAT 2763
QY 889 LysIleAsnArgIleSerThrGluAlaIleAsnIleArgSerAlaAla 904
Db 2764 AGA---AATGTACGTAAACACTTACACCGGTAATTTCAAAATCATCCAGT 2808

RESULT 8
ADP18627
ID ADP18627 standard; DNA; 2817 BP.
XX
AC ADP18627;
DT 12-AUG-2004 (first entry)
XX
DE Photobhabdus luminescens W-14 tccC5 encoding DNA SEQ ID NO:15.
KW tcd; Photobhabdus luminescens W-14; transgenic plant; Toxin A;
KW orally active insect toxin; insect toxin; tccC5; gene; da.
XX
OS Photobhabdus luminescens.
XX
FH Key Location/Qualifiers
FT CDS 1..2817
FT /tag= a
FT /product= "tccC5"
XX
PN WO2004044217-A2.
XX
XX 27-MAY-2004.
XX
XX 12-NOV-2003; 2003WO-1B005553.
XX
XX 12-NOV-2002; 2002US-0425672P.
XX
XX (UYBA-) UNIV BATH.
XX
XX Pfreuch-Constant RH, Waterfield NR;
XX
XX WPI; 2004-411735/38.
XX
XX P-PSDB; ADP18628.
XX
XX New isolated Photobhabdus luminescens nucleic acids, useful for
XX expressing orally active insect toxin or for generating transgenic plants
XX with enhanced resistance to insects.
XX
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Db 2149 CATGAATCATGACCAACACCTAGTGATAGATT-----ACCCCAATT 2193
 QY 719 SerGlyTyrLeuLeuSerHisGluGluLeuLeuGlyLeuGlySerGlnIle 738
 Db 2194 AAAAATACACACAGATACCTACAAATTAATGCCGCGATAAGGAAATCGTATTACG 2253
 QY 739 TyrSerArgLeuGluGluLeuSerSerLeuSerGlyLeuSerHisLeuSerLeu 758
 Db 2254 CCAGCAGTGGAAAGTTTAGACGCGACATATTATTCCTCAAGATAGACAAATGAGGGTA 2313
 QY 759 GlySerGluIleSerGlyTyrMetAlaArgThr----- 769
 Db 2314 ACTATCGGGTGATGACCTATGATAGATAATTCACGCCATCGCTTGGCACTGCCACAG 2373
 QY 770 -----lGlnAspThrIleSerGluTyrAla-----Glu 779
 Db 2374 GAAGGAAATAGTAAATTAATGTTGGTGATATCGTTTCGGATAACGCTTATTATCAACATCG 2433
 QY 780 GluHisLysTyrArgSerAsn-----HisProAspPheTyrSerGluThrAspPhe--- 796
 Db 2434 GCCCATCGTGTGTTTCTGAAATTTGTTTCACAAAAAGAAACACCACTGCAATCGATACGTC 2493
 QY 797 ---PheAlaLeuMetAspLysSerGluLysAsn-----AspTyr 808
 Db 2494 AAGATGGCATTTTAAACGAATGCGGGTGTCATGTCCACGACGATCTATGTATATAAT 2553
 QY 809 SerGlyGluArgLysIleTyrAlaAlaMetGluValLysValTyrHisAspLeuLysAsn 828
 Db 2554 GCTGGCGAGGAGCAAGTATTAAATG-----GATTTAAAGCAT 2592
 QY 829 LysGlnSerGluLeuHisValAsnTyrAlaLeuAlaHisProTyrThrGlnLeuSerAsn 848
 Db 2593 TCAAGAAAAAGCCCTGCTGAAAAATTAATAACTAAGAGTCAGTGGACCAACAATCGGACAA 2652
 QY 849 GluGluArgAlaLeuLeuGlnGluThrGluProAlaIleAlaLeuAspArgGluTyrAsn 868
 Db 2653 GCGGAATATTACTACTAGGGAACACAGTTCGAAAGTTGTT-----TCAATGAA 2703
 QY 869 PheLysGlyValGlyLysPheLeuThrMetLysAlaIleLysLysSerLeuLysGlyHis 888
 Db 2704 CATCAGGCGAGATACCTATGTATTATTGCAAGATATTAAACATCCGACCATCAT 2763
 QY 889 LysIleAsnArgIleSerThrGluAlaIleAsnIleArgSerAlaIa 904
 Db 2764 AGA---AATGTACGTAACACTTACACCGGTAATTTCAAATCATCCAGT 2808

RESULT 10
 ID ACF69434 standard; DNA; 2817 BP.
 AC ACF69434;
 XX 20-NOV-2003 (first entry)
 DT
 DE
 KW Photorhabdus luminescens nucleotide sequence #7901.
 KW Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;
 KW detection; food; gene expression; plant; animal; microorganism; toxin;
 KW antibiotic; biopesticide; virulence factor; disease model; plague;
 KW whooping cough; gene; ds.
 XX
 OS Photorhabdus luminescens.
 XX
 XX W0200294867-A2.
 PN
 XX
 XX 28-NOV-2002.
 XX
 XX 07-FEB-2002; 2002WO-IB003040.
 XX
 XX 07-FEB-2001; 2001FR-00001659.
 PR
 XX (INSP) INST PASTEUR.

(CNRS) CNRS CENT NAT RECH SCI.
 Duchaud E, Taourit S, Glaser P, Frangeul L, Kunat F, Danchin A;
 Buchrieser C;
 WPI; 2003-148459/14.
 Genomic sequence of Photorhabdus luminescens and encoded polypeptides,
 useful e.g. as therapeutic antimicrobials and agricultural pesticides.
 Claim 2; SEQ ID NO 7901; 1205pp; French.
 The invention relates to the isolation of genes and their encoded
 proteins from Photorhabdus luminescens. The isolated sequences are
 sources of probes and primers for detecting the genome of P. luminescens
 and related species; to study polymorphisms; for gene analysis and for
 detection/amplification of the genes. Antibodies (Ab) raised against the
 polypeptides encoded by the genes are used for detection/identification
 of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that
 carry a gene-containing vector are used to select compounds that
 modulate, regulate, induce or inhibit expression of the genes in plants,
 animals or microorganisms other than P. luminescens and are able to alter
 response or sensitivity to toxins and antibiotics produced by P.
 luminescens. Cells transformed to express the genes are useful for
 recombinant production of the proteins, particularly toxins and
 antibacterials useful as insecticides, bactericides and fungicides. The
 genes, proteins, vectors containing the genes and Ab are also useful
 therapeutically (to treat microbial infection by bacteria or fungi that
 are sensitive to P. luminescens-encoded toxins or antibiotics) and as
 biopesticides. Other uses of the genes and the proteins are as virulence
 factors and for identifying targets of human diseases for which P.
 luminescens is a model (particularly plague and whooping cough). This
 sequence represents one of the isolated P. luminescens genes
 XX
 SQ Sequence 2817 BP; 922 A; 682 C; 588 G; 625 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1,46e-200 Length: 2817
 Score: 2845.50 Matches: 578
 Percent Similarity: 71.01% Conservative: 71
 Best Local Similarity: 63.24% Mismatches: 150
 Query Match: 60.03% Indels: 115
 DB: 10 Gaps: 11
 US-10-647-956A-6 (1-915) x ACF69434 (1-2817)
 QY 1 MetSerSerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn 20
 Db 1 ATGAAACCATTTGACCCCTAAACTTTATCACCATATACCGCGCTCAGTGTTCACGATAAC 60
 QY 21 ArgLysLeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAsnSerAsp 40
 Db 61 CGTGGACTCGCTATCCGTAAATATTAGTTTACCGCGCTACCGCAGAACCAATACCGAT 120
 QY 41 GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro 60
 Db 121 CCGCGTATTACTCGCCATCAATATAATGCGCGGATATTGAACCAAGCATTGATCCT 180
 QY 61 Arg-----LysAsnLysAsnGlnSerGlyProAsnPheIleArgValPhe 75
 Db 181 CCCTGTATGTATGCTAAGCAGACTAACACCGCGCTAACACCGAATTTTATCTGGCAGCAT 240
 QY 76 AsnLeuAlaGlyGlnValLeuArgGluSerValAspAlaGlyArgThrIleThrLeu 95
 Db 241 AATTGACCGCAATATCTCTGGACAGAGAGCGGTGATGCTGGCGCAACATATTACCTC 300
 QY 96 AsnAspIleGluSerArgProValLeuIleIleAsnAlaThrGlyValArgGlnAsnHis 115
 Db 301 AACGATATTGAAGTGCCTCGCGGTATTGACCATCATGCGCAACCGGTGTCGCCCAAAATCAC 360
 QY 116 ArgTyrGluAspAsnThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAla 135
 Db 361 CTTTATGAAGATAACACCTTACCGGTGCTCTACTCGCAATCACCGCAACACGACACACA 420

136 GlyGluLysThrThrGluArgLeuIleThrAlaGlyAsnThrProGlnGluLysAspTyr 155
156 AsnLeuAlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAsnSer 175
481 AACCTTGTGGTCAGTCAGCCGTCATTACGATACCCGCGGACTCGCTCAACTCAACAGC 540
176 LeuSerLeuAlaGlyValValLeuSerGlnSerGlnGlnGlnLeuLeuThrAspAsnGlnAsp 195
541 CTTGCCCTGACCGCGCGCTTTTATCAATCTCAACACCGCTCGTCGATAACCAAGAT 600
196 AlaAspTrpThrGlyGluAspGlnSerLeuTrpGlnGlnLysLeuSerSerAspValTyr 215
601 GCCGACTGGACAGGTGAAGACAGAGCGCTCTGGCAGCAAAAACCTAGTAGTGTCTAT 660
216 IleThrGlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGly 235
661 ACCACCCAAAATAAAACCGATGCCACCGGGTTTTACTTACCACAGCCGATGCTAAAGGC 720
236 AsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLysGlySerTrpLeuThrLeu 255
721 AACATTACGGCGAAGCTATGATGTGGCGGTCAAGAGGAGCTGGCTAACATTA 780
256 LysGlyGlnAlaGlnValIleIleLysSerLeuThrTyrSerAlaAlaGlyGlnLys 275
781 AAAGTCAAGCCGMAACAAGTGATTTCAATTCGCTGACCTACTCCGCGCGCGNACAAAA 840
276 LeuArgGluGluHisGlyAsnGlyIleValThrGluTyrSerTyrGluProGluThrGln 295
841 TTACGCGAAGACGACGGTAAACGGCATTTATACCGAATACAGCTATGAACCGGAACCTCAG 900
296 ArgLeuIleGlyIleThrThrArgArgProSerAspAlaLysValLeuLeuAspLeuArg 315
901 CGGCTTATCGGCATTACCACTCGCGCTCCATCAGACGCCAAGGTGTTCAGACACTACGC 960
316 TyrGlnTyrAspProValGlyAsnValIleAsnIleArgAsnAspAlaGluAlaThrArg 335
961 TATCAATATGACCCGGTAGGCATGTGATCAATATCCGTAAACGATGGGAAGCCACCCGC 1020
336 PheTrpArgAsnGlnLysValAlaProGluAsnSerTyrThrTyrAspSerLeuTyrGln 355
1021 TTTTGGCGCAATCAAAAAGTCATCCGAGAAATAGCTATACCTACGATTCCTCTGTATCAG 1080
356 LeuIleSerAlaThrGlyArgGluMetAlaAsnIleGlyGlnGlnAsnAsnGlnLeuPro 375
1081 CTTATCAGTCCCGACCGGACGCGTGAATGGCCAATATAGGTCAAGCCAAAATAACCCCACTCCCC 1140
376 SerProAlaLeuProSerAspAsnAsnThrTyrThrAsnTyrThrArgSerTyrSerTyr 395
1141 TCCCTCGGCTACTCGTCTGATTAACACACCTACTACTACCCGCGCACCTATAGTTAT 1200
396 AspHisSerGlyAsnLeuThrGlnIleArgHisSerSerProAlaThrGlnAsnAsnTyr 415
1201 GACCGTGGCGCAATTGGATGAAATTCAGCATAGTTCCACCTGCACGCAAAAATAACTAC 1260
416 ThrValAlaIleThrLeuSerAsnArgSerAsnArgGlyValLeuSerThrLeuThrThr 435
1261 ACGACGAATATAACGGTTTCTAATTTACAGCAACCGTGCCTGATTAAGTACACTGACCGAA 1320
436 AspProAsnGlnValAspThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuPro 455
1321 GATCAACCCCAAGTTGATCGCTTATTTGATTCGGAGGCCATCAACCAACTTATATCC 1380
456 GlyGlnThrLeuIleTrpThrProArgGlyGluLeuLysGlnValAsnAsnGlyProGly 475
1381 GGTCAAGTTCTAATATGACACCGCGAGCGCAATTTGAAACAAGTCAACAGTAGCGCAGGA 1440
476 AsnGluTrpTyrArgTyrAspSerAsnGlyMetArgGlnLeuLysValSerGluGlnPro 495
1441 AATGAGTGGTATCACTACGATAGCAACCGCACACGACGCTAAAAGTGAATGAACAA 1500

496 ThrGlnAsnThrThrGlnGlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThr 515
1501 ACTCAAAATATCGCGCAACAGCAAGAGTCACTTATCTCGCGGGCTAGAACTACGCACA 1560
516 ThrGlnSerAsnAlaThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGly 535
1561 ACCCAACATGGCAGTACTACCGGAATATTTGCAAGTATTACACTCGGTAAAGCTGGT 1620
536 ArgAlaGlnValArgValLeuHisTrpGluSerGlyLysProGluAspValAsnAsn 555
1621 CGTGCACAGTCCGGGTATTACATTTGGGAGAGCGGAAACCCGAAAGATATCAACACAT 1680
556 GlnLeuArgTyrSerTyrAspAsnLeuIleGlySerSerGlnLeuGluLeuAspAsnGln 575
1681 CAACTTCGTTACAGTACGATACGATAATCTTATCGGTTCCAGCAACTTGAATTAGATAGCGAA 1740
576 GlyGlnIleSerGlnGluTyrTyrProPheGlyGlyThrAlaLeuTrpAlaAla 595
1741 GGCACAAATTATCAGTCAGGAAGAATATTATCCATTTGGCGGTACAGCTCTGTGGCGAGCA 1800
596 AsnSerGlnThrGluAlaSerTyrLysThrIleArgTyrSerGlyLysGluArgAspAla 615
1801 AGGAATCAAAACCGAACCGAGCTATAAAACCATTCGTTATTCAGTAAAGACGGATGCT 1860
616 ThrGlyLeuTyrTyrTyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTrpLeuSer 635
1861 ACCGGCTGTATTATTACGGCTACCGTTATTACCAACCGTGGTGGCGAGATGTTAAGT 1920
636 AlaAspProAlaGlyThrIleAspGlyLeuAsnLeuTyrArgMetValArgAsnAsnPro 655
1921 CGCGACCCCGCGGAACCATTTGATGGCTGCAATTTATATCGCATGTGTGAGAAAATAATCCG 1980
656 ValSerLeuGlnAspGluAsnGlyLeuAlaPro----- 666
1981 GTGACCAATTTGATGTTTCAGGATTTATCTCGGCTAACAGAACAGNAGCGATAATA 2040
667 GluLysGlyLysTyrThrLysGluValAsnPhePheAspGluLeuLysPheLysLeuAla 686
2041 AAACGGTTCCTTTTACAGCA-----ATGGAAGAAGCCGTTTATAAAAAATG 2088
687 AlaLysSer----- 689
2089 GCGAAACCTCAAACTTTCAACCGCCAAAGAGCTATCGCTACCCAAACAGAGCAAGAGCC 2148
689 ----- 689
2149 CATCAATTTGACCAACAATCCCGGTGTAGATACTAGCCCAATTAAAGATTACACCACG 2208
690 -----SerHisValValLysTyr 695
2209 GATAGCTCGCAATTAATCTGCAATAAGAGAAAAACCGTATTACATCGATAGTGAAGAT 2268
696 AsnGluLysGluSerSerTyrThrLysAsnLysSerLeuLysVal----- 710
2269 TTAGATTCTCTATTATCTGCCCTGCAAGATAGACAAATACGGGTAACTTTATCGAGTGATG 2328
711 -----Val 711
2329 ACCTATATAGATAATTTCAAGCCCTCCCTCGCACTCTCCACAGNAGNAGNATAGCATC 2388
712 ArgValGlyAsp-----SerAspProSerGlyTyrLeu-----LeuSerHisGluGlu 727
2389 AACGTTGGTGATATCGTTTCAGAT---AATGCTTATTATCAACATCGGCCCATCGTGGT 2445
728 LeuLeuLysGlyLeuGluLysSerGlnIleIleTyrSerArgLeuGluGluAsnSerSer 747
2446 TTTCTGAATTTGTGCAATAAAAGAAACCAACCGATCGAATATGTCAAATGGCAATTT 2505
748 LeuSerGlu-----LysSerLysThrAsnLeuSerLeuLys 760
2506 TTACCAATACAGGTGCAATGTGGCAGCAAAATCTAAGTATTAATACGAAATGCGGAG 2565
761 GluIleSerGlyTyrMetAlaArgThrIleGlnAspThrIleSerGluTyrAlaGluGlu 780

Db	2566	AAAATA-----TTTAAGATGGATTAGATGATTCGGTGGAAAAAGCTTTGTTGAAAAA	2616
Qy	781	HisLysTyrArgSerAsnHisProAsp-----PheTyrSerGlu	793
Db	2617	TTGAAATAAGAGCAATGACCAAGAGCGGGGCAACGAGAAATACTATCTCCACAGAA	2676
Qy	794	ThrAspPhePheAlaLeuMetAspLysSerGluLysAsnAsp	807
Db	2677	ACACCGTTTCAAGTTGTTTCAATGAGACATCAAGGTAGAGAT	2718
RESULT 11			
ACF65386_5/c			
Continuation (6 of 7) of ACF65386 from base 500001 (Photorhabdus luminescens nucleotide			
WP Sequence split into 7 fragments LOCUS ACF65386 Accession ACF65386			
WP	Fragment Name	Begin	End
WP	ACF65386_0	1	110000
WP	ACF65386_1	100001	210000
WP	ACF65386_2	200001	310000
WP	ACF65386_3	300001	410000
WP	ACF65386_4	400001	510000
WP	ACF65386_5	500001	610000
WP	ACF65386_6	600001	700779
Alignment Scores:			
Pred. No.:	1.22e-198	Length:	110000
Score:	2845.50	Matches:	578
Percent Similarity:	71.01%	Conservative:	71
Best Local Similarity:	63.24%	Mismatches:	150
Query Match:	60.03%	Indels:	115
DB:	10	Gaps:	11
US-10-647-956A-6 (1-915) x ACF65386_5 (1-110000)			
Qy	1	MetSerSerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn	20
Db	15073	ATGAAATAACATTACCCCTTAACATTTATACCATACCGCCACCTCAGTGTTCACGATAAC	15014
Qy	21	ArgLysLeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAsnSerAsp	40
Db	15013	CGTGGACTCGCTATCGGTAATATTAGTTTACCGCGGTACCCGAGAGCAAAATACCGAT	14954
Qy	41	GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro	60
Db	14953	CCGCGTATTACTCGCATCAATATAATCGCGCGGATATTGAACCAAAAGCATTGATCCT	14894
Qy	61	Arg-----LysAsnLysAsnGlnSerGlyProAsnPhelleArgValPhe	75
Db	14893	CGCTGTATGATGCTAAGCAGACTAAACACCGCGTACACCGGAATTTTATCTGGCAGCAT	14834
Qy	76	AsnLeuAlaGlyGlnValLeuArgGluSerValAspAlaGlyArgThrIleThrLeu	95
Db	14833	AAITTGACCGCAATATCTTCGCAACAGAGAGGCTGATGCTGCGCAACAAATTACCTC	14774
Qy	96	AsnAspIleGluSerArgProValLeuIleAsnAlaThrGlyValArgGlnAsnHis	115
Db	14773	AACGATATTGAAGTCCCGCGTATTGACCATCAGCGCAACCGGTGTCCGCCAAAATCAC	14714
Qy	116	ArgTyrGluAspAsnThrLeuProGlyArgLeuLeuAlaIleThrGlnValGlnAla	135
Db	14713	CTTTATGAAGATAAACCCCTTACCCGTCGCTACTCGCATATCCGAAACAGACAGACA	14654
Qy	136	GlyGluLysThrThrGluArgLeuIleThrAlaGlyAsnThrProGlnGluLysAspTyr	155
Db	14653	GAAGAGAAAACAACCGAGCGCTTTTCTGGCGCGCAATACGCGCGAGGAAAAGAGTAC	14594
Qy	156	AsnLeuAlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAsnSer	175
Db	14593	AACCTTTGTTGTCAGTGTACCGCTCATACGATACCGCGGACTCGCTCAACTCAACAGC	14534
Qy	176	LeuSerLeuAlaGlyValValLeuSerGlnSerGlnLeuLeuThrAspAsnGlnAsp	195
Db	14533	CTTGCCCTGACCGGCGCGTTTTTATCACAAATCTCAACACCGCTCGTCGATACCAAGAT	14474

Qy	196	AlaAspTTrpThrGlyGluAspGlnSerLeuTrpGlnGlnLysLeuSerSerAspValTyr	215
Db	14473	GGCGACTGCACAGGTGAGACACAGAGCCCTCTGGCAGCAAAAACCTAGTAGTGTCTAT	14414
Qy	216	IleThrGlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGly	235
Db	14413	ACACCCAAAATAAAACCCATGCCACCGGGTTTTACTTACCAGACCGATGCTAAAGGC	14354
Qy	236	AsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLeuLysGlySerTrpLeuThrLeu	255
Db	14353	ACATTCAGCGGCAAGCCTATGATGGCGGTCAGCTAAAGGGAGCTGGCTAAACATTA	14294
Qy	256	LysGlyGlnAlaGluGlnValIleLysSerLeuThrTyrSerAlaAlaGlyGlnLys	275
Db	14293	AAAGGTGACAGCGAAACAAGTGATTAATAAATCGCTACTCTCCGCCGCGGACAAAA	14234
Qy	276	LeuArgGluGluHisGlyAsnGlyIleValThrGluTyrSerTyrGluProGluThrGln	295
Db	14233	TTACGCGAAGAGCAGCGTAAACGCGATTAATCCGAATACAGCTATGAACCGGAATCTAG	14174
Qy	296	ArgLeuIleGlyIleThrThrArgArgProSerAspAlaLysValLeuGlnAspLeuArg	315
Db	14173	CGGCTTATCGGCATTTACCACTCGCGTCCATCAGACGCCAGGTGTTCAGACCTACGC	14114
Qy	316	TyrGlnTyrAspProValGlyAsnValIleAsnIleArgAsnAspAlaGluAlaThrArg	335
Db	14113	TATCAATATGATCCCGGTAGGCAATGTGATCAATATCCGTAAACGATCGGAAGCCACCGC	14054
Qy	336	PheTrpArgAsnGlnLysValAlaProGluAsnSerTyrThrTyrAspSerLeuTyrGln	355
Db	14053	TTTTGGCGCAATCAAAAAGTCATCCCGAGAAATAGCTATACCTTACGATTCTCTGTATCAG	13994
Qy	356	LeuIleSerAlaThrGlyArgGluMetAlaAsnIleGlyGlnGlnAsnAsnGlnLeuPro	375
Db	13993	CTTATCAGTGCACCGAGCTGAATGGCAATATAGGTTCAGCCAAATAACCCACTCCCC	13934
Qy	376	SerProAlaLeuProSerAspAsnAsnThrTyrThrAsnTyrThrArgSerTyrSerTyr	395
Db	13933	TCCCTTGCCTACCTGCTGATTAACAACACTACACTTAACACCGCACCTATAGTTAT	13874
Qy	396	AspHisSerGlyAsnLeuThrGlnIleArgHisSerSerProIleThrGlnAsnAsnTyr	415
Db	13873	GACCGTGGCGGCAATTTGATGAAATTCAGCATAGTTCACTGCCACGCAAAAATAACTAC	13814
Qy	416	ThrValAlaIleThrLeuSerAsnArgSerAsnArgGlyValLeuSerThrLeuThrThr	435
Db	13813	ACGACGAATATTAACGGTTTCTAATTAACAACACCGTCCGCTTTAAGTACACTGACCGAA	13754
Qy	436	AspProAsnGlnValAspThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuPro	455
Db	13753	GATCCAAACCAAGTTGATGCTTATTTGATTCGGGAGGCCATCAACACCACTTATTATCC	13694
Qy	456	GlyGlnThrLeuIleTrpThrProArgGlyGluLeuLysGlnValAsnAsnGlyProGly	475
Db	13693	GGTCAAGTTCTAATATGGACACCGCGAGCGCAATTTGAAACAAGTCAACACTAGCGCAGA	13634
Qy	476	AsnGluTTrpTyrArgTyrAspSerAsnGlyMetArgGlnLeuLysValSerGluGlnPro	495
Db	13633	AATGAGTGTATCATTACCATAGCAACGCAACGACAGCTAAAGTGAATGAACAAACAA	13574
Qy	496	ThrGlnAsnThrThrGlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThr	515
Db	13573	ACTCAGATATTCGCGCAACAGCAAGAGTCACTTATCTCCGGGGCTAGAACTACGCACA	13514
Qy	516	ThrGlnSerAsnAlaThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGly	535
Db	13513	ACCAACATGGCAGTACTACCGCAATATTTCGAAGTTATCACACTCGTAAAGTGTGT	13454
Qy	536	ArgAlaGlnValArgValLeuHisTrpGluSerGlyLysProGluAspValAsnAsn	555
Db	13453	CGTGGCAAGTCCGGGTATTACATTTGGGAGAGCGGAAACCCGGAAGATATCAACAACAT	13394

Db 1 ATGATTCTGTTACAATTCTGCAATTAACCGAATAATACCCCATCTCTGCTAGCGTACGAGATAAT 60
Qy 21 ArgLysLeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAspGlu---AsnSer 39
Db 61 CGAGGGTTAAATATACATACGCTGGAATATCTCGGGACTCAAGCTGATGAACCAATAGC 120
Qy 40 AspGluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAsp 59
Db 121 AACCAATTTGATCATCTCGCTATCAATTTAATACTACAGGACTTCAGAGCTTCAAGTAAAAAGCACAGAC 180
Qy 60 ProArgLysAsnLysAsnGlnSerGlyProAsnPheIleArgValPheAsnLeuAlaGly 79
Db 181 CCACGTAGATATAAAACACAGAGTGGTTCAAATCTCACTCGTATCTTTAGTCTCGCTGGG 240
Qy 80 GlnValLeuArgGluGluSerValAspAlaGlyArgThrIleThrLeuAsnAspIleGlu 99
Db 241 AATACACTGGCTGAGAAAGTATCGATGCTGGCGGAACGATTACCTTGAACGATATCGAA 300
Qy 100 SerArgProValLeuIleIleAsnAlaThrGlyValArgGlnAsnHisArgTyrGluAsp 119
Db 301 GGACGCCAGTACTGACTATCAATGCAATCGCGGCTCGTCAGACCCCATCACTATGAAGGT 360
Qy 120 AsnThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGlyGluLysThr 139
Db 361 AATACCTTGGCCCGCGCTTGGCTGGCTGTCCCGAGTTAATACAAAGAACGAGAAACC 420
Qy 140 ThrGluArgLeuIleTrrAlaGlyAsnThrProGlnGluLysAspTyrAsnLeuAlaGly 159
Db 421 ACGAGGCGCTTATTTGGGCAACAATACAGATGCGAGAGAAACACAGAACTCTCGCGGG 480
Qy 160 GlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAsnSerLeuSerLeuAla 179
Db 481 CAATGTATACGCCATTATGATCTCGCGGGCTGCTACAACTGGAAAGTTTGTCTTAAACA 540
Qy 180 GlyValValLeuSerGlnSerGlnGlnLeuLeuThrAspAsnGlnAspAlaAspTrrThr 199
Db 541 GGATCGGTTTTATCACAGTCTCTGCTCAATTAATAGCCGACGATCAGGAAGCTGATGGCGC 600
Qy 200 GlyGluAspGlnSerLeuTrrGlnGlnLysLeuSerSerAspValTyrIleThrGlnSer 219
Db 601 GGTGATGATGAATAATAGCTGGCTGACAAATCAATGCGCAACATATTCAGACTCAACAT 660
Qy 220 AsnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGlyAsnIleGlnArg 239
Db 661 AAAACTGATGCCATTGGTCTCTGCTAACTCAATCGACGCCAAGGCAATATGCAACGG 720
Qy 240 LeuAlaTyrAspValAlaGlyGlnLeuLysGlySerTrrPleuThrLeuLysGlyGlnAla 259
Db 721 CTGGCTTATGATGTGCGGGCCCAACTGAAAGGTAGCTGGTTAAACACTAAAGGCCAAGCC 780
Qy 260 GlnGlnValIleLysSerLeuThrTyrSerAlaAlaGlyGlnLysLeuArgGluGlu 279
Db 781 GAAAAGTTATGTACAGTCTATTACTGCTGAGCGCCGACAAATAATACAGAGAGAG 840
Qy 280 HisGlyAsnGlyIleValThrGluTyrSerTyrGluProGluThrGlnArgLeuIleGly 299
Db 841 CACGGTAATGGCGTTATTACGAATATACCTCTAATCGACCCACGAGACCCCAACGATTAAATAC 900
Qy 300 IleThrThrArgProSerAspAla---LysValLeuGlnAspLeuArgTyrGlnTyr 318
Db 901 ATTACAAACCCCGCAACTAGAGATAGTACAAAAACCACTACAAGATTTCGTTATGAATAT 960
Qy 319 AspProValGlyAsnValIleAsnIleAtqAsnAspAlaGluAlaThrArgPheTrrArg 338
Db 961 GATCCCGTTGGCAATGTGATCAATATTCGTAATGTCAGAGCAACCCGATTCGCGGT 1020
Qy 339 AsnGlnLysValAlaProGluAsnSerTyrThrTyrAspSerLeuTyrGlnLeuIleSer 358
Db 1021 AATCAGAAAAATAGTCGGAATAATGCATATTCCTATGATCTCTGTACCAACTCATCCAA 1080
Qy 359 AlaThrGlyArgGluMetAlaAsnIleGlyGlnAsnGlnLeuProSer----- 376
Db 1081 GCAACCGCGCGGAAATGGCTAACTTGGTTCAGCAAGGAAGCCAGCTCCCTCTCTTAATT 1140

Qy 377 ProAlaLeuProSerAspAsnAsnThrTyrThrAsnTyrThrArgSerTyrSerTyrAsp 396
Db 1141 ACCCTCTTCTTACCGATGACAATACTTATCTAACTATATTCGTATCTATACCTACGCAC 1200
Qy 397 HisSerGlyAsnLeuThrGlnIleArgHisSerSerProAlaThrGlnAsnAsnTyrThr 416
Db 1201 GATAGCGGCAACCTGCACANAATCCAGCAGCTGCTCCGGCAAGTAACATAACTACACC 1260
Qy 417 ValAlaIleThrLeuSerAsnArgSerAsnArgGlyValLeuSerThrLeuThrThrAsp 436
Db 1261 ACNAATATCACCATTTCAAAACCGTAATAACCGGGTGTCTCTCAGTACCTCACCACGAC 1320
Qy 437 ProAsnGlnValAspThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuProGly 456
Db 1321 CCNAATCTCGTTGATACATTTCTTTGATGAGGTGGTCAACCAACAGTCTGTTCTCAGGG 1380
Qy 457 GlnThrLeuIleTrrProArgGlyGluLeuLysGlnValAsnAsnGlyProGlyAsn 476
Db 1381 CAATCCTTAACTGGACACCCAGGGAGAACTACAAACAGTGAACCAAGT---GGTAAT 1437
Qy 477 -----GluTrrTyrArgTyrAspSerAsnGlyMetArgGlnLeuLysValSerGlu 493
Db 1438 ACCGCGCTGAGTGGTACCACTATGACAGTACGGCATCGGGCTACTGAAATAAAGCAA 1497
Qy 494 GlnProThrGlnAsnThrThrGlnGlnAlaGlyValIleTyrLeuProGlyLeuGluLeu 513
Db 1498 CAGCAAACTCAATACCAACGAGCAACAGTCACTATCTCGCAGGGTTGGAATTA 1557
Qy 514 ArgThrThrGlnSerAsnAlaThrThrGluGluLeuHisValIleThrLeuGlyGlu 533
Db 1558 CACACACACAAGCGGCACCAATATCACCGAAGACTTCAAGTTATTACTGTGACGACAA 1617
Qy 534 AlaGlyArgAlaGlnValArgValLeuHisTrrGluSerGlyLysProGluAspValAsn 553
Db 1618 GCAGGAAAGCACAGTACGCTACTACTGGAAGAAAGGCCCAACCCACCGCATAAAT 1677
Qy 554 AsnAsnGlnLeuArgTyrSerTyrAspAsnLeuIleGlySerSerGlnLeuGluLeuAsp 573
Db 1678 AAGCATCAAGTCAGATATAGTACGATAATCTTACACACAGCAGCAAGTATAGAACTGGAT 1737
Qy 574 AsnGlnGlyGlnIleSerGluGluTyrTyrProPheGlyGlyThrAlaLeuTrr 593
Db 1738 ATGCACGGAGAAATGATGATTTGGGAAGAGTATATACCCCTATGTGTGGCCACCGCATGG 1797
Qy 594 AlaAlaAsnSerGlnThrGluAlaSerTyrLysThrIleArgTyrSerGlyLysGluArg 613
Db 1798 GCAGCAAGAATCAGATTGAGCTGGTTACAAACCACTTCGTTATTTCAGGTAAAGAACGT 1857
Qy 614 AspAlaThrGlyLeuTyrTyrGlyTyrArgTyrTrrArgTyrGlnProTrrAlaGlyArgTrr 633
Db 1858 GATGCAACGGGACTGTACTATTACGGCTACCGCTATTATCAACCGTGGCGCGGTAGATGG 1917
Qy 634 LeuSerAlaAspProAlaGlyThrIleAspGlyLeuAsnLeuTyrArgMetValArgAsn 653
Db 1918 TTAAGCGCTGACCGCGCTGGAACCGTAGATGGTCTGAATTTGTACCGTATGGTAAGAAAT 1977
Qy 654 AsnProValSerLeuGlnAspGluAsn----- 662
Db 1978 AATCCAATGACCGGCATAGATGAAGTGGCGGTATGTTTAAACCCGTAGCAACAGGTGCA 2037
Qy 663 -----GlyLeuAlaProGluLysGlyLysTyrThrLysGlu----- 674
Db 2038 TTAGGCATTTGGCGGTATGTCATACGAGCTTTACAAATATATAAAATCAACAGTTGAAAAG 2097
Qy 675 -----ValAsnPheAspGluLeuLysPheLysLeuAla 686
Db 2098 CCTCAGATGCCATCTCCTCTCTGTAATCCTACGGTATCTGAATTTGTACCGTATGGTAAGAAAT 2157
Qy 687 AlaLysSerSer----- 690
Db 2158 CAAAAAGCGAGTCTTTAAAGCAAACTATGACCCGATGAGCAGATGCGCCCAATACATA 2217

691 -----HisValVallystrpAenGluLysGluSerSerTyr 702
|||...
2218 ACGGGCGTAAGAGCCGAGACATCTCGCAGGGTCAAGTCCCTGGCGTCAAGCA 2277
703 ThrLysAsnLysSerLeuLysValValGlyAspSerAspProSerGlyTyrLeu 722
|||...
2278 ATAAAGAGGGCAAGCTAGTTCGGCGCTGCCGAGAAATTTGCTGGCGGTGGCAATGTC 2337
723 -----LeuSerHisGluGluLeuLeuLys----- 730
|||...
2338 GGTGAACATAACAAACACCGCTAACAAAGCCGCGCCGCCGACGCAATTAATAATTTT 2397
731 -----GlyIleGluLys-----SerGlnIle 737
2398 AGTCTACCTTGGACGGTATATAAAGATTTTAAAGCAGCGCGGTAGTGTACCGTTC 2457
738 IleTyrSerArgLeuGluGlu-----AsnSerSerLeuSerGluLysSerLys 753
|||...
2458 AGCCACGAAATTTGAAGAGCTGCAAAAGCACTGATGATTTAAAGAGGTGCGCAACA 2517
754 ThrAsnLeuSerLeuGlySerGluLysSerGlyTyrMetAlaArgThrIleGln----- 771
2518 GATACGCTAATTAACGGGGATCGCTAGGTGCGACAGTGGAGCCACACTGGATACCGCC 2577
771 ----- 771
2578 GCCGCGGTGTCGCACACCCCGGTAGCCAAAGTGGCACTCAAGGTCTGTCTATGGCATGG 2637
772 -----AspThrIleSerGluTyrAlaGluGluHisLys 782
|||...
2638 AAAGTTACCGCATTTGTTACACCCGCAAGAGATTAAGCGAGCTCGCAGAAAAACATAAG 2697

RESULT 13
ACF67367_39/c
Continuation (40 of 57) of ACF67367 from base 3900001 (Photorhabdus luminescens nucleoti
WP Sequence split into 57 fragments LOCUS ACF67367 Accession ACF67367

Fragment Name	Begin	End
ACF67367_00	1	110000
ACF67367_01	100001	210000
ACF67367_02	200001	310000
ACF67367_03	300001	410000
ACF67367_04	400001	510000
ACF67367_05	500001	610000
ACF67367_06	600001	710000
ACF67367_07	700001	810000
ACF67367_08	800001	910000
ACF67367_09	900001	1010000
ACF67367_10	1000001	1110000
ACF67367_11	1100001	1210000
ACF67367_12	1200001	1310000
ACF67367_13	1300001	1410000
ACF67367_14	1400001	1510000
ACF67367_15	1500001	1610000
ACF67367_16	1600001	1710000
ACF67367_17	1700001	1810000
ACF67367_18	1800001	1910000
ACF67367_19	1900001	2010000
ACF67367_20	2000001	2110000
ACF67367_21	2100001	2210000
ACF67367_22	2200001	2310000
ACF67367_23	2300001	2410000
ACF67367_24	2400001	2510000
ACF67367_25	2500001	2610000
ACF67367_26	2600001	2710000
ACF67367_27	2700001	2810000
ACF67367_28	2800001	2910000
ACF67367_29	2900001	3010000
ACF67367_30	3000001	3110000
ACF67367_31	3100001	3210000
ACF67367_32	3200001	3310000
ACF67367_33	3300001	3410000
ACF67367_34	3400001	3510000
ACF67367_35	3500001	3610000

WP	ACF67367_36	3600001	3710000
WP	ACF67367_37	3700001	3810000
WP	ACF67367_38	3800001	3910000
WP	ACF67367_39	3900001	4010000
WP	ACF67367_40	4000001	4110000
WP	ACF67367_41	4100001	4210000
WP	ACF67367_42	4200001	4310000
WP	ACF67367_43	4300001	4410000
WP	ACF67367_44	4400001	4510000
WP	ACF67367_45	4500001	4610000
WP	ACF67367_46	4600001	4710000
WP	ACF67367_47	4700001	4810000
WP	ACF67367_48	4800001	4910000
WP	ACF67367_49	4900001	5010000
WP	ACF67367_50	5000001	5110000
WP	ACF67367_51	5100001	5210000
WP	ACF67367_52	5200001	5310000
WP	ACF67367_53	5300001	5410000
WP	ACF67367_54	5400001	5510000
WP	ACF67367_55	5500001	5610000
WP	ACF67367_56	5600001	5648894

Alignment Scores:
Pred. No.: 1.6e-182 Length: 110000
Score: 2627.50 Matches: 528
Percent Similarity: 69.78% Conservative: 100
Best Local Similarity: 58.67% Mismatches: 153
Query Match: 55.43% Indels: 119
DB: 10 Gaps: 13

US-10-647-956A-6 (1-915) x ACF67367_39 (1-110000)

Qy	1 MetSerSerTyrAsnSerAlaIleAaspGlnLysThrProSerIleLysValLeuAaspAsn 20
Db	49602 ATGATCGTTACAAATCTGCAATTAACCCCAATATCTGTCAGCGTACGAGATAAT 49543
Qy	21 ArgLysLeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAaspGlu---AsnSer 39
Db	49542 CGAGGGTTAAATATACATACGCTGGAAATATCTGCGGACTCAAGCTGATGAACCAATAGC 49483
Qy	40 AspGluLeuIleThrPheTyrGluPheAenIleProGlyPheGlnValLysSerThrAasp 59
Db	49482 AACGAATTGATCACTCGCTATCAATTAATTAATCACTCAGCGACTTCAAGTAAAGACACAGAC 49423
Qy	60 ProArgLysAsnLysAsnGlnSerGlyProAsnPheIleArgValPheAenLeuAlaGly 79
Db	49422 CCACGTAGATATAAAACCAGAGTGGTCAAACTTCACGTAATCTTTAGTCTCGCTGGG 49363
Qy	80 GlnValLeuArgGluGluSerValAaspAlaGlyArgThrIleThrLeuAsnAaspIleGlu 99
Db	49362 AATACACTGGGTGAAGAAAGATATCGATGCTGGCCGAACGATTACCTTGAACGATATCGAA 49303
Qy	100 SerArgProValLeuIleleAenAlaThrGlyValArgGlnAenHisArgTyrGluAasp 119
Db	49302 GGACGCCAGTACTGACTATCAATCAATCGCGGCTCGTCAGACCCATCACTATGAAGGT 49243
Qy	120 AsnThrLeuProGlyArgLeuAlaIleThrGluGlnValGlnAlaGlyGluLysThr 139
Db	49242 AATACCTTGCCCGCGCTTGTGGGTGTCACCGAGTTAATACAAAGAACGAGAAACC 49183
Qy	140 ThrGluArgLeuIleTrpAlaGlyAenThrProGlnGluLysAaspTyrAsnLeuAlaGly 159
Db	49182 ACCGAGCGCTTATTTGGGGCAACATACAGATGCAGAGAAACCCAGAAATCTCGCCGGG 49123
Qy	160 GlnCysValArgHisTyrAaspThrAlaGlyLeuThrGlnLeuAenSerLeuSerLeuAla 179
Db	49122 CAATGTATACGCCATTATGATCTCTCGGGGCTGGTACCACTGGAAGTTTGTCTCTTAACA 49063
Qy	180 GlyValValLeuSerGlnSerGlnLeuThrAaspAenGlnAaspAlaAaspTyrThr 199
Db	49062 GGATCGGTTTTATCACAGTCTCGTCAATTAATAGCCAGCATCAGGAAGCTGATGGCGC 49003
Qy	200 GlyGluAaspGlnSerLeuTrpGlnGlnLysLeuSerSerAaspValTyrIleThrGlnSer 219


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QY 614 AspAlaThrGlyLeuTyrTyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTyr 633
DB 77192 GATGCAACGGGACTGTACTATTACGGCTACCGCTATTATCAACCGTGGCGGTAGATGG 77251
QY 634 LeuSerAlaAspProIleGlyThrIleAspGlyLeuAsnLeuTyrArgMetValArgAsn 653
DB 77252 TTAAGCGCTGACCGCGCTGGAACCGTAGATGGTCTGAATTTGTACGTATGGTAAGAAAT 77311
QY 654 AsnProValSerLeuGlnAspGluAsn----- 662
DB 77312 ATCCCAATGACCGGCTAGATGAAGATGGCGGTATGTTTAAACCGTAGCAACAGGTGCA 77371
QY 663 -----GlyLeuAlaProGluLeuGlyGlyTyrThrLysGlu----- 674
DB 77372 TTAGGCATTGGCGGTATGGCATACGAGCTTTACAAATATAAAATCAACAAGTTGAAAG 77431
QY 675 -----ValAsnPhePheAspGluLeuLysPheLysLeuAla 686
DB 77432 CCTCAGATGCCATCTCTGTCTGAATCCTACGGTGATCAACAAGTCAGCAAAATCACC 77491
QY 687 AlaLysSerSer----- 690
DB 77492 CAAAAGCGAGTCTCTTAAAGCAAACTATGACCCGATGAGCAGATGGCCCATACATA 77551
QY 691 -----HisValValLysTyrAsnGluLysGluSerTyr 702
DB 77552 ACGGGCGTTAAGACCGCAGAACATCTCGCACAGGCTCAAGTCCCTCGCGCTCAAGCA 77611
QY 703 ThrLysAsnLysSerLeuLysValValArgValGlyAspSerAspProSerGlyTyrLeu 722
DB 77612 ATAAAGAAGGGCAAGCTTAGTTCGGCGTTCGGGAGAAATTTCTCGCGGTGCAATGTC 77671
QY 723 -----LeuSerHisGluLeuLeuLys----- 730
DB 77672 GGTGAATAACAAACACCGCTAACAAAGCCCGCCGACCGCAAGCAATTAATAATTT 77731
QY 731 -----GlyIleGluLys-----SerGlnIle 737
DB 77732 AGTCTCACCTTGGACGGTATATAAAGGTATTTAAGCAGCGCGGTAGTGTACCGTC 77791
QY 738 IleTyrSerArgLeuGlu-----AsnSerSerLeuSerGluLysSerLys 753
DB 77792 AGCCAGAAAAATTTGAAGAGCTGCAAAAGCAACTGATGATTTAAAGAGAGTTCGCAACA 77851
QY 754 ThrAsnLeuSerLeuGlySerGluIleSerGlyTyrMetAlaArgThrIleGln----- 771
DB 77852 GATACGCTAATTACCGGGGTCATCGCTAGTGGCAGACAGTCGGAGCCACACTGGATACCGCC 77911
QY 771 ----- 771
DB 77912 GCCGCGTCTGTCACACCGCGTAGCCAAAGTGGCACTCAAGGTCTGTCTATTGGCATGG 77971
QY 772 -----AspThrIleSerGluTyrAlaGluGluHisLys 782
DB 77972 AAAGTTACCGGCATTGTTTCACCGCAGAGAAGATTAAGCGAGCTCGCAGAAAAACATAAG 78031
RESULT 15
ID ACF71155
AC ACF71155 standard; DNA; 2898 BP.
AC ACF71155;
XX
XX 20-NOV-2003 (first entry)
XX
XX Photorhabdus luminescens nucleotide sequence #9622.
XX
XX Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;
XX detection; food; gene expression; plant; animal; microorganism; toxin;
XX antibiotic; biopesticide; virulence factor; disease model; plague;
XX whooping cough; gene; ds.
XX
XX Photorhabdus luminescens.
XX
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PN WO200294867-A2.
XX
PD 28-NOV-2002.
XX
PF 07-FEB-2002; 2002WO-IB003040.
XX
XX 07-FEB-2001; 2001PR-00001659.
PR
XX (INSP ) INST PASTEUR.
PA (CNRS ) CNRS CENT NAT RECH SCI.
XX
XX Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;
PI Buchrieser C;
XX
XX WPI; 2003-148459/14.
DR
PT Genomic sequence of Photorhabdus luminescens and encoded polypeptides,
PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.
XX
PS Claim 2; SEQ ID NO 9622; 1205pp; French.
XX
XX The invention relates to the isolation of genes and their encoded
XX proteins from Photorhabdus luminescens. The isolated sequences are
XX sources of probes and primers for detecting the genome of P. luminescens
XX and related species; to study polymorphisms; for gene analysis and for
XX detection/amplification of the genes. Antibodies (Ab) raised against the
XX polypeptides encoded by the genes are used for detection/identification
XX of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that
XX carry a gene-containing vector are used to select compounds that
XX modulate, regulate, induce or inhibit expression of the genes in plants,
XX animals or microorganisms other than P. luminescens and are able to alter
XX response or sensitivity to toxins and antibiotics produced by P.
XX luminescens. Cells transformed to express the genes are useful for
XX recombinant production of the proteins, particularly toxins and
XX antibacterials useful as insecticides, bactericides and fungicides. The
XX genes, proteins, vectors containing the genes and Ab are also useful
XX therapeutically (to treat microbial infection by bacteria or fungi that
XX are sensitive to P. luminescens-encoded toxins or antibiotics) and as
XX biopesticides. Other uses of the genes and the proteins are as virulence
XX factors and for identifying targets of human diseases for which P.
XX luminescens is a model (particularly plague and whooping cough). This
XX sequence represents one of the isolated P. luminescens genes
XX
XX Sequence 2898 BP; 978 A; 640 C; 632 G; 648 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 8,29e-181 Length: 2898
Score: 2578.50 Matches: 532
Percent Similarity: 68.82% Conservative: 97
Best Local Similarity: 58.21% Mismatches: 184
Query Match: 54.40% Indels: 101
DB: 16 Gaps:
US-10-647-956A-6 (1-915) x ACF71155 (1-2898)
QY 1 MetSerSerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAen 20
DB 1 ATGAACAACCTTGACCCCAAAATTTACCAACACACTCCCACTATCTGTTACGATAAC 60
QY 21 ArgLysLeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAsnSerAsp 40
DB 61 CGTGGGTGGATGTCGGTGAATCCATTATCACCAGACTACCGCAGAAAAAATAGTGAT 120
QY 41 GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro 60
DB 121 ATCCGTATCACCGCTCATCAGTATGATGTTCTCGACACCTGACCACCAAGATTGACCCA 180
QY 61 Arg-----LysAsnLysAsnGlnSerGlyProAsnPheIleArgValPhe 75
DB 181 CGCTGTATGACCGCTGGCAGAAAGATAGCTCGGTAAACCCCAATTTCTCTGCAGTAT 240
QY 76 AsnLeuAlaGlyGlnValLeuArgGluSerValAspAlaGlyArgThrIleThrLeu 95
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QY 775 SerGluTyrAlaGluGluHisLysTyrArgSerAsnHisProAspPheTyrSerGluThr 794
Db 2386 -----GAGAAAGAGGATGGACATTTAATTATAAGAT----- 2418
QY 795 AspPhePheAlaLeuMetAspLysSerGluLysAsnAspTyrSerGlyGluArgLysIle 814
Db 2419 GAATTTGTTAACTTAAAGATAA--GAAATATCC-----TTAGGAAAGGAAATTA 2469
QY 815 TyrAlaAlaMetGluVal-----LysValTyr 823
Db 2470 TTCCTGGTGTGGAACCTCTGCCGATAATCCAGAGCACTATAAAGTTCAAGATGTTAGC 2529
QY 824 HisAspLeuLysAsnLysGlnSerGluLeuHisValAsnTyrAlaLeuAlaHisProTyr 843
Db 2530 GAATTTATTCTGGGATTGAATCCGCTACAAAAATAATCGAGTAGAGTTACATCCATT 2589
QY 844 ThrGln-----LeuSerAsnGluGlu 850
Db 2590 ACATCATCATTAATTAATAAACACATCTTAAATAATGNAGAG 2631
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Search completed: December 14, 2005, 10:29:56
Job time : 1738 secs

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November 2005

Published_Applications_Nucleic Acid and Published_Applications_Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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